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RESULT 3
AR222273 LOCUS 1788 bp mRNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6429289.
ACCESSION AR222273
VERSION AR222273.1 GI:23329756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1788)
AUTHORS Krieger,M., Acton,S.L. and Pearson,A.M.
TITLE Class BI and CI scavenger receptors
JOURNAL Patent: US 6429289-A 3 06-AUG-2002;
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LOCUS Cricetulus griseus CD36-related class B scavenger receptor haSR-Bi
(haSR-bi) mRNA, complete cds.
ACCESSION U11453
VERSION U11453.1 GI:562021
KEYWORDS modified lipoprotein receptor; oxidized low density lipoprotein; adipocytes.
SOURCE Cricetulus griseus (Chinese hamster)
ORGANISM Cricetulus griseus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Cricetidae; Cricetinae; Cricetulus.
REFERENCE 1 (bases 1 to 1788)
AUTHORS Acton, S.L., Scherer, P.E., Lodish, H.F. and Krieger, M.
TITLE Expression cloning of SR-BI, a CD36-related class B scavenger receptor
JOURNAL J. Biol. Chem. 269 (33), 21003-21009 (1994)
PUBMED 7520436
REFERENCE 2 (bases 1 to 1788)
AUTHORS Acton, S.L.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Susan L. Acton, Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA

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ACCESSION		AR112115					
VERSION		AR112115.1		GI:14092015			
KEYWORDS							

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1825)
AUTHORS Acton, S. Laurence.
TITLE Human, intronic, and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 3 10-OCT-2000;
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DEFINITION Sequence 3 from patent US 6228581.
ACCESSION ARI49157
VERSION ARI49157.1 GI:15113748
KEYWORDS Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1825)
AUTHORS Acton, S.L. and Ordovas, J.M.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6228581-A 3 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..1825
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 99.9%; Score 1786; DB 6; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACCTGCAGGGCTACTGCTGCTCGGGCACTGCTGAGACTCAGCTTGTCTGGAACGGT 60
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RESULT 8
LOCUS CQ868666
DEFINITION Sequence 78 from Patent WO2004074321.
ACCESSION CQ868666
VERSION CQ868666.1
KEYWORDS GI:51998641
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
MORRIS, D.W. and MALANDRO, M.S.
Novel therapeutic gpcr targets in cancer
Patent: WO 2004/074321-A 78 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
source
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/organism="Mus musculus"
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ORIGIN
Query Match 80.6%; Score 1441.2; DB 6; Length 2496;
Best Local Similarity 88.3%; Pred. No. 1.5e-301;
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1;
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RESULT 9
BC004656
LOCUS
DEFINITION

BC004656 2512 bp mRNA linear ROD 09-JUL-2005
Mus musculus scavenger receptor class B, member 1, mRNA (cDNA clone
MGC:5988 IMAGE:3498018), complete cds.

818 TTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTTCAGGGGCTCCAGAAATTC 877
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ORIGIN

Query Match 77.8%; Score 1390.6; DB 9; Length 2392;
 Best Local Similarity 88.1%; Pred. No. 1.4e-230;
 Matches 1524; Conservative 0; Mismatches 204; Indels 1; Gaps 1;

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RESULT 12

BC076504

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BC076504 2408 bp mRNA linear ROD 07-JUL-2004
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 clone MGC:91637 IMAGE:7099863), complete cds.

BC076504
 BC076504.1 GI:49904284
 MGC.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.

1 (bases 1 to 2408)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dickenson, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Schectz, E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Cartancini, P., Prange, C., Faha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Mallek, J.A., Gounatne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

2 (bases 1 to 2408)
Strausberg, R.
Direct Submission
Submitted (06-JUL-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgti.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 175 Row: f Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13928729.

Location/Qualifiers
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ORIGIN

Query Match 77.8%; Score 1390.6; DB 9; Length 2408;
Best Local Similarity 88.1%; Pred. No. 1.4e-290;
Matches 1524; Conservative 0; Mismatches 204; Indels 1; Gaps 1;

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QY 175 CGCGCTGGTGGCGGTGGGCTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGG 234
Db 131 CAGCGTGGTGGGCTGGGCTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGG 190
QY 235 TTATGATCTCGTGATGCCCTCGCTCATCAACAGCAGGTACTGAAGATGTCGATAG 294
Db 191 TCATGATTCATGGTGGCTCGCTCATCAAGCAGGAGGTGCTCAAGATGTCGATAG 250
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Db 251 ACCCCAGCAGCTGTCTTGTGGATGTGGAGAGAGATCCCTGTCTTCTACTTGTCCG 310
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Db 311 TCTACTTCTTCGAGGTGGTCAATCCAGCAGGAGTCTTAAATGGCCAGAGCAGTAGTCC 370
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QY 595 TGATGGAGCAGTCTGCGAGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 654
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LOCUS			
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LOCUS ARI95310 1785 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7 from patent US 6350859.
ACCESSION ARI95310
VERSION ARI95310.1 GI:20244747
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Krieger,M., Acton,S.L. and Rigotti,A.
TITLE Class BI and CI scavenger receptors
JOURNAL Patent: US 6350859-A 7 26-FEB-2002;
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Best Local Similarity 88.6%; Pred. No. 4.4e-286;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
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QY 230 TGTGGTTATGATCCCTGCTGATGCCCTCGCTCATCAACAGCAGGTACTCAAGAAATGTCGG 289
DB 125 CGTTGTATGATCCTCATGGTGCCTTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCGG 184
QY 290 CATAGACCCAGCAGCCTGTCTCTTGTGCAATGTGAAGGAGATCCCTGTACCCCTTCTACTT 349
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DB 245 GTCTGTCTACTTCTTCAGGTGGTCAACCCAAACAGGTCTTCAACGCGCAGAGCCAGT 304

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:34:57 ; Search time 1079.41 Seconds
(without alignments)
11039.845 Million cell updates/sec

Title: US-08-765-108-3

Perfect score: 1788
Sequence: 1 GCCACCTGCGGGCTACTGC.....CTCTCAGCGGACAGTCGC 1788

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s.*
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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1788	100.0	1788	2 AAT10116	Aat10116 Hamster s
2	1788	100.0	1788	2 AAX23403	Aax23403 Hamster s
3	1788	100.0	1788	6 AAZ30615	Aaz30615 Hamster S
4	1788	100.0	1788	6 ABS53744	AbS53744 cDNA enco
5	1788	100.0	1788	6 AAD33915	Aad33915 Hamster s
6	1788	100.0	1788	12 ADJ53334	Adj53334 Hamster S
7	1786	99.9	1825	9 ACD44926	Acd44926 Human cdn
8	1786	99.9	1825	12 ADJ46120	Adj46120 Human var
9	1718	96.1	1788	14 AEB03941	Aeb03941 Hamster S
10	1441.2	80.6	2496	13 ABD33431	Abd33431 Murine ca
11	1441.2	80.6	2496	13 ADR67032	Adr67032 Mouse can
12	1441.2	80.6	2513	14 ADZ13454	Adz13454 Murine ca
13	1413	79.0	2497	10 ADB58616	AdB58616 Toxicity-
14	1413	79.0	2497	10 ADB53264	AdB53264 Primary r
15	1413	79.0	2497	10 ABT42207	Abt42207 Toxicity
16	1413	79.0	2497	13 ADV41414	Adv41414 Rat cardl
17	1369.8	76.6	1785	2 AAX23404	Aax23404 Mouse sca
18	1369.8	76.6	1785	2 AAZ30616	Aaz30616 Mouse sca
19	1369.8	76.6	1785	6 ABI99330	Abi99330 Mouse isc

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21	1369.8	76.6	1785	12 ADJ53336	Adj53336 Murine SR
22	1359.8	76.1	1785	14 AEB03942	Aeb03942 Murine Sc
23	1358	76.0	1718	14 AEB03937	Aeb03937 Hamster S
24	1255.8	70.2	1531	13 ADS73684	AdS73684 Rat SRB-I
25	1247.8	69.8	1546	14 AEA33429	Aea33429 SR-BI CDN
26	1243.8	69.6	1607	6 ABL46318	AbL46318 Mouse sca
27	1233	69.0	2382	14 ADZ13452	Adz13452 Murine ca
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31	1139.4	63.7	2630	9 ACD44925	Acd44925 Human CDN
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33	1137.8	63.6	2558	4 ABA09256	AbA09256 Human SR-
34	1136.2	63.5	2565	2 AAZ32194	Aaz32194 Human CLA
35	1136.2	63.5	2566	3 AAA40750	Aaa40750 Wild type
36	1136.2	63.5	2566	9 AAL62623	Aal62623 Human CD3
37	1136.2	63.5	2566	12 ADL61166	AdL61166 Human tyr
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39	1135.4	63.5	3144	13 ABD33433	Abd33433 Human can
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43	1129.8	63.2	2630	2 AAX24589	Aax24589 Human SR-
44	1120.4	62.7	2604	10 ADE09617	Ade09617 Novel DNA
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ALIGNMENTS

RESULT 1

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XX	29-MAR-1996	(first entry)
XX	Hamster scavenger receptor class B-I CDNA.	
XX	Scavenger receptor class BI; HaSR-BI; low density lipoprotein;	
KW	atherosclerosis; CHO; Chinese hamster ovary; lipoprotein receptor;	
KW	cholesterol; ds.	
XX	Cricetulus sp.	
XX	Key	Location/Qualifiers
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FT		/*tag= a
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XX	WO9600288-A2.	
XX	04-JAN-1996.	
XX	19-JUN-1995;	95WO-US007721.
XX	23-JUN-1994;	94US-00265428.
XX	(NASI) MASSACHUSETTS INST TECHNOLOGY.	
XX	Krieger M, Acton SL, Pearson AM, Rigotti A;	
XX	WPI; 1996-068872/07.	
DR	P-PSDB; AAR88465.	
XX	Class BI and CI scavenger receptor proteins - used to develop products	
PT	for treating or preventing atherosclerosis, fat uptake by adipocyte(s)	
PT	and immune disorders.	
XX	XX	
PS	Claim 14; Page 56-57; 84pp; English.	
XX		

CC A cDNA clone (AAT10116) codes for a new hamster class B-I scavenger
 CC receptor, hasR-BI (AAR88465), that selectively binds to low density
 CC lipoprotein (LDL) and to acetylated LDL. It was isolated using a cDNA
 CC expression library prep. from CHO line Var-261 mRNA that was transfected
 CC into COS cells, with subsequent visible screening for endocytosis of
 CC fluorescent acetylated LDL. The isolated cDNA can be used as a probe to
 CC screen libraries for the presence of related receptors, to screen patient
 CC samples, and to screen for drugs that modulate receptor activity and/or
 CC expression

XX Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;

Query Match 100.0%; Score 1788; DB 2; Length 1788;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	CCTGAGCCCGCAGCCCGCGCCGACACGCGGACATGGCGGCGAGCGCGCGCT	180
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QY	181	GGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGATGA	240
DB	181	GGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGATGA	240
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DB	241	TCCTCGTGATGCTCTGCTCATCAACAGCAGAGTACTGAGGAATGTCGCGATAGACCCCA	300
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QY	781	TTGAGATGAACTACAGTCTGGGCTCTTCACTGTGTTTACGGGCGTCCAGACTTCA	840
DB	781	TTGAGATGAACTACAGTCTGGGCTCTTCACTGTGTTTACGGGCGTCCAGACTTCA	840
QY	841	GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCAATTCAG	900

DB	841	GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCAATTCAG	900
QY	901	ACGAGTGCACATGATCAATGACACTTCCGGGCGAGATGCGGCGACCATTCATGACACCCC	960
DB	901	ACGAGTGCACATGATCAATGACACTTCCGGGCGAGATGCGGCGACCATTCATGACACCCC	960
QY	961	AGTCCTCGCTGGAATTCCTTTCAGTCCGGAAGCCTGCAAGGTCTATGAAGCTCACCTACCATG	1020
DB	961	AGTCCTCGCTGGAATTCCTTTCAGTCCGGAAGCCTGCAAGGTCTATGAAGCTCACCTACCATG	1020
QY	1021	ATTTCAGGGTGTGTTGAAGCATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG	1080
DB	1021	ATTTCAGGGTGTGTTGAAGCATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG	1080
QY	1081	CCAATGGGTCTGTTTACCCACCAATGAAGTTTCTGCGGTGCTTGAATCCGGCATTC	1140
DB	1081	CCAATGGGTCTGTTTACCCACCAATGAAGTTTCTGCGGTGCTTGAATCCGGCATTC	1140
QY	1141	AAAAATGTCAGCACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCCCTCACTTCTACA	1200
DB	1141	AAAAATGTCAGCACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCCCTCACTTCTACA	1200
QY	1201	ATGACAGCCCTGTGCTTATCAGAAAGCGTTCTGGGTCTGAAACCTTGACCCCAAGGAGCAT	1260
DB	1201	ATGACAGCCCTGTGCTTATCAGAAAGCGTTCTGGGTCTGAAACCTTGACCCCAAGGAGCAT	1260
QY	1261	CTTTGTTCTTGCATCCATCCGCTCACTGGGATCCCACTGACTTCTGTGAACTGTC	1320
DB	1261	CTTTGTTCTTGCATCCATCCGCTCACTGGGATCCCACTGACTTCTGTGAACTGTC	1320
QY	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGCAATGGGCAAAAGGAGATCGAGCCCG	1380
DB	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGCAATGGGCAAAAGGAGATCGAGCCCG	1380
QY	1381	TGTCCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGGCGCGGAGCCCTGAACA	1440
DB	1381	TGTCCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGGCGCGGAGCCCTGAACA	1440
QY	1441	CGTTCTACAGCAGCTGGTGTGATGTCGCCCGGAGTACTTCACTATGTGCAAGTGTGCTGC	1500
DB	1441	CGTTCTACAGCAGCTGGTGTGATGTCGCCCGGAGTACTTCACTATGTGCAAGTGTGCTGC	1500
QY	1501	TGGGGCTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1560
DB	1501	TGGGGCTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1560
QY	1561	AATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGCAGGATAAGGAGGCGCATTCAGG	1620
DB	1561	AATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGCAGGATAAGGAGGCGCATTCAGG	1620
QY	1621	CCTACTCTGAGTCTCTGATGTCAAGCTGTCAGGCGGCGGCTGCTGCAAGAGCCAGC	1680
DB	1621	CCTACTCTGAGTCTCTGATGTCAAGCTGTCAGGCGGCGGCTGCTGCAAGAGCCAGC	1680
QY	1681	TGTAGGGTCCCAAGACACACAGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
DB	1681	TGTAGGGTCCCAAGACACACAGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
QY	1741	CCAGCCCTTACACCCCGCTTCTTGGAGTCTTCTCAGCGGACAGTCCG	1788
DB	1741	CCAGCCCTTACACCCCGCTTCTTGGAGTCTTCTCAGCGGACAGTCCG	1788

RESULT 2

AA23403

ID AAX23403 standard; DNA; 1788 BP.

XX AAX23403;

AC 17-JUN-1999 (first entry)

XX Hamster scavenger receptor class B-I DNA.

DE

XX Scavenger receptor class B type I; hamster; steroid production; HDL;
KW cholesterol; cholesteryl ester transport; high-density lipoprotein;
KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;
KW treatment; disorder; overproduction; underproduction; menopause;
KW breast cancer; prostate cancer; endometriosis; fibroid tumour; ss.
XX Cricetulus griseus.
XX WO9911288-A1.
XX 11-MAR-1999.
XX 04-SEP-1998; 98WO-US018463.
XX 05-SEP-1997; 97US-0057943P.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX Krieger M;
XX WPI; 1999-204984/17.
XX P-PSDB; AAW93574.
XX Modification of steroid production in mammals - by administering
XX modulator of SR-BI expression or activity.
XX Disclosure; Page 77; 86pp; English.
XX CC This invention describes a method for modifying steroid production in a
XX mammal which comprises administering a compound that alters cholesterol
XX or cholesteryl ester transport from high-density lipoprotein (HDL) or
XX other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger
XX receptor class B type I). This method is useful for female contraception,
XX for treating disorders characterised by overproduction of steroids, for
XX treating disorders characterised by underproduction of steroids, for
XX especially menopause, for treating disorders that can be treated by
XX decreasing steroid production, especially breast cancer, prostate cancer,
XX endometriosis or fibroid tumours
XX SQ Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;

Query Match 100.0%; Score 1788; DB 2; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCGAGGCTACTGCTGCTCCGGCCACCTGCTGAGACTCACCTTGTGGAAGCTG 60
DB 1 GCCACCTGCGAGGCTACTGCTGCTCCGGCCACCTGCTGAGACTCACCTTGTGGAAGCTG 60

QY 61 AGCTCGGCTTCTGTCATCTCTGCGGCTCTGTCGCTTCTGTCGCTGCTCCCTTTCAGTC 120
DB 61 AGCTCGGCTTCTGTCATCTCTGCGGCTCTGTCGCTTCTGTCGCTGCTCCCTTTCAGTC 120

QY 121 CCTGAGCCCCCGGAGCCCGGCGCCACACGCGGACATGCGCGGAGCGCGCGCGCT 180
DB 121 CCTGAGCCCCCGGAGCCCGGCGCCACACGCGGACATGCGCGGAGCGCGCGCGCT 180

QY 181 GGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 240
DB 181 GGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 240

QY 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGAGTACTGAAGATGTCGCGATAGACCCCA 300
DB 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGAGTACTGAAGATGTCGCGATAGACCCCA 300

QY 301 GCAGCCTGTCTTTGCAATGGAAGAGATCCCTGTACCCTTTCTACTTGTCCGTCTACT 360
DB 301 GCAGCCTGTCTTTGCAATGGAAGAGATCCCTGTACCCTTTCTACTTGTCCGTCTACT 360

QY 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAGAGCCAGTAGTGGGGAGC 420

QY 421 GTGGAACCTATGCTTACAGGGAATTGACATTAAGGCCAACATCACCTTCAATGACAATG 480
DB 421 GTGGAACCTATGCTTACAGGGAATTGACATTAAGGCCAACATCACCTTCAATGACAATG 480
QY 481 ATACTGTGCTCTTTGTGGAGCACGCGAGCTTCATTTCCAGCCGAGCAGAGTCCACGGCT 540
DB 481 ATACTGTGCTCTTTGTGGAGCACGCGAGCTTCATTTCCAGCCGAGCAGAGTCCACGGCT 540
QY 541 CTGAGAGTGACTACTATATATCTGCCTAAACATTTCTGGTCTTTGGGGGGCGCAGTAATGATG 600
DB 541 CTGAGAGTGACTACTATATATCTGCCTAAACATTTCTGGTCTTTGGGGGGCGCAGTAATGATG 600
QY 601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTTGGGGCTGGCCACCTTGGGGCCAGC 660
DB 601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTTGGGGCTGGCCACCTTGGGGCCAGC 660
QY 661 GTGCGCTTTATGAACCGAACAGATTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
DB 661 GTGCGCTTTATGAACCGAACAGATTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
QY 721 ATTTTATCAACAATACTTACAGAGCATGTTCCCATCAAGGGCAAGTTCGGGCTGTTTG 780
DB 721 ATTTTATCAACAATACTTACAGAGCATGTTCCCATCAAGGGCAAGTTCGGGCTGTTTG 780
QY 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
QY 841 GCAAGATCCACCTGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGGATTCAG 900
DB 841 GCAAGATCCACCTGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGGATTCAG 900
QY 901 AGCAGTGCAACATGATCAATGSCACTTCCGGGAGATGCGGACCATTCATGACACCCC 960
DB 901 AGCAGTGCAACATGATCAATGSCACTTCCGGGAGATGCGGACCATTCATGACACCCC 960
QY 961 AGTCCTCGCTGGAATTTCTTCACTGCGGAAAGCTTCAGAGTCTATGAAGCTCACCTACCATG 1020
DB 961 AGTCCTCGCTGGAATTTCTTCACTGCGGAAAGCTTCAGAGTCTATGAAGCTCACCTACCATG 1020
QY 1021 ATTGAGGGTGTGGAAGGATCCCACTATCGCTTTCAGAGCCCTTAAACCTTTGTTG 1080
DB 1021 ATTGAGGGTGTGGAAGGATCCCACTATCGCTTTCAGAGCCCTTAAACCTTTGTTG 1080
QY 1081 CCAATGGGCTGTTTACCCCAATGAAGTTCCTGCGGCTGCTTGAATCCGGCAATC 1140
DB 1081 CCAATGGGCTGTTTACCCCAATGAAGTTCCTGCGGCTGCTTGAATCCGGCAATC 1140
QY 1141 AATAATGTCAGCACTGTCAGGTTGGTGCAACCTGTTTCTGTCAACCTTCACTTCTACA 1200
DB 1141 AATAATGTCAGCACTGTCAGGTTGGTGCAACCTGTTTCTGTCAACCTTCACTTCTACA 1200
QY 1201 ATGAGACCTGTGCTATCAGAAAGCTTCTGGGTCTGAACCTGACCCAGGAGGAGCAT 1260
DB 1201 ATGAGACCTGTGCTATCAGAAAGCTTCTGGGTCTGAACCTGACCCAGGAGGAGCAT 1260
QY 1261 CTTTGTCTTGAATCCATCCGCTCACTGGGATCCCATGAATCTGTTGTGAAGTTC 1320
DB 1261 CTTTGTCTTGAATCCATCCGCTCACTGGGATCCCATGAATCTGTTGTGAAGTTC 1320
QY 1321 AGATAAGCTCTACATCAAAAGCTGTCAAGGCAATGGGCAACAGGGAAGATCGAGCCCG 1380
DB 1321 AGATAAGCTCTACATCAAAAGCTGTCAAGGCAATGGGCAACAGGGAAGATCGAGCCCG 1380
QY 1381 TGGTCTCTCCATTTGCTGTTGAGCAGAGCGGTGCCATGGGCGGAGGCCCTGAACA 1440
DB 1381 TGGTCTCTCCATTTGCTGTTGAGCAGAGCGGTGCCATGGGCGGAGGCCCTGAACA 1440
QY 1441 CGTTCTACAGCAGCTGGTGTGATGTCGCCAGGACTTCACTATGTGCAAGTATGTCGTC 1500
DB 1441 CGTTCTACAGCAGCTGGTGTGATGTCGCCAGGACTTCACTATGTGCAAGTATGTCGTC 1500

QY 1081 CCAATGGGCTGTTTACCCACCAATGAAGGTTTCTGCCGCTGCTTGAATCCGGCATTC 1140
 DB 1081 CCAATGGGCTGTTTACCCACCAATGAAGGTTTCTGCCGCTGCTTGAATCCGGCATTC 1140
 QY 1141 AAAATGTCAGCACTTGCGAGTTTGGTGCACCCCTGTTTCTGTACACCCCTCACTTCTACA 1200
 DB 1141 AAAATGTCAGCACTTGCGAGTTTGGTGCACCCCTGTTTCTGTACACCCCTCACTTCTACA 1200
 QY 1201 ATGCAGACCTCTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACCCCAAGGAGCAT 1260
 DB 1201 ATGCAGACCTCTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACCCCAAGGAGCAT 1260
 QY 1261 CTTTGTCTTGTGATCATCCGCTCACTGGGATCCCATGAACTGTTCTGTGAAGTTGC 1320
 DB 1261 CTTTGTCTTGTGATCATCCGCTCACTGGGATCCCATGAACTGTTCTGTGAAGTTGC 1320
 QY 1321 AGATAAGCCTCTACATCAAGAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCCG 1380
 DB 1321 AGATAAGCCTCTACATCAAGAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCCG 1380
 QY 1381 TGGTCTCTCCATGCTGCTGTTGAGCAGAGCGGTGCGGCGGCGAGCCCTGAACA 1440
 DB 1381 TGGTCTCTCCATGCTGCTGTTGAGCAGAGCGGTGCGGCGGCGAGCCCTGAACA 1440
 QY 1441 CGTTCTACAGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
 DB 1441 CGTTCTACAGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
 QY 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTGCGAGGATTAAGGAGCCCATTCAGG 1620
 DB 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTGCGAGGATTAAGGAGCCCATTCAGG 1620
 QY 1621 CCTACTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 DB 1621 CCTACTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TGTAGGCTCCAAAGACACCAAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 DB 1681 TGTAGGCTCCAAAGACACCAAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 QY 1741 CCAGCCCTACACCCGCTTCTTGGAGTCTCTCTCAGCGGACAGTCCG 1788
 DB 1741 CCAGCCCTACACCCGCTTCTTGGAGTCTCTCTCAGCGGACAGTCCG 1788

RESULT 4

ABS53744

ID ABS53744 standard; cDNA; 1788 BP.

XX AC ABS53744;

XX DT 20-NOV-2002 (first entry)

XX DE cDNA encoding hamster scavenger receptor type B1 (hasR-B1).

XX KW Hamster; scavenger receptor protein type B1; low density lipoprotein;

XX KW LDL; cholesterol; endothelial; adipose; macrophage; lipoprotein receptor;

XX KW receptor; gene; ss.

XX OS Crictetus griseus.

XX Key Location/Qualifiers

XX FT 156..1685

XX FT /*tag= a

XX FT /product= "Hamster scavenger receptor type B1 (hasR-B1)"

XX FT

XX PN US6429289-B1.

XX

PD 06-AUG-2002.

XX 23-JUN-1994; 94US-00265428.

XX 23-JUN-1994; 94US-00265428.

XX (WASI) MASSACHUSETTS INST. TECHNOLOGY.

XX Krieger M, Acton SL, Pearson AM;

XX WPI; 2002-689668/74.

XX P-PSDB; ABG33056.

XX New scavenger receptor protein type B1 useful for screening for drugs

XX that inhibit the uptake of cholesterol in endothelial or adipose cells or

XX macrophages.

XX Claim 3; Col 27-28; 31pp; English.

XX The present invention relates to a new scavenger receptor protein type B1

XX which selectively binds to low density lipoprotein (LDL) and modified

XX lipoprotein with the characteristics of acetylated LDL. The invention is

XX useful for screening for drugs that inhibit the uptake of cholesterol in

XX endothelial or adipose cells or macrophages, and for screening for other

XX lipoprotein receptors. The present nucleic acid sequence encodes the

XX hamster scavenger receptor protein type B1 (hasR-B1) of the invention

XX Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1788; DB 6; Length 1788;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGAGGCTACTGCTGCTCGGGCACCTGCTGAGACTCACCTGCTGGAACGTG 60

DB 1 GCCACCTGAGGCTACTGCTGCTCGGGCACCTGCTGAGACTCACCTGCTGGAACGTG 60

QY 61 AGCCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120

DB 61 AGCCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 121 CCTGAGCCCGGAGCCCGGGCGGCGACAGCGGACATGGCGGCGAGCGCGCGGCGCT 180

DB 121 CCTGAGCCCGGAGCCCGGGCGGCGACAGCGGACATGGCGGCGAGCGCGCGGCGCT 180

QY 181 GGTGCGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 240

DB 181 GGTGCGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 240

QY 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

DB 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 301 GCAGCCTGCTCTTGTGCAATGTGGAAGAGATCCCTGTACCTCTTCTACTTGTGCTGCTACT 360

DB 301 GCAGCCTGCTCTTGTGCAATGTGGAAGAGATCCCTGTACCTCTTCTACTTGTGCTGCTACT 360

QY 361 TCTTCCAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAGAGCCAGTAGTCCGGGAGC 420

DB 361 TCTTCCAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAGAGCCAGTAGTCCGGGAGC 420

QY 421 GTGGACCTATGCTACAGGGAATTCAGACATTAAGGCCCAACATCACCTTCAATGACAATG 480

DB 421 GTGGACCTATGCTACAGGGAATTCAGACATTAAGGCCCAACATCACCTTCAATGACAATG 480

QY 481 ATACTGTGCTCTTGTGGAGCACCGGAGCTCCATTTCAGCCGCGGACAGGTCCCAAGGCT 540

DB 481 ATACTGTGCTCTTGTGGAGCACCGGAGCTCCATTTCAGCCGCGGACAGGTCCCAAGGCT 540

QY 541 CTGAGAGTGACTACATTATATGCTGCTTAACTTCTGCTTGGGGGGCGGAGTAAATGATGG 600

DB 541 CTGAGAGTGACTACATTATATGCTGCTTAACTTCTGCTTGGGGGGCGGAGTAAATGATGG 600

PA (KOZA/) KOZARSKY K.
PA (RIGO/) RIGOTTI A.
PA (KRIE/) KRIEGER M.
XX
PI Kozarsky K, Rigotti A, Krieger M;
XX WPI; 2004-246237/23.
DR P-PSDB; ADJ53335.
XX
PT Screening for agents that influence lipid transport, useful e.g. for
PT treating or preventing atherosclerosis, based on modulation of the SR-BI
PT scavenge receptor.
XX
XX Disclosure; SEQ ID NO 1; 22pp; English.
XX
CC The invention relates to a method for screening compounds that alter
CC transport of lipids, cholesterol, lipoproteins or their components,
CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
CC homologue. The test compound is administered to an animal and cholesterol
CC or bile acid levels, production levels of steroid hormones or alterations
CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
CC hormones, bile acids and Vitamin A is measured. Agents that alter
CC transport of lipids, cholesterol or lipoproteins are potentially useful
CC for the treatment or prevention of atherosclerosis, fat uptake by
CC adipocytes and some endocrine disorders. This sequence represents cDNA
CC encoding the hamster SR-BI scavenger receptor of the invention.
XX
XX Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 1788; DB 12; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCGAGGGTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTCTGGAACGCTG 60
DB 1 GCCACCTGCGAGGGTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTCTGGAACGCTG 60

QY 61 AGCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 AGCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 CCTGAGCCCGCGAGCCCGGCGCGCACACGCGACATGCGCGGCGAGCGCGCGCGCT 180
DB 121 CCTGAGCCCGCGAGCCCGGCGCGCACACGCGACATGCGCGGCGAGCGCGCGCGCT 180

QY 181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240
DB 181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240

QY 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGTACTGAGAAATGTCGCGCATAGACCCCA 300
DB 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGTACTGAGAAATGTCGCGCATAGACCCCA 300

QY 301 GCAGCTGTCTCTTGCAATGTGGAAGAGATCCCTGTACCCTTCTACTTTCGCGTCTACT 360
DB 301 GCAGCTGTCTCTTGCAATGTGGAAGAGATCCCTGTACCCTTCTACTTTCGCGTCTACT 360

QY 361 TCCTCGAGGTGGTCAATCCAGGAGATCCCTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
DB 361 TCCTCGAGGTGGTCAATCCAGGAGATCCCTAAGGGTGAGAGCCAGTAGTGGGGAGC 420

QY 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCGCAACATCACCTTCAATGACAATG 480
DB 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCGCAACATCACCTTCAATGACAATG 480

QY 481 ATACTGTGCTCTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGAAGAGTCCACCGCT 540
DB 481 ATACTGTGCTCTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGAAGAGTCCACCGCT 540

QY 541 CTGAGAGTACTACATTTATCTGCTAACTTCTGGTCTTGGGGGGCGCAGTAAATGATGG 600
DB 541 CTGAGAGTACTACATTTATCTGCTAACTTCTGGTCTTGGGGGGCGCAGTAAATGATGG 600

QY 601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACCTTTGGGCCAGC 660
DB 601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACCTTTGGGCCAGC 660

QY 661 GTGCCCTTATGAACCGAACAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCTGTGA 720
DB 661 GTGCCCTTATGAACCGAACAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCTGTGA 720

QY 721 ATTTTATCAACAATACTTACCAGACATGTTCCCATCAAGGCGAGTTCCGGCTCTTTG 780
DB 721 ATTTTATCAACAATACTTACCAGACATGTTCCCATCAAGGCGAGTTCCGGCTCTTTG 780

QY 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTCAAGGCGCTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTCAAGGCGCTCCAGAACTTCA 840

QY 841 GCAAGATCCACTGTGTGGAAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG 900
DB 841 GCAAGATCCACTGTGTGGAAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG 900

QY 901 AGCAGTGAACATGATCAATGGCACTTCCGGCGAGATGCGGCACCATTCATGACACCCC 960
DB 901 AGCAGTGAACATGATCAATGGCACTTCCGGCGAGATGCGGCACCATTCATGACACCCC 960

QY 961 AGTCCTCGCTGGAATTTCTTCACTCCGGAAGCTGCAAGCTCTATGAAGCTCACCTACCATG 1020
DB 961 AGTCCTCGCTGGAATTTCTTCACTCCGGAAGCTGCAAGCTCTATGAAGCTCACCTACCATG 1020

QY 1021 ATTTCAGGGTGTGTTGAAGGATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG 1080
DB 1021 ATTTCAGGGTGTGTTGAAGGATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG 1080

QY 1081 CCAATGGGCTGTGTTTACCCCAATGAAGGTTTTCGCCGCTGCTTGAATCCGGCATTC 1140
DB 1081 CCAATGGGCTGTGTTTACCCCAATGAAGGTTTTCGCCGCTGCTTGAATCCGGCATTC 1140

QY 1141 AAAATGTGAGCACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCTCTCACTTCTACA 1200
DB 1141 AAAATGTGAGCACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCTCTCACTTCTACA 1200

QY 1201 ATGCAGACCTGTGCTATCAGAAAGCGTTCTGGGCTGAACCTGTGACCCCAAGGAGCAT 1260
DB 1201 ATGCAGACCTGTGCTATCAGAAAGCGTTCTGGGCTGAACCTGTGACCCCAAGGAGCAT 1260

QY 1261 CTTTGTCTTCCATCCTCCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CTTTGTCTTCCATCCTCCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

QY 1321 AGATAAGCCTCTACATCAAGGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
DB 1321 AGATAAGCCTCTACATCAAGGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380

QY 1381 TGTCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGGCGCGGAGCCCTGAAACA 1440
DB 1381 TGTCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGGCGCGGAGCCCTGAAACA 1440

QY 1441 CGTTCTACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CGTTCTACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

QY 1501 TGGGGCTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 TGGGGCTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

QY 1561 AATGCTTTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGGATAGAGGCGCATTCAGG 1620
DB 1561 AATGCTTTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGGATAGAGGCGCATTCAGG 1620

QY 1621 CCTACTCTGAGTCTCTGATGTACAGCTGCCAAGGGCGAGTGGTGGCAGAGCCCAAGC 1680
DB 1621 CCTACTCTGAGTCTCTGATGTACAGCTGCCAAGGGCGAGTGGTGGCAGAGCCCAAGC 1680

QY 1681 TGTAGGGTCCCAAGACACACGAGCCCCCCCCAACTGTAGTCTTGTCTGAGACGACCAT 1740

Db 1681 TGTAGGTTCCAAAGACACACAGAGCCCCCAACCTGTAGTGTGTGACACAGCCAT 1740
Qy 1741 CCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTCGC 1788
Db 1741 CCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTCGC 1788

RESULT 7

ACD44926
ID ACD44926 standard; cDNA; 1825 BP.

XX ACD44926;

XX 10-SEP-2003 (first entry)

XX Human cDNA encoding scavenger receptor BI, splice variant.

XX Human; ss; gene; scavenger receptor BI; SR-BI; cardiant; antilipemic;
KW high density lipoprotein; HDL; hormone replacement therapy;
KW postmenopausal female; cardiovascular disorder; coronary heart disease;
KW atherosclerosis; stroke; ischaemia; restenosis; congestive heart failure;
KW gangrene; SNP; single-nucleotide polymorphism.

XX Homo sapiens.

XX US2003044782-A1.

XX 06-MAR-2003.

XX 08-FEB-2001; 2001US-00779152.

XX 10-JUL-1997; 97US-00890979.

XX 27-FEB-1998; 98US-00031626.

XX (ACTO/) ACTON S L.

XX (MCCA/) MCCARTHY J J.

XX Acton SL, McCarthy JJ;

XX WPI; 2003-503489/47.

XX P-PSDB; ABO27241.

XX Determining if a subject has or is at risk of developing abnormally low
PT high density lipoprotein level, involves determining identity of allelic
PT variant of polymorphic region of SR-BI gene of the subject.

XX Example 1; Fig 3; 84pp; English.

XX The invention relates to determining whether a subject has, or is at risk
CC of developing, an abnormally low high density lipoprotein (HDL) level,
CC involves determining the identity of the allelic variant of a polymorphic
CC region of the SR-BI (scavenger receptor BI) gene of the subject, and
CC comparing the allelic variant of the subject with allelic variants
CC associated with abnormally low HDL levels. Also included are a kit for
CC determining whether a subject has, or is at risk of developing, a low HDL
CC level (comprises a probe or primer which is capable of hybridising to an
CC SR-BI gene, and thus identifying whether the SR-BI gene contains an
CC allelic variant of a polymorphic region which is associated with a low
CC HDL level), and predicting the effect of hormone replacement therapy on
CC the HDL level in a female subject (by identifying one or more allelic
CC variants of the SR-BI gene which are associated with abnormally low HDL
CC levels in females (especially postmenopausal females), thus predicting
CC the effect of hormone replacement therapy on the HDL level in the
CC subject). Also disclosed are methods of treating low HDL levels and
CC resulting cardiovascular disorders (e.g. coronary heart disease,
CC atherosclerosis, stroke, ischaemia, restenosis, congestive heart failure
CC and gangrene) by administering a compound that increases HDL levels, when
CC the subject has been identified as having the common allele at residue 41
CC of exon 8. The present sequence is a cDNA encoding a SR-BI protein

XX Sequence 1825 BP; 377 A; 525 C; 496 G; 427 T; 0 U; 0 Other;

Query Match 99.9%; Score 1786; DB 9; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACCTGCAGGGCTACTGCTGCTCCGGCCACATGCTGAGACTCACCTTCTGGAACTG 60
Db 1 GCACCTGCAGGGCTACTGCTGCTCCGGCCACATGCTGAGACTCACCTTCTGGAACTG 60
Qy 61 AGCCTCGGCTTCTGTCATCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCT 120
Db 61 AGCCTCGGCTTCTGTCATCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCT 120
Qy 121 CTTGAGCCCGGAGCCCGGCGCCGACACGCGACATGCGCGGAGCGCCAGCGCGGCT 180
Db 121 CTTGAGCCCGGAGCCCGGCGCCGACACGCGACATGCGCGGAGCGCCAGCGCGGCT 180
Qy 181 GCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 GCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 241 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 301 GCAGCCTGCTCTTTGCAATGTGGAAGAGATCCCTGTACCTTCTACTTCTCGTCTACT 360
Db 301 GCAGCCTGCTCTTTGCAATGTGGAAGAGATCCCTGTACCTTCTACTTCTCGTCTACT 360
Qy 361 TCTTCAGGTGCTCAATCCAGCGAGATCCTTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
Db 361 TCTTCAGGTGCTCAATCCAGCGAGATCCTTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
Qy 421 GTGACCCCTATGCTACAGGGAAATCAGACATGAAGGCCAATCACCCTTCAATGACAATG 480
Db 421 GTGACCCCTATGCTACAGGGAAATCAGACATGAAGGCCAATCACCCTTCAATGACAATG 480
Qy 481 ATACTGTGCTCTTTGTGGAGACCCGAGCTCCATTTCCAGCCGAGAGCTCCACCGGCT 540
Db 481 ATACTGTGCTCTTTGTGGAGACCCGAGCTCCATTTCCAGCCGAGAGCTCCACCGGCT 540
Qy 541 CTGAGAGTGAATACATTAATCTGCTTAACTTCTGCTTGGGGGGGGGAGTAATGATGG 600
Db 541 CTGAGAGTGAATACATTAATCTGCTTAACTTCTGCTTGGGGGGGGGAGTAATGATGG 600
Qy 601 AGAGCAAGCTGTCAGCGCTGGAAGCTGATGATGATGATGATGATGATGATGATGATG 660
Db 601 AGAGCAAGCTGTCAGCGCTGGAAGCTGATGATGATGATGATGATGATGATGATG 660
Qy 661 GTGCTTTTATGAACCGAAGAGATTTGGTGAATCTGTGGGCTATGAGGATCCCTTCGTGA 720
Db 661 GTGCTTTTATGAACCGAAGAGATTTGGTGAATCTGTGGGCTATGAGGATCCCTTCGTGA 720
Qy 721 ATTTTATCAAAATACTTACAGACATGTTCCCATCAAGGGCAAGTTGCGGCTGTTTG 780
Db 721 ATTTTATCAAAATACTTACAGACATGTTCCCATCAAGGGCAAGTTGCGGCTGTTTG 780
Qy 781 TTGAGATGAACAACTCAGACTCTGSGCTTCTACTGTGTTTTCAGGGCGTCCAGAACTTCA 840
Db 781 TTGAGATGAACAACTCAGACTCTGSGCTTCTACTGTGTTTTCAGGGCGTCCAGAACTTCA 840
Qy 841 GCAAGATCCACCTGCTGGAGAGATGGAATGGGCTCAGCAGAGTCAACTACTGGCAATTCAG 900
Db 841 GCAAGATCCACCTGCTGGAGAGATGGAATGGGCTCAGCAGAGTCAACTACTGGCAATTCAG 900
Qy 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCATTCATGACACCCC 960
Db 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCATTCATGACACCCC 960
Qy 961 AGTCTCTGCTGGAATTTCTCAGTCCCGAGAGCTGAGGCTCTATGAAGCTCACCTACCATG 1020
Db 961 AGTCTCTGCTGGAATTTCTCAGTCCCGAGAGCTGAGGCTCTATGAAGCTCACCTACCATG 1020
Qy 1021 ATTCAGGGGTGTTTGAAGGCAATCCCACTATCGCTTTCAGAGCCCTTAAACTTTGTTTG 1080

[illegible]

RESIT.T 8

RESUL 8
AD.T46120

ADU46120
TD AD.T

ADJUSTED

XX AD.T

XX
AC
ADU

DT 06-1

33

DE
Human

XX

KW Human

KW gins

KW
care

KW high

KW meta

XX

OS
Home

XX

PN
US21

XX DE-1

05-105

XX	05-AUG-2002; 2002US-00212848.
XX	05-AUG-2002; 2002US-00212848.
XX	(VITI-) VITIVITY INC.
XX	McCarthy J;
XX	WPI; 2004-224681/21.
DR	P-PSDB; ADJ46121.
XX	Determining the presence of abnormally high triglyceride (TG) level or
PT	TG:high density lipoprotein cholesterol ratio comprises determining if
PT	the subject has an allelic variant of a polymorphic region of the CD36L1
PT	gene.
XX	Disclosure; SEQ ID NO 3; 80pp; English.
XX	The invention relates to determining whether a subject has, or is at risk
CC	of developing, abnormally high triglyceride (TG) level or an abnormally
CC	high TG:high density lipoprotein cholesterol (HDL-C) ratio, comprises
CC	determining whether the subject has an allelic variant of a polymorphic
CC	region of the CD36L1 gene (scavenger receptor class B type 1) that is
CC	associated with abnormally high TG levels or TG:HDL-C ratios. Also
CC	include are a method of diagnosing or aiding in the diagnosis of
CC	abnormally high TG level or TG:HDL-C ratio in a subject, a method for
CC	treating a subject having a disease or disorder associated with specific
CC	allelic variants of a CD36L1 gene, a kit for determining whether a
CC	subject has, or is at risk of developing, abnormally high TG level or an
CC	abnormally high TG:HDL-C ratio (comprising a probe or primer capable of
CC	hybridising to a polymorphic region of a CD36L1 gene and identifying
CC	whether the CD36L1 gene contains an allelic variant of a polymorphic
CC	region associated with abnormally high TG level or TG:HDL-C ratio, and
CC	instructions for use), a method for predicting the effect of hormone
CC	replacement therapy on the TG level or TG:HDL-C ratio in a female
CC	subject, a medical information system for assessing a subject's risk for
CC	developing an abnormally high TG level or TG:HDL-C ratio (comprising
CC	means for obtaining biological information from the individual to obtain
CC	a CD36L1 genetic profile, means for representing the CD36L1 genetic
CC	profile as digital molecular data, means for electronically processing
CC	the CD36L1 digital genetic profile to generate a risk assessment report
CC	for displaying an abnormally high TG level or TG:HDL-C ratio and means
CC	for displaying the risk assessment report on an output device, where the
CC	presence of a polymorphic region of CD36L1 indicates an increased risk
CC	for developing an abnormally high TG level or TG:HDL-C ratio), a
CC	computerised method of providing medical advice to a subject, a method
CC	for a health care provider to generate a personal health assessment
CC	report for an individual and a method of assessing the health of an
CC	individual. The composition and methods are useful for identifying risk
CC	factors for abnormal lipid levels and their associated diseases and
CC	disorders. These may be used for diagnosing, prognosing or treating
CC	subjects having a disease or disorder associated with abnormal lipid
CC	levels, such as vascular (e.g. coronary artery disease, atherosclerosis,
CC	cardiovascular disease, myocardial infarction, stroke and gangrene) or
CC	metabolic (e.g. diabetes or obesity) diseases or disorders. The present
CC	sequence is a cDNA encoding human CD36L1.
XX	Sequence 1825 BP; 377 A; 525 C; 496 G; 427 T; 0 U; 0 Other;
SQ	Query Match 99.9%; Score 1786; DB 12; Length 1825;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTCGAGACTCACCTTGTGGAACTGTG 60
Db	1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTCGAGACTCACCTTGTGGAACTGTG 60
Qy	61 AGCCTCGGCTTCTGTCACTCTGTGGCCTCTGTGCCTTCTGTGCCTGTCCCTTCAGTC 120
Db	61 AGCCTCGGCTTCTGTCACTCTGTGGCCTCTGTGCCTTCTGTGCCTGTCCCTTCAGTC 120
Qy	121 CCTGAGCCCCGAGCCCGGGCGGCCACACGCGGACATGGGGCGGCAGGGCGCGCT 180

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Db 121 CTTGAGCCCGGAGCCCGGCGCCGACACGCGGACATGGGCGGCGAGCCGCGCGCGCT 180
Qy 181 GGGTGGCGGTGGGGCTGGGCGTGGTGGGCGTCTGTGGCGTGTCTCGGTGGTGGTTATGA 240
Db 181 GGGTGGCGGTGGGGCTGGGCGTGGTGGGCGTCTGTGGCGTGTCTCGGTGGTGGTTATGA 240
Qy 241 TCCTCGTATGATCCCTCGCTCATCAAAACAGAGAGTACTGAAGAAATGTCCGCATAGACCCCA 300
Db 241 TCCTCGTATGATCCCTCGCTCATCAAAACAGAGAGTACTGAAGAAATGTCCGCATAGACCCCA 300
Qy 301 GCAGCCTGTCTCTTGTGCAATGTGGAGAGAGATCCCTGTACCTCTTACTGTTCGCTACT 360
Db 301 GCAGCCTGTCTCTTGTGCAATGTGGAGAGAGATCCCTGTACCTCTTACTGTTCGCTACT 360
Qy 361 TCTTCGAGGTGGTCAATCCCGAGAGATCTTAAAGGGTGAAGAGCCAGTAGTGGGGAGC 420
Db 361 TCTTCGAGGTGGTCAATCCCGAGAGATCTTAAAGGGTGAAGAGCCAGTAGTGGGGAGC 420
Qy 421 GTGACCCATGTCTACAGGGAATTCAGACATAGAGGCCAAATCACCTTCAATGACAAATG 480
Db 421 GTGACCCATGTCTACAGGGAATTCAGACATAGAGGCCAAATCACCTTCAATGACAAATG 480
Qy 481 ATACTGTGTCTTGTGAGACCGCAGCCTCCATTTCCAGCCGACAGGTCCCAACGCT 540
Db 481 ATACTGTGTCTTGTGAGACCGCAGCCTCCATTTCCAGCCGACAGGTCCCAACGCT 540
Qy 541 CTGAGAGTGAATACATATATCTGCTTAACTTCTGGTCTTGGGGGGCGCAGTATGATGG 600
Db 541 CTGAGAGTGAATACATATATCTGCTTAACTTCTGGTCTTGGGGGGCGCAGTATGATGG 600
Qy 601 AGACAACTGTGAGGCTGAAGCTGATGATGACTTGGGGCTGGCCACCTTGGGGCAGC 660
Db 601 AGACAACTGTGAGGCTGAAGCTGATGATGACTTGGGGCTGGCCACCTTGGGGCAGC 660
Qy 661 GTGCTTTATGAACCGACAGTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Db 661 GTGCTTTATGAACCGACAGTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Qy 721 ATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTGTTG 780
Db 721 ATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTGTTG 780
Qy 781 TTGAGATGAACAACTCAGACTCTGGGCTTTCACTGTGTTCAAGGGCTCCAGAACTTCA 840
Db 781 TTGAGATGAACAACTCAGACTCTGGGCTTTCACTGTGTTCAAGGGCTCCAGAACTTCA 840
Qy 841 GCAGATCCACCTGGTGAAGATGGAATGGGCTCAGCAAGGTCAACTCTGGCAATTCAG 900
Db 841 GCAGATCCACCTGGTGAAGATGGAATGGGCTCAGCAAGGTCAACTCTGGCAATTCAG 900
Qy 901 AGCAGTCAACATCATCAATGGCACTTCCGGGAGATGGGGACCACTTCATGACACCC 960
Db 901 AGCAGTCAACATCATCAATGGCACTTCCGGGAGATGGGGACCACTTCATGACACCC 960
Qy 961 AGTCTCGCTGGAATTTCTCAGTCCGGAAGCTCAGAGTCTATGAAGCTCACCTACCATG 1020
Db 961 AGTCTCGCTGGAATTTCTCAGTCCGGAAGCTCAGAGTCTATGAAGCTCACCTACCATG 1020
Qy 1021 ATTGAGGGGTGTTGAAGGCATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG 1080
Db 1021 ATTGAGGGGTGTTGAAGGCATCCCACTATCGCTTCAAGCCCTTAAACCTTTGTTG 1080
Qy 1081 CCAATGGTCTGTTTACCCCAATGAAGTTCCTGCGGTGCTTGAATCCGGGCATTC 1140
Db 1081 CCAATGGTCTGTTTACCCCAATGAAGTTCCTGCGGTGCTTGAATCCGGGCATTC 1140
Qy 1141 AAAATGTGACACTTGCAGGTTTGGTGACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
Db 1141 AAAATGTGACACTTGCAGGTTTGGTGACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
Qy 1201 ATGAGACCTTGTCTATCAAGCCGCTTCTGGTCTGAACCCCTGAGCCCAAGGAGCAT 1260
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Db 1201 ATGCAGACCCCTGTGCTATCAAGACCCGCTTCTGGTCTGAACCCCTGAGCCCAAGGAGCAT 1260
Qy 1261 CTTTGTTCCTTGACATCATCCGCTCACTGGGATCCCATGAACCTGTTCTGTGAAGTTGC 1320
Db 1261 CTTTGTTCCTTGACATCATCCGCTCACTGGGATCCCATGAACCTGTTCTGTGAAGTTGC 1320
Qy 1321 AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCG 1380
Db 1321 AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCG 1380
Qy 1381 TGGTCTCCCATCTGCTGTGTTTGGAGCAGAGCGGTGTCATGGGCGGCGAGCCCTGAACA 1440
Db 1381 TGGTCTCCCATCTGCTGTGTTTGGAGCAGAGCGGTGTCATGGGCGGCGAGCCCTGAACA 1440
Qy 1441 CGTTCTACACGAGCTGGTGTCTGATGCCCGAGGTACTTCAAGTATGTGAGTATGTGCTGC 1500
Db 1441 CGTTCTACACGAGCTGGTGTCTGATGCCCGAGGTACTTCAAGTATGTGAGTATGTGCTGC 1500
Qy 1501 TGGGGCTGGGCGGCTCTCTGCTGTGTCGTCCTCATCTACCAATGTCGAGCCAGGAGA 1560
Db 1501 TGGGGCTGGGCGGCTCTCTGCTGTGTCGTCCTCATCTACCAATGTCGAGCCAGGAGA 1560
Qy 1561 AATGCTTTTATTTTGGAGTGGTAAAGGGCTCGCAGGATAGGAGGCCATTCAGG 1620
Db 1561 AATGCTTTTATTTTGGAGTGGTAAAGGGCTCGCAGGATAGGAGGCCATTCAGG 1620
Qy 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGSCAGGTGCTCAAGAGGCCAAGC 1680
Db 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGSCAGGTGCTCAAGAGGCCAAGC 1680
Qy 1681 TGAGGGTCCCAAGACACCAAGGCCCCCCTCACTGATGCTTGGTCTGAGCCAGCCAT 1740
Db 1681 TGAGGGTCCCAAGACACCAAGGCCCCCCTCACTGATGCTTGGTCTGAGCCAGCCAT 1740
Qy 1741 CAGCCCTTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGTC 1786
Db 1741 CAGCCCTTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGTC 1786
```

RESULT 9

AEBO3941
ID AEBO3941 standard; cDNA; 1788 BP.

XX AEBO3941;

XX AC

XX 25-AUG-2005 (first entry)

XX Hamster Scavenger Receptor Class B-1 coding sequence, 'SEQ ID 1 #2.

XX Antilipemic; transgenic animal; Scavenger Receptor Class B-1;

XX high density lipoprotein receptor; cholesterol; lipid; gene; ss.

XX Cricetulus griseus.

XX Key Location/Qualifiers

XX CDS 156..1685

XX FT /*tag= a

XX FT /product= "SR-BI"

XX US2005136005-A1.

XX 23-JUN-2005.

XX 02-SEP-2004; 2004US-00933037.

XX 23-JUN-1994; 94US-00265428.

XX 19-JUN-1995; 95WO-US007721.

XX 15-NOV-1996; 96US-00749907.

XX 27-MAR-1997; 97US-00765108.

XX 30-AUG-1999; 99US-00385799.

XX (NASI) MASSACHUSETTS INST TECHNOLOGY.
PA (TYPE-) UNIV PENNSYLVANIA.

XX Kozarsky K, Rigotti A, Krieger M;
PI WPI; 2005-457475/46.
DR P-PSDB; AEB03938.
XX
PT New genetically engineered mouse or derivative cells with inactivated SR-
PT BI gene expression or activity, useful as a model for designing drugs
XX that can modulate cholesterol transport.
XX
PS Disclosure; SEQ ID NO 1; 21pp; English.
XX
CC The present invention relates to a novel genetically engineered mouse, or
CC cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene
CC expression or SR-BI activity has been inactivated. SR-BI is a high
CC density lipoprotein (HDL) receptor. It was found that estrogen
CC downregulates SR-BI under conditions of upregulation of the low density
CC lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
CC adrenal membranes and other non-placental steroidogenic tissues from
CC animals treated with estrogen, but not in other non-placental non-
CC steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
CC tissue causes a decrease in blood cholesterol levels. The animal is
CC useful as a model for designing drugs that can modulate cholesterol
CC transport or that can stimulate or inhibit the binding to and lipid
CC movements mediated by SR-BI and redirect uptake and metabolism of lipids
CC and cholesterol by cells. The present sequence is a coding sequence for
CC SR-BI, which was used to illustrate the invention. Note: The SEQ ID 1
CC given in the sequence listing (the sequence shown in AEB03937) is stated
CC to be 1788 nucleotides in length. However, there appears to be a 1 to 3
CC nucleotide deletion at the end of each line of the sequence shown in the
CC sequence listing, resulting in a sequence that is 1718 nucleotides in
CC length. Therefore a corrected version of the sequence has been produced
CC with Ns added to replace the missing nucleotides (the sequence shown in
CC AEB03941). SEQ ID 1 is stated to encode SEQ ID 2 (given in AEB03938).
XX
SQ Sequence 1788 BP; 354 A; 492 C; 468 G; 404 T; 0 U; 70 Other;

Query Match 96.1%; Score 1718; DB 14; Length 1788;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1718; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGCTACTGCTGCCGGCCACTGCCGTGAGACTCACCTTGCTGGAACTGG 60
DB 1 GCCACCTGCAGGCTACTGCTGCCGGCCACTGCCGTGAGACTCACCTTGCTGGAACTGG 60
QY 61 AGCCTCGGCTTCTGTCATCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTG 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTG 120
QY 121 CCTGAGCCCCCGAGCCCGGCGCGACACGCGGACATGGSCGCGAGCGCCGAGGCGCGCT 180
DB 121 CCTGAGCCCCCGAGCCCGGCGCGACACGCGGACATGGSCGCGAGCGCCGAGGCGCGGN 180
QY 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTG 240
DB 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTG 240
QY 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 GCAGCCTGCTCTTGGCAATGTGAAGGAGATCCCTGTACCCTTCTACTTGTCCGCTCTACT 360
DB 301 GCAGCCTGCTCTTGGCAATGTGAAGGAGATCCCTGTACCCTTCTACTTGTCCGCTCTANN 360
QY 361 TCTTCGAGGTGGTCAATCCGAGGAGATCCTAAGGGGTGAGAGCCAGTAGTGCAGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCGAGGAGATCCTAAGGGGTGAGAGCCAGTAGTGCAGGAGN 420
QY 421 GTGACCCCTATGCTACAGGGAATTCAGACATTAAGGCCAAACATCATCTTCAATGACAATG 480
DB 421 GTGACCCCTATGCTACAGGGAATTCAGACATTAAGGCCAAACATCATCTTCAATGACAANN 480

QY 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCGCTCCATTTCCAGCGGACAGGTGCCACGCT 540
DB 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCGCTCCATTTCCAGCGGACAGGTGCCACGNN 540
QY 541 CTGAGAGTCACTACATTATATATATGCTTAACTTGTCTTGGGGGCGCAGTAAATGATGG 600
DB 541 CTGAGAGTCACTACATTATATATGCTTAACTTGTCTTGGGGGCGCAGTAAATGATNN 600
QY 601 AGAGCAAGTCTGCGAGCCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 AGAGCAAGTCTGCGAGCCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 GTGCGCTTTATGAACCAAGCAAGTTGGTGGATCTGCTGGGGCTATGAGGATCCCTTCGTGA 720
DB 661 GTGCGCTTTATGAACCAAGCAAGTTGGTGGATCTGCTGGGGCTATGAGGATCCCTTCGTNN 720
QY 721 ATTTTATCAACAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTTCGGGCTGTTG 780
DB 721 ATTTTATCAACAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTTCGGGCTGTTNN 780
QY 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTGCAGAACTTCA 840
DB 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTGCAGAACTTNN 840
QY 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTCTGCGATTTCAG 900
DB 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTCTGCGATTTCNN 900
QY 901 AGCAGTGCACAACTGATCAATGGCACCTCCGGGCGAGATGGGGCACCATTCATGACACCCC 960
DB 901 AGCAGTGCACAACTGATCAATGGCACCTCCGGGCGAGATGGGGCACCATTCATGACACCCN 960
QY 961 AGTCTCGCTGGAAATCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTACATG 1020
DB 961 AGTCTCGCTGGAAATCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTACATNN 1020
QY 1021 ATTCAGGGGTGTTGAAGGCATCCCGACCTATCGCTTACAGCCCTTAAACCTTCTGTTG 1080
DB 1021 ATTCAGGGGTGTTGAAGGCATCCCGACCTATCGCTTACAGCCCTTAAACCTTCTGTTNN 1080
QY 1081 CCAATGGGTCTGTTTACCCACCAATGAAGTTCCTGCGCGCTTGAATCGGCANNN 1140
DB 1081 CCAATGGGTCTGTTTACCCACCAATGAAGTTCCTGCGCGCTTGAATCGGCANNN 1140
QY 1141 AAAATGTGACGACTTGCGAGTTTGGTGCAACCTGTTCTGTCTGACACCTCATTCTACA 1200
DB 1141 AAAATGTGACGACTTGCGAGTTTGGTGCAACCTGTTCTGTCTGACACCTCATTCTNN 1200
QY 1201 ATGCGAGCCCTGCTGCTATCAGAAAGCGTTCTGGGTCTGAACCTGACCCAGGGAGCAT 1260
DB 1201 ATGCGAGCCCTGCTGCTATCAGAAAGCGTTCTGGGTCTGAACCTGACCCAGGGAGCINN 1260
QY 1261 CTTTGTTCCTTGACATCCATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAAGTTGC 1320
DB 1261 CTTTGTTCCTTGACATCCATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAAGTTNN 1320
QY 1321 AGATAAGCCTCTACATCAAGCTGTCAAGGGATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
DB 1321 AGATAAGCCTCTACATCAAGCTGTCAAGGGATTTGGGCAAAACAGGGAAGATCGAGCINN 1380
QY 1381 TGGTCTCCCTTGTGTTGAGCAGAGCGGTGTCATGGGGCTGAGCGCCCTGCAACA 1440
DB 1381 TGGTCTCCCTTGTGTTGAGCAGAGCGGTGTCATGGGGCTGAGCGCGAGCCCTGCAANN 1440
QY 1441 CGTTCCTACACGAGCTGCTGATGCCCGCAGGACTTCAGTATGTGCAAGTGTGCTGC 1500
DB 1441 CGTTCCTACACGAGCTGCTGATGCCCGCAGGACTTCAGTATGTGCAAGTGTGCTNN 1500
QY 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 AATGCTTTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCGCAGGATAGAGGGCCATTCAGG 1620

Db	1561	AATGCTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCGCAGGATAAGGAGGCCATTCCNN	1620
Qy	1621	CCTACTCTGAGTCTCTGATGTCACCAAGTGCACAGGGCACGGTCTGCAAGAAGCCAAAGC	1680
Db	1621	CCTACTCTGAGTCTCTGATGTCACCAAGTGCACAGGGCACGGTCTGCAAGAAGCCANN	1680
Qy	1681	TGTAGGTTCCAAAGACACCAAGTGCACCAAGTGCACCAAGTGCACCAAGTGCACCAAGTGC	1740
Db	1681	TGTAGGTTCCAAAGACACCAAGTGCACCAAGTGCACCAAGTGCACCAAGTGCACCAAGTGC	1740
Qy	1741	CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTGGC	1788
Db	1741	CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTGGC	1788
RESULT 10			
ABD33431			
ID	ABD33431	standard; cDNA; 2496 BP.	
XX	ABD33431;		
XX			
DT	18-NOV-2004	(first entry)	
DE	Murine cancer-associated (CA) cDNA MR07-081.		
XX			
KW	Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;		
KW	ss; cancer; cytostatic.		
OS	Mus musculus.		
PN	WO2004058146-A2.		
PD	15-JUL-2004.		
PP	15-DEC-2003; 2003WO-US040081.		
XX			
PR	17-DEC-2002; 2002US-00322281.		
XX			
PA	(SAGR-) SAGRES DISCOVERY INC.		
PI	Morris DW, Malandro MS;		
DR	WPI; 2004-499109/47.		
DR	P-PSDB; ABO84950.		
XX			
PT	Novel human cancer associated protein encoded within open reading frame		
PT	of cancer associated gene, useful as targets for diagnosing cancer.		
PS	Disclosure; SEQ ID NO 564; 182pp; English.		
XX			
CC	The invention relates to cancer-associated proteins (CAP) and the cancer-		
CC	associated (CA) nucleic acids encoding them. The invention also relates		
CC	to a method for treating cancers involving administering to a patient an		
CC	inhibitor of CAP, and a method of screening for anticancer activity in a		
CC	potential drug involving providing a cell that expresses a CA gene,		
CC	contacting a tissue sample derived from a cancer cell with an anticancer		
CC	drug candidate and monitoring the effect of the anticancer drug candidate		
CC	on expression of the CA gene. The CAP proteins are useful for detecting		
CC	cancer associated with expression of a CAP protein in a test cell sample		
CC	and for screening for a bioactive agent capable of modulating the		
CC	activity of a CAP protein. The CA nucleic acids are useful for diagnosing		
CC	cancer, involving determining the expression of a CA nucleic acid in a		
CC	tissue. This sequence represents murine CA cDNA of the invention. Note:		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences		
XX			
SQ	Sequence 2496 BP; 517 A; 741 C; 660 G; 578 T; 0 U; 0 Other;		
Query Match 80.6%; Score 1441.2; DB 13; Length 2496;			
Best Local Similarity 88.3%; Pred. No. 0;			
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1;			

Qy	1	GCACCTGCAGGGCTACTGCTGCTCCGGCCACATGCGCTGAGACTCACCTTGCTGGAAGCTG	60
Db	39	GCCACCTGCAGGGCTACTGCTGCTCCGGCCACCGCCAGGCACACACTTGCTGCTGAGGG	98
Qy	61	AGCCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCGTCTTGTGCGTGTGCTCCCTTCAGTC	120
Db	99	AGTCTCGGCTTCTGTCATCTCTGTGGCCTCGTCACTCTGTCTCCGT-CTCCTTCAGGT	157
Qy	121	CCTGAGCCCGCGAGCCCGGGCCGCAACGCGGACATGCGCGGCGACGCGCAGGGCGCGCT	180
Db	158	CCTGAGCCCGGAGAGCCCTTCCGCGACGCGGACATGGCGGCGACTCCTCAGGGCGCGCT	217
Qy	181	GGGTGGCGGTGGGGCTGGGGGCTCGTGGGGCTGCTGTGCGTGTGCTCGGTGTGTTATGA	240
Db	218	GGGTGGCCTTGGGGTGTGGGGCCCTGGGGGCTGTGTGTTGCTGCGCTCGCGGTGTTCATGA	277
Qy	241	TCCTCGTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCCGATAGACCCCA	300
Db	278	TCCTCATGTGCCCCCTCCCTCATCAGCAGCAGGTGTCAAGANTGTCCGCATFAGACCCGA	337
Qy	301	GCAGCCTGTCTTTTGAATGTGGAAGGAGATCCCTGTACCCCTTCTACTTTGTCGGTCTACT	360
Db	338	GCAGCCTGTCTTTGGGAGTGTGAAGGAGATCCCCTGCCCTTCTACTTGTCTGTCTACT	397
Qy	361	TCTTCGAGGTGTCAATCCAGCGAGATCCTAAAGGGTGAGAACCCAGTAGTGCGGGAGC	420
Db	398	TCTTCGAAGTGTCAACCCAAACGAGTCTCTAACGGCCAGAAAGCCAGTAGTCCGGGAGC	457
Qy	421	GTGGACCTATGTCACAGGGAATTCAGACATGAAGCCACATCACCTTCAATGACAAATG	480
Db	458	GTGGACCTATGTCACAGGAGTTCAGACAAAGGTCAACATCACCTTCAATGACAAAG	517
Qy	481	ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGGACAGTCCCAACGGCT	540
Db	518	ACACCGTGTCTTGTGGAGAACCGCAGCTCAATTTCCAGCCTGACAAAGTCGATGGCT	577
Qy	541	CTGAGAGTGACTACATATATCTGCCATAACATCTGTGCTTTGGGGGGCGCAGTAATGATGG	600
Db	578	CAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCTCTGGGGGGCTCGATATTTGATGG	637
Qy	601	AGAGCAAGTCTGCAGCGCTTGACGTGATGATGACCTTTGGGCTGGGCCACTTGGGGCCAGC	660
Db	638	AGAGCAAGCGCTTGAGCCTGAAGCTGATGATGACCTTGGCGCTGGTCCACCATGGGCCAGC	697
Qy	661	GTGCCCTTATGAACCGAACAGTTGGTGAGATCCTGTGGGGCTATGAGGATGCCCTTCGTGA	720
Db	698	GTGCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGGCTATGACGATCCCTTCGTGC	757
Qy	721	ATTTTATCAACAAATACTTACAGACATGTTCCCATCAAGGGCAAGTGTGGCCTGTTTG	780
Db	758	ATTTTCTCAACAGTACTCTCCACAGCATGCTTCCCATAAAGGGCAAAATTTGGCCTGTGTTG	817
Qy	781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTCAGGGGGTCCAGAACTTCA	840
Db	818	TTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGCTTTCAGGGCGTCCAGAAATTTCA	877
Qy	841	GCAAGATCCACTGTGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTCTGSCATTTGAG	900
Db	878	GCAGGATCCATCTGGTGGACAAATGGAACGGACTCAGCAAGATCGAATATTGGCATTTGAG	937
Qy	901	AGCAGTGAACAACTGATCAATGGCACTTCCGGGCGAGATGTGGGCAACATTCATGACACCCC	960
Db	938	AGCAGTGAACATGATCAATGGGACTTCCGGGCGAGATGTGGGCAACCTTCATGACACCCG	997
Qy	961	AGTCTCGCTGGAATTTCTTCAGTCCGGAAGCCTGCAAGGTCTATGAAGTCACTTCAATG	1020
Db	998	AATCTCTCGCTGGAATTTCTTCAGCCCGGCGACATGCAAGGTCCATGAAGCTGACCTCAACAG	1057
Qy	1021	ATTTAGGGGTGTTTGAAGGATCCCACTATCGCTTCACAGGCCCTTAAACTTTGTTTG	1080
Db	1058	AATCAAGGGGTGTTTGAAGGATTTCCACGCTATCGCTTTCAGGCCCGCCGATATCTGTGTTG	1117

Query Match 80.6%; Score 1441.2; DB 13; Length 2496;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 1577; Conservative 0; Mismatches 208; Indels 1;

QY 361 TCTTCAGGCTGCTCAATCCCAAGCGAGATCTTAAAGGGTGAAGCCAGTAGTGTGGGAGC 420
DB 398 TCTTCAGGCTGCTCAATCCCAAGCGAGTCTTCAACGGCCAGAGCCAGTAGTGTGGGAGC 457
QY 421 GTGACCCCTATGTCTACAGGGAATTCAGACATAGGCGCAACATCACCTTCAATCACAATG 480
DB 458 GTGACCCCTATGTCTACAGGGAATTCAGACATAGGCGCAACATCACCTTCAATCACAATG 517
QY 481 ATACTGTGTCTTGTGTGAGCAGCGCAGCTCCATTTCCAGCGGACAGAGTCCCAACGGCT 540
DB 518 ACACGGTGTCTTGTGTGAGCAGCGCAGCTCCATTTCCAGCGGACAGAGTCCCAACGGCT 577
QY 541 CTGAGAGTACTACATTATATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGATG 600
DB 578 CAGAGAGTACTACATTATATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGATG 637
QY 601 AGACAGTCTGACAGGCTGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCGAGC 660
DB 638 AGACAGGCTGTGAGCGTGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCGAGC 697
QY 661 GTGCTTTTATGAACCGAACTGCTGGTCTGAGATCTTGTGGGGCTATGAGATCCCTTCTGTA 720
DB 698 GTGCTTTTATGAACCGCACTGCTGGTCTGAGATCTTGTGGGGCTATGAGATCCCTTCTGTA 757
QY 721 ATTTTATCAAAATATCTTACGACATGTTCCCATCAAGGGCAAGTTCGGGCTGTTG 780
DB 758 ATTTTCTCAACACCTGCTCCGACATGCTTCCCATCAAGGGCAAGTTCGGGCTGTTG 817
QY 781 TTGAGATGACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
DB 818 TTGGGATGAACAACTCAGAACTTCTGGGGCTTCTCACTGTCTTACGGGGCTCCAGAACTTCA 877
QY 841 GCAAGATCCACCTGCTGACAGATGGAATGGGCTCAGCAAGTCAACTCTTGGGCACTTCA 900
DB 878 GCAGATCCATCTGGTGGACAAATGGAACGAGCTCAGCAAGATCGATTTGGGCACTTCA 937
QY 901 AGCAGTGCACATGATCAATGGCACTTCCGGGGAGATGTGGGCACTTCAATGACACCCC 960
DB 938 AGCAGTGTAACTGATCAATGGGCACTTCCGGGGAGATGTGGGCACTTCAATGACACCCC 997
QY 961 AGTCTCGCTGGAAATCTTCTGAGTCCGAGAGCTCAGAGTCTATGAAGCTCCTTACCAGT 1020
DB 998 AATCTCGCTGGAAATCTTCTGAGTCCGAGAGCTCAGAGTCTATGAAGCTCCTTACCAGT 1057
QY 1021 ATTCAGGGGTGTTTGAAGGCAATCCCACTATGCTTCTCAGAGCCCTTAAAGCTTGTGTTG 1080
DB 1058 AATCAAGGGGTGTTTGAAGGCAATCCCACTATGCTTCTCAGAGCCCTTAAAGCTTGTGTTG 1117
QY 1081 CCAATGGGTCTGTTTACCCCAATGAAGTGTCTGCGGCTGCTTGAATTCGGGCACTT 1140
DB 1118 CCAAGGGTCTGTTTACCCCAATGAAGTGTCTGCGGCTGCTTGAATTCGGGCACTT 1177
QY 1141 AATATGTGACGACTGTGAGTGTGGTGAACCCCTGTTTCTGTGACACCTTCACTTCTACA 1200
DB 1178 AGAATGTGACGACTGTGAGTGTGGTGAACCCCTGTTTCTGTGACACCTTCACTTCTACA 1237
QY 1201 ATGACAGCCTGTGCTATCAGAGCGTCTTGGGTCTGAACCTTCAACCCCAAGGGAGCAT 1260
DB 1238 ACGCGGACCTGTTGTGAGAGCTGTTCTTGTGCTGAACCTTCAACCCCAAGGGAGCAT 1297
QY 1261 CTTTGTCTTGTGACATCCCGTCTACTGGGATCCCATGAACTGTTCTGTGAAGTTGC 1320
DB 1298 CTTTGTCTTGTGACATCCCGTCTACTGGGATCCCATGAACTGTTCTGTGAAGTGC 1357
QY 1321 AGATAAGCTCTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCAGGCGCG 1380
DB 1358 AGCTGAGCCTCTACATCAAACTCTGTCAAGGGCATTTGGGCAACAGGGAAGATCAGGCGCG 1417
QY 1381 TGTGCTCTCCATCTGCTGTTTGTGAGCAGAGCGGTGCTTGGGGCGGCGGCTTGAACA 1440
DB 1418 TAGTTCTGCGCTGCTGTTGTTGAGCAGAGCGGAGCAATGGGGTGGCAAGCCCTTGAGCA 1477

QY 1441 CGTTCTACACGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
DB 1478 CGTTCTACACGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1537
QY 1501 TGGGGCTGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1538 TGGGGCTGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1597
QY 1561 AATGCTTTTTTATTTTGGAGTGGTAGTAAAGAGGCTCGCAGGATAGGAGGCGCATTCAGG 1620
DB 1598 AATGCTTTTTTATTTTGGAGTGGTAGTAAAGAGGCTCGCAGGATAGGAGGCGCATTCAGG 1657
QY 1621 CCTACTCTGATGCTCTGATGCTCAGAGTCCCAAGGCGCGTCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1658 CCTACTCTGATGCTCTGATGCTCAGAGTCCCAAGGCGCGTCTGCTGCTGCTGCTGCTGCTGCTG 1717
QY 1681 TGTAGGGTCCCAAGACACACGAGCGGCTTCTTGGAGTCTCTCTCAGCGGACAGTC 1740
DB 1718 TATAGGGTCTCTGAGACACTATAAGCGGCTTCTTGGAGTCTCTCTCAGCGGACAGTC 1777
QY 1741 CCAAGCTTACACCGCGCTTCTTGGAGTCTCTCTCAGCGGACAGTC 1786
DB 1778 CCAAGCTTACACCGCGCTTCTTGGAGTCTCTCTCAGCGGACAGTC 1823

RESULT 12

ADZ13454

ID ADZ13454 standard; cDNA; 2513 BP.

XX AC ADZ13454;

XX DT 16-JUN-2005 (first entry)

XX DE Murine cancer-associated cDNA #109.

XX DX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

XX KW cytoskeletal; gene; ss.

XX OS Mus sp.

XX PN W02005031001-A2.

XX PD 07-APR-2005.

XX PF 23-SEP-2004; 2004WO-US031617.

XX PR 23-SEP-2003; 2003US-00669920.

XX PA (CHIR) CHIRON CORP.

XX PI Morris DW, Malandro MS;

XX PF WPI; 2005-273395/28.

XX DR P-PSDB; ADZ13455.

XX PT Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.

XX PS Disclosure; SEQ ID NO 974; 198pp; English.

XX CC The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA

1368	AGTGTAGTCTGTACATCAAAATCCGTCAAGGGCGTCGGGCAAAACAGAGGAAGATCGAGCCAG	1427
Qy	TGFTCTCTCCATTCCTGTGTGTTTTAGCAGAGCGGTGTCATGGGCGGCGAGCCCTGAAACA	1440
Db	TAGTCTCTGCCATTGCTGTGTGTTCCGACAGAGCGGATGATGGGTGGCAAGACCTGAAACA	1487
Qy	CGTTCTACACGACCTGGTGTGATGCCCCAGGTACTTACAGTATGTCGATATGTGCTGC	1500
Db	CGTTCTACACGACCTGGTGTGATGCCCCAGGTCTTCACTACGCGCATGTGTGCTGC	1547
Qy	TGGGGCTTGGCGGGCTCTCGCTGCTGGTGGCCGCTCATCTACCAAGTTTGGCGAGCCAGGAGA	1560
Db	TGGGGCTTGGAGGGCTCTCTGTTCTGGTGCCCATCATTTACCAACTGCGCAGCCAGGAGA	1607
Qy	AATGCTTTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCGCAGGATAAGGAGGCCATTTCAGG	1620
Db	AATGCTTTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCGCAGGATAAGGAGGCCATTGCAGG	1667
Qy	CCTACTCTGAGTCTCTGATGTCAACCAGCTGCGAAGGGCAGGGTGCTGCCAAGAGCCCAAGC	1680
Db	CCTACTCTGAGTCTCTGATGTCAACCAGCTGCGAAGGGCAGGGTACTGCCAAGAGGCCCAAGC	1727
Qy	TGTAGGGTCCCAAGAGACACCAAGAGCCCCCCCACCTGTATAGCTTGGTTCAGACCCAGCCAT	1740
Db	TGTAGGGCCCCAAGAGACACCAAGAGCCCCCCCACCAACTGTATAGCTTGGTTCAGACCCAGCCG	1787
Qy	CCAGCCCTTACACCCCGCTTCTTGGAGACTCTCTTCAGCGGACA	1783
Db	CCAGTCCCTACACCCCACTTCTCGAGACTCTCTTCAGCGGACA	1830

RESULT 14

RESOL 14
AD853264AD53264
ID ADB53264 standard: DNA: 2497 BP.

AD853264:

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEO ID NO:3806.

toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

KW toxicity marker; toxicity progression; drug screening;

KW primary rat hepatocyte toxicity modelling; gene; ds.

OS *Rattus norvegicus*.

PN WO2003065993-A2.

PD 14-AUG-2003.

04-FEB-2003: 2003WO-US003482.

PR 04-FEB-2002: 2002US-0353171P.

PR 13-MAR-2002: 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.
DE 10 APR 2002 2002US 0372603P
DE 10 APR 2002 2002US 0372603P

PR 19-APR-2002; 2002US-037360IP.

PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P

22-AFK-2002; 2002US-0374139F.
08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002: 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0378665P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

04-SEP-2002; 2002US-0407688P.

XX
PA (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
PI
XX
DR WPI; 2003-731472/69.
XX
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
XX Claim 44; SEQ ID NO 3806; 874pp; English.
XX
XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
XX Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property Organization

XX Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

Query Match 79.0%; Score 1413; DB 10; Length 2497;
 Best Local Similarity 87.9%; Pred. No. 0;
 Matches 1567; Conservative 0; Mismatches 205; Indels 11; Gaps 2;

Qy 1 GCCACCTGAGGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTGCTGGAACGCTG 60
 Db 59 GCCACCTGAGGGCTACTGCTGCTTCTGGCCACTGTGAGGCACACACCTTGCTG----- 111

Qy 61 AGCTCGGCTTCTGTCATCTCTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 112 ---CTCGGTTCTGTCATCTCTGCGGCTCTGCGGCTCTGTCGCGT-CCCCCTTCAGGT 167

Qy 121 CCTGAGCCCGGAGCCCGGCGGCACACGCGGACATGGGCGGCGAGCGGCGCGCT 180
 Db 168 CCTGAGCCCGAGGACTCTCGGCGGCGGACGCGGCGGCTGAGCTCCAGGGCAGCT 227

Qy 181 GGGTGGCGGTGGGCTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGGGCT 240
 Db 228 GGGTGGCTTGGGCTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGGGCTGGTGGGCT 287

Qy 241 TCCTCGTGATCCCTCGCTCATCAACAGCAGGACTGAGAGATGTCGCGATAGACCCCA 300
 Db 288 TTCTCATGGTGGCTCGCTCATCAAGCAGGAGTGTCAAGATGTCCGATAGACCCCA 347

Qy 301 GCAGCTGTCTTTGCAATGGAAGAGATCCTGTACCTTCTACTTCTCGCTTACT 360
 Db 348 GCAGCTGTCTTTGGGATGTGAGAGAGATCCTGTCTCTTCTACTTCTCGCTTACT 407

Qy 361 TCTTCGAGGTGGTCAATCCGAGGAGATCTTAAGGGTGAAGCCAGTATGTCGGGAGC 420
 Db 408 TCTTCGAGGTGGTCAATCCGAGGAGTCTTAATGGCCAGAGCCAGTATGTCGGGAGC 467

Qy 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCCCAATCACCTTCAATGCAATG 480
 Db 468 GCGGACCTATGCTACAGGAGTTCAGACAAAGGTTAACTCACCTTCAATGCAATG 527

Qy 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGAGCAGGCTCCACGCT 540
 Db 528 ACAGGTGTCTTACATAGAGACCGAAGCCTTGGTTCCAGCCAGACAGTCCAGGGCT 587

Qy 541 CTGAGAGTACTACATTAATCTGCTAACATCTGGTCTTTGGGGGGCGCAGTAAATGAG 600
 Db 588 CAGAGAGTACTACATTTGCTGCTAACTCTGGTCTCTGGAGGGGCGAGTATGATGG 647

Qy 601 AGACAGTCTGAGGCTGAGCTGATGATGACCTTGGGCTGGCCACCTTGGGCCAGC 660
 Db 648 AGGACAGCCCAAGGCTGAGCTGATGATGACCTTGGGCTGGTCCACATGGGCCAGC 707

Qy 661 GTGCTTTTATGAACCGAAGTGTGGTGGATCTGCTGGGCTGATGAGATCCCTTCGTGA 720
 Db 708 GGGCTTTTATGAACCGCAGCGTGTGGTGGATCTGCTGGGCTGATGAGATCCCTTTGTGA 767

Qy 721 ATTTTATCAAAATCTTACAGACATGTTCCCATCAAGGGCAAGTTCGGGCTGTTTG 780
 Db 768 ATTTCTCTCAGCAATAATTTCCAGACATGTTCCCATCAAAAGGCAAAATTTGGGCTGTTG 827

Qy 781 TTGAGATGAACACTCAGACTCTGGGCTCTTCACTGTGTTTCAGGGGCTCCAGAACTTCA 840
 Db 828 TTGGGATGAACGACTCAGTCTGGGCTCTTCACTGTGTTTCAGAGGTGTTCCAGAAATTTCA 887

Qy 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGATTTCAG 900

Db 888 GCAAGATCCATCTGGTGGATAAGTGGAAACGGCTCAGCGAGGTCAACTATTGGCAATTCGG 947
 Qy 901 AGCAGTGGCAACATGATCAATGSCACTTCCGGGAGATGTGGGACCACTTTCATGACACCCC 960
 Db 948 AACAGTGGCAACATGATCAATGTTACTTGGCCGGCAGATGTGGGACCACTTTCATGACACCCC 1007
 Qy 961 AGTCTCTCGCTGGAATTTCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTACCATG 1020
 Db 1008 ATCTCTCATCTGGANTTCTTCAGCCCAAGGCTGCAAGTCTATGAAGCTCACCTACCATG 1067
 Qy 1021 ATTCAAGGGTGTGTTGAAGGCATCCCACTATCGCTTTCACAGCCCTTAAACTTTGTTG 1080
 Db 1068 AATCAAGGGTGTGTTGAAGGCATCCCACTATCGCTTTCACGGCCCGGATCTTTGTTG 1127
 Qy 1081 CCAATGGGCTGTGTTTACCCACCAATGAAGGTTTCTGCCCGTGCCTTGAATCGGCAATTC 1140
 Db 1128 CCAACGGGTCGCTCTTACCCACCAATGAAGGTTTCTGCCCGTGCCTGCGGATTC 1187
 Qy 1141 AAAATGTCAGCACTTGCAGGTTTGGTGACCCCTGTTCTGTACACCCCTCACTTCTTACA 1200
 Db 1188 AGAATGTGAGCACTGCAAGTTTGGTGGCCCTGTTTCTTCCAGCCCGGATCTTCTACA 1247
 Qy 1201 ATGCAAGCCCTGTGCTTATCAGAAGCCGTTCTGGGCTCTGAACCTTGACCCCAAGGGAGCAT 1260
 Db 1248 ATGCTGACCCCGTGTCTCAGAAGCTGTTCTTGGTCTGAACCTTGACCCCAAGGGAGCAT 1307
 Qy 1261 CTTTGTCTTGCATCTCATCCGCTCATCGGATCCCAATGAACTGTTCTGTGGAAGTTC 1320
 Db 1308 CTTTGTCTTGCATCTCATCCGCTCATCGGATCCCAATGAACTGTTCTGTGGAAGTTC 1367
 Qy 1321 AGATAGCCCTTACATCAAGCTGTCAAGGCAATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
 Db 1368 AGCTGAGTCTGTACATCAAAATCCGTCAAGGGCTCGGGCAAAACAGGGAAGATCGAGCCAG 1427
 Qy 1381 TGTCTCTCCCTTGTCTGTGTTTGTGAGCAGAGGGGTGCCATGGGCGGCGAGCCCTTGAACA 1440
 Db 1428 TAGTCTCTGCCATGTCTGTGTTTGTGAAACAGAGCGGATGATGGTGGCAAGACCTTGAACA 1487
 Qy 1441 CGTTTACAGCAGCTGTGCTGATGCCCCAGGTACTTCAGTATGTGCAAGTATGTGCTGC 1500
 Db 1488 CGTTTACAGCAGCTGTGCTGATGCCCCAGGTACTTCACCTACGCGCAGTATGTGCTGC 1547
 Qy 1501 TGGGGCTGGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1548 TGGGGCTTGGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1607
 Qy 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGAGGAGGCAATTCAGG 1620
 Db 1608 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGAGGAGGCAATTCAGG 1667
 Qy 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCGAGGGGACGGTGTGCGAAGAGCCAGC 1680
 Db 1668 CCTACTCTGAGTCTCTGATGTCAACAGCTGCGAAGGGGACGGTGTGCGAAGAGCCAGC 1727
 Qy 1681 TGTAGGGTCCCAAGACACACGAGCCCGCCCAACTGATAGCTGCTGCTGAGCCAGCCAT 1740
 Db 1728 TGTAGGGTCCCAAGAGACACACGAGCCCGCCCAACTGATAGCTGCTGCTGAGCCAGCCAT 1787
 Qy 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTCTCAGCGGACA 1783
 Db 1788 CCAGTCCCTACACCCCGCTTCTCAGGAGTCTCTCAGCGGACA 1830

Search completed: February 23, 2006, 18:39:34
 Job time : 1086.41 secs


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Qy 1141 AAAATGTCAGCACTTGCAGGTTTGGTGACCCCTGTTCTGTGTCTACACCCCTCACTTCTACA 1200
Db 1179 AGAATGTGCAGCACTTGCAGGTTTGGTGACCCCTGTTCTGTGTCTACACCCCTCACTTCTACA 1238
Qy 1201 ATGCAGACCCCTGCTATCAGAAGCCCTTCTGGTCTGTGAACCCCTGACCCCAAGGAGCAATT 1260
Db 1239 ACGCCGACCCCTGTTGTGTCAAGAGCTGTCTTGTGTCTGAACCCCTTAACCCCAAGGAGCAATT 1298
Qy 1261 CTTTGTTCCTTGACATCCATCCGCTCACTGGGATCCCATGAACCTGTCTGTGAAGTTGC 1320
Db 1299 CTTTGTTCCTTAGACATCCATCCGCTCACTGGGATCCCATGAACCTGTCTGTGAAGTTGC 1358
Qy 1321 AGATAAGCCTTACATCAAGCTCTCAAGGCAATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
Db 1359 AGCTGAGCCTTACATCAAACTCTGTCAAGGCAATCGGGCAAAACAGGGAAGATCGAGCCAG 1418
Qy 1381 TGTCTCTCCCATGCTGTGTTTGTAGCAGAGCGGTGCGATGGCGGGCGGCGCCCTGAACA 1440
Db 1419 TAGTCTTCCGTTGCTGTGTTGCGAAGCAGAGCGGCAATGGGTGGCAAGCCCTGAGCA 1478
Qy 1441 CGTCTTACAGCAGCTGTGCTGATGCCCGCAGGTACTTTCAGTATGTGCAGTATGTGCTGC 1500
Db 1479 CGTCTTACAGCAGCTGTGCTGATGCCCGCAGGTACTTTCAGTATGTGCAGTATGTGCTGC 1538
Qy 1501 TGGGGCTTGGCGGCTCTCTGCTGTGTTGGTGGCCGTCATCTACAGTTCGCGCAGCCAGGAGA 1560
Db 1539 TGGGGCTTGGAGGCTCTCTGCTGTGTTGGTGGCCCATCATCTGCCACTTGGCAGCCAGGAGA 1598
Qy 1561 AATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGAGGATAAGAGGCAATTCAGG 1620
Db 1599 AATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGAGGATAAGAGGCAATTCAGG 1658
Qy 1621 CCTACTCTGAGTCTCTCATGTCACAGCTGCGAGGCGAGGCTGCTGCAAGAGCCCAAGC 1680
Db 1659 CCTACTCTGAGTCTCTCATGTCACAGCTGCGAGGCGAGGCTGCTGCAAGAGCCCAAGC 1718
Qy 1681 TGTAGGCTCCCAAGACACCAAGCAGGCCCCCCCCACCTGATAGCTTGTGTGAGCAGCCAT 1740
Db 1719 TATAGGCTCTTGAAGACACTATAGCCCCCCCCCAACCTGATAGCTTGTGTGAGCAGCCAT 1778
Qy 1741 CGAGCCCTTACACCCCGCTTCTGAGAGCTCTCTCAGCGGACATC 1786
Db 1779 CCACTCCCTACACCCCGCTTCTGAGAGCTCTCTCAGCGGACATC 1824

RESULT 2
AK033114
LOCUS
DEFINITION
Mus musculus 15 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:8030433C21 product:scavenger receptor class
B1, full insert sequence.
ACCESSION
AK033114
VERSION
AK033114.1 GI:26328836
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2 10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
PUBMED
11042159
REFERENCE
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AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, Y., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Kashiwagi, K.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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11076861

PUBMED

4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
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AUTHORS

5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

6 (bases 1 to 2441)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

REFERENCE

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

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Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

FEATURES

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genomic survey sequence.
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VERSION AY412682.1 GI:39768647
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1364)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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VERSION			
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Hominidae; Homo.			
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AUTHORS			
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,			
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,			
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,			
Adams, M.D. and Cargill, M.			
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Inferring nonneutral evolution from human-chimp-mouse orthologous			
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JOURNAL			
Science 302 (5652), 1960-1963 (2003)			
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,			
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,			
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Adams, M.D. and Cargill, M.			
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Direct Submission			
JOURNAL			
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,			
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COMMENT			
This sequence was made by sequencing genomic exons and ordering			
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AY412681
LOCUS
DEFINITION
Pan troglodytes SCAR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY412681
VERSION
AY412681.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Pan.
REFERENCE
1 (bases 1 to 1364)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 1364)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1364
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1364
/gene="SCAR1"
/locus_tag="HCM4638"

ORIGIN
Query Match 45.9%; Score 821.4; DB 10; Length 1364;
Best Local Similarity 70.4%; Pred. NO. 4.3e-207;
Matches 960; Conservative 0; Mismatches 404; Indels 0; Gaps 0;
Qy 318 ATGTGGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACTTCTTCTGAGGTGGTCAAT 377
Db 1 ATGTGGAAGGAGATCCCTGTATCCCTTCTATCTCTCCGTCTACTTCTTTGAGGTCAATGAAC 60
Qy 378 CCCAGCAGATCTTAAGGGTGAAGACCAAGTGTGCGGGAGCGTGACCCCTATGTCTAC 437
Db 61 CCCAGCAGATCTTGAAGGGCGAAGACCGAGTGTGCGGGAGCGGGCCCTACGTGTAC 120
Qy 438 AGGGAATTCAGACATAAGGGCCCAACATCACCTTCAATGACAAATGATACGTGTCTTTGTG 497
Db 121 AGGAGTTTACGGCAAAAGCAACATCACCTTCAACAAACGACACCGGTGCTCTTCCCT 180
Qy 498 GAGCACCGCAGCTTCCATTTCCAGCCGGAAGAGTGTCCACCGCTCTGAGAGTGAATCAAT 557
Db 181 GAGTACCGCAGCTTCCAGTTTCCAGCTTCCAGTCCCAAGTCCCAAGCTCGAGAGCGACTACATC 240
Qy 558 ATACTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGATGAGAGCAAGTCTGACAGG 617
Db 241 GTCATGCCCAACATCTCTGGTCTTGGGTGCGCGGTGATGATGGAGAATAAGCCCATGACC 300
Qy 618 CTGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGCGAGCGTCTTTATGACCGA 677
Db 301 CTGAAGCTCATGACCTTGGGCAATTCACCACTTGGGCAAGCGTCTTTCATGAACCGC 360
Qy 678 ACAGTTGGTGAATCTCTGGGCTATGAGGATCCCTTCTGGAATTTTATCAACAATATC 737
Db 361 ACTGTGGTGAATCATGTGGGCTACAGGACCCCTTGTGAATCTCATCAACAGTAC 420
Qy 738 TTACAGACATGTTCCCAATCAAGGGCAAGTGTGGCTGTTTGTGAGATGAACAATCA 797
Db 421 TTTCCAGGCAATGTTCCCTTCAAGGCAAGTGTGGATTAATTTGTGAGCTCAACAATCC 480
Qy 798 GACTCTGGCTTCTACTGTGTTCAAGGGGCTCCAGAACTTCAGCAGATCCACCTGGTG 857
Db 481 GACTCTGGCTTCTACGGTGTTCACGGGGTCCAGAACTTCAGCAGATCCACCTGGTG 540
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Db 541 GACAAGTGAACGGGCTGAGCAAGTGTGACTTCTGGCAATTCAGTCAAGTCAATGATC 600
Qy 918 AATGGCACTTCCGGGAGATGTGGGCAACATTCATGACACCCAGTCTCTCGTGGAAATC 977
Db 601 AATGGAATCTTGGGCAAAATGTGGCCGCTTCTATGACTCTGAGTCTCTCGTGGAGTTC 660
Qy 978 TTCACTCCGAGAGCTCAGCTCTATGAGCTCACTACCTACCTGATGATCAGGGGTGTTGAA 1037
Db 661 TACAGCCGGAGGCTCCGCAATCATGAAGCTAATGTACAGGAGTCAAGGGGTGTTGAA 720
Qy 1038 GGCAATCCCACTTCTGCTTCCAGAGCCCTTAAACTTTGTTGCAATGGGTCTGTTTAC 1097
Db 721 GGCAATCCCACTTCTGCTTCCAGAGCCCTTAAACTTTGTTGCAATGGGTCTGTTTAC 780
Qy 1098 CCACCAATGAAGTGTCTGCGGCTTGAATTCGGCAATTCAGAAATGTCAGCACTTGC 1157
Db 781 CCACCAATGAAGTGTCTGCGGCTTGAATTCGGCAATTCAGAAATGTCAGCACTTGC 840
Qy 1158 AGGTTTGTGACCCGCTTCTGCTCAACCTTCTACATGATGAGACCTTGTGCTA 1217
Db 841 AGGTTTGTGACCCGCTTCTGCTCAACCTTCTACATGATGAGACCTTGTGCTA 900
Qy 1218 TCAGAAGCCGTTCTGGGTCTGAAACCTTGACCCAGGAGGAGTCTTTGTTCTTGCATC 1277
Db 901 GCAGAAGGGGTGATGCGCTTGACCTTAAACAGAGAGGCACTCTTGTCTTCTGGACATC 960
Qy 1278 CATCCGCTCACTGGGATCCCATGAATGTTCTGTGAAGTGTGAGATGAAGCTCTTACATC 1337
Db 961 CACCCGCTCAAGGAAATCCCATGAATGTTCTGTGAAGTGTGAGATGAAGCTCTTACATC 1020
Qy 1338 AAAGCTGTCAAGGCAATGGGCAACAGGAGAGATGAGCCGCTGCTCCCAATGCTG 1397
Db 1021 AAATCTGTGAGGCAATGGGCAACAGGAGAGATGAGCCGCTGCTCCCAATGCTG 1080
Qy 1398 TGGTTTGACGAGAGCGGTGCTTGGGGGCGAGCCCTGAAACGTTTCTACACGAGCTG 1457
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Qy 438 AGGGAATTCACACATAAGGCCAACATCACCTTCAATGACATGATGATCTGTGCTCTTTG 497
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Qy 498 GAGCACCGCAGCCTCCATTTCCAGCCGAGACAGTCCCAAGGCTCTGAGAGTACATCATT 557
Db 181 GAGTACCGCAGCCTCCAGTTCAGGCTCCAGTCCCAAGTCCCAAGGCTCGGAGAGGACTATC 240
Qy 558 ATACTGCTCAACATTTCTGGTCTTGGGGGGCGCAGTAAATGATGAGAGCAAGTCTGCGAGC 617
Db 241 GTCATGCCCAACATCTGGTCTTGGGTGCGCGGTGATGATGAGAGATAAGCCCATGACC 300
Qy 618 CTGAAGCTGATGATGACCTTGGGGCTGGCCAGCTTGGGCCAGCGTGCCTTTATGAACCGA 677
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Qy 678 ACAGTGTGTGATGATCTGTGGGCTATGAGGATCCCTTCGTGAAATTTATCAACAATATC 737
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Qy 738 TTACGACAGATGTTCCCATCAAGGCGCAAGTTTCGGCTGTTTGTGAGATGAACAACTCA 797
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Qy 798 GACTCTGGGCTTTCACTGTGTTTCAAGGCGTCCAGAACTTTCAGAAAGATCCACCTGGTG 857
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Qy 858 GACAGATGGAATGGCTCAGCAAGGTCAACTACTGGCATTCAGAGCAGTGAACATGATC 917
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Db 601 AATGGAATCTTGGGCAATGTGGCGCTTTCATGACTCTGAGTCTCTGCTGAGTTC 660
Qy 978 TTCAGTCCGGAAGCCTGAGGCTTATGAAGCTCACCTACCATGATTCAGGGGTGTTTGA 1037
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Qy 1038 GGCATCCCACCTATGCTTCACAGCCCTTAAACTTGTGTCATGGTCTGTTTAC 1097
Db 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
Qy 1098 CCACCAATGAAGGTTTCTGCCCGTCTTGAATCCGCGCATTCACAAATGTCAGCACTTC 1157
Db 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840
Qy 1158 AGGTTTGTGACCCCTGTTTCTGTCAACCCCTCACTTCTCAATGACAGACCCCTGTGCTA 1217
Db 841 NNNNNNGTGCCTTGTCTCTCCATCTCTCACTTCTCAACGCGCGACCGGTTCTG 900
Qy 1218 TCAGAAGCGTTCTGGGTCTGAACCTTGACCCAGGAGGATCTTTTGTCTCTTGAATC 1277
Db 901 GCAGAAGCGGTGACTGGGCTGCACCCCTAAACCCAGGAGGACACACTCTTGTCTCTGACATC 960
Qy 1278 CATCCGCTGACTGGATCCCATCAACTGTTCTGTGAGTTCAGATGAAGCTCTACATC 1337
Db 961 CACCGGTGACGGGAATCCCATGAACTGCTGTGAACTGACGCTGAGCCTCTACATG 1020
Qy 1338 AAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCGCTGCTTCCCAATTCCTG 1397
Db 1021 AATCTGTGACGAGCATTTGACAAATCTGGGAGATGATGAGCTGTGTCTCTGCGCTGCTC 1080
Qy 1398 TGGTTTGAAGAGCGGTGTCATGCGGCGGAGCCCTTGAAACAGCTTCTACACGAGCTG 1457
Db 1081 TGGTTTGAAGAGCGGCGGTCATGAGGCGGAGACTCTTCAACATTTCTACACCGAGCTG 1140
Qy 1458 GTGCTGATGCCCAAGTACTTCACTATGTGAGTATGCTGTCTGCGGCTGGGGGCTC 1517
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Qy 1518 CTGCTGCTGTGCGCGTCACTACAGTTCGCGAGCCAGGAGAAATGCTTTTATTTGG 1577
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Qy 1578 AGTGGTAGTAAAGAGGCTCGCAGGATAAGGAGGCCATTTCAGGCTACTCTGAGTCTCTG 1637
Db 1261 AGTGGTAGTAAAGAGGCTCAAGAGATAGGAGGCCATTTCAGGCTACTCTGAGTCTCTG 1320
Qy 1638 ATGTCAACAGCTGCCAAGGCGACGGTCTGCAAGAAGCCAAAGCT 1681
Db 1321 ATGACATCAGCTCCCAAGGCGCTCTGTGCTGCGAGGAGCAAAACT 1364

RESULT 9
BU517714 902 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCY 10165932 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6515330 5', mRNA_sequence.
BU517714
BU517714.1 GI:22825240
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 902)
AUTHORS
NIH-MGC http://mgc.ncl.nih.gov/
TITLES
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@b-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14092 row: b column: 03
High quality sequence stop: 700.
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Location/Qualifiers
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/clone="IMAGE:6515330"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 38.1%; Score 681.2; DB 5; Length 902;
Best Local Similarity 87.3%; Pred. No. 8.5e-170;
Matches 757; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

Qy 525 GACAGTCCACGGCTCTGAGAGTGAATATATGCTTACTGCTTCTGCTTCTGGG 584
Db 1 GACAAGTGGATGGCTCAGAGAGTGAATATGCTTACTGCTTAACTCTTGGTCTGGG 60
Qy 585 GCGCGAGTAAATGATGAGAGCAAGTCTGACAGGCTGAAGCTGATGATGACCTTGGGCTG 644
Db 61 GGCTCGATTTGATGAGAGCAAGCTGTGAGCTGAAGCTGATGATGACCTTGGGCTG 120
Qy 645 GCACCTTGGGCGAGGCTGCTTTATGAACCCAGTGTGGTGAAGTCTGTGGGCTAT 704
Db 121 GTCACATGGGCGAGGCTGCTTTTATGAACCCAGTGTGGTGAAGTCTGTGGGCTAT 180
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Db      661  TCTGCAACTCGCAGCAGGAGAAATCTTTT--GTTTGGAGTGGTAGTAAAGGGCT 718
Qy      1597  GCAGGATAAGAGGCCATTTCAGGCTACTCTGAGTCTCTGATGTCACCAAGTCGCAAGG 1656
Db      719  CCCAGGATAAGAGGCCATTTCAGGCTACTCTGAGTCTCTGATGTCACCAAGTCGCAAGG 778
Qy      1657  GCAGGCTGCTCAAGAACCCAGCTGTAGGTGTCCTCAAGACACACAGAGCCGCCCAA-- 1714
Db      779  GCAGGCTGCTCAAGAACCCAGCTGTAGGTGTCCTCAAGACACACAGAGCCGCCCAA 838
Qy      1715  CCTGATAGTCTGTCAGACACAGCCATCCAGCCCTCAGACCC 1755
Db      839  CTGATTAGTCTGTCAGACACAGCCATCCAGCTCTCAAGGCC 879

RESULT 11
BM553238 1088 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6572721 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5467120
DEFINITION 5', mRNA sequence.
ACCESSION BM553238
VERSION BM553238.1 GI:18791793
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo
1 (bases 1 to 1088)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1968 row: j column: 17
High quality sequence stop: 698.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5467120"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 37.9%; Score 677.6; DB 3; Length 1088;
Best Local Similarity 78.5%; Pred. No. 8.2e-169;
Matches 849; Conservative 0; Mismatches 229; Indels 4; Gaps 3;

Qy      330  ATCCCTGTACCTCTTACTGTGCGTCTACTTCTTCGAGGTGGTCAATCCAGCGAGATC 389
Db      1 ATCCCTATCCCTCTTACTTCTCGTCTACTTCTTTGACGTCATGAACCCAGCGAGATC 60
Qy      390  CTAAGGGTGAGAGCCAGTAGTGGCGGAGGTGACCCCTATGTCACAGGGAATTGAGA 449

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RESULT 12
B0917716

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 35.7%; Score 639; DB 2; Length 907;
Best Local Similarity 84.4%; Pred. No. 1.5e-158;
Matches 754; Conservative 0; Mismatches 135; Indels 4; Gaps 3;
Qy 804 GGGCTTCTACTGTGTTTCACGGGCGTCCAGAACTTCAGCAAGATCCACCTGGTGACAGA 863
Db 1 GGGGTCTTCTACTGTCTTTCACGGGCGTCCAGAACTTCAGCAAGATCCACCTGGTGACAAA 60
Qy 864 TGGATGGCTCAGCAAGGTCACTACTGCGATTCAGAGCATGCAATCATCAATGCGC 923
Db 61 TGGACGGACTCAGCAAGATCGATTATGGCAATTCAGAGCATGTAACATGATCAATGCGG 120
Qy 924 ACTTCCGGGAGATGTGGGCAACCAATTCATGACACCCAGTCTCGCTGGAAATTTCTAGT 983
Db 121 ACTTCCGGGAGATGTGGGCAACCAATTCATGACACCCAGTCTCGCTGGAAATTTCTAGC 180
Qy 984 CCGAAGCTTCAGGTCTATGAAGCTCACTTACATGATTCAGGGGTGTTTGAAGGCATC 1043
Db 181 CCGGAGGCATCGAGTCCATGAAGCTGACCTTACAAAGATCAAGGGTGTGTTGAAGGCAT 240
Qy 1044 CCGACCTATCGCTTCAGAGCCCTTAAACTTTGTTGGCAATGGTCTGTTTACCCACCC 1103
Db 241 CCGACGTATCGCTTCAGGGCCCGGATACCTCTGTTGGCAACGGGTCCGTCTACCCACCC 300
Qy 1104 AATGAAGTCTTCTCGGCTGCTTGAATCCGGCATTCAGAAATGTCAGCACTTGCAGGTTT 1163
Db 301 AACGAAGCTTCTCGGCTGCTTGAATCCGGCATTCAGAAATGTCAGCACTTGCAGGTTT 360
Qy 1164 GGTGACCCCTGTTTCTGTCAACACCTCACTTCAATGATGAGACCCCTGTGCTATCAGAA 1223
Db 361 GGTGCGCTGTTTCTGTCAACACCTCACTTCAATGATGAGACCCCTGTGCTATCAGAA 420
Qy 1224 GCCGTTCTGGTCTGAACCTTGACCAAGGAGCATTTTGTGCTTGAATCATCCATCCG 1283
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Db 481 GTCACTGGATCCCATGAATGTTGTTGAAGTTGCAATGAGCTTCAATCAATCT 540
Qy 1344 GTCAAGGCGCATTTGGGCAACAGGGAAGATCGAGCCGCTGCTCCATGCTGTGTTT 1403
Db 541 GTCAAGGCGCATTTGGGCAACAGGGAAGATCGAGCCGCTGCTCCATGCTGTGTTT 600
Qy 1404 GAGCAGCGGTGCCATGGGCGGAGCCCTGAAACAGTTCATACAGCAGCTGGTGTG 1463
Db 601 GAAACAGCGGAGCAATGGGTGGCAAGCCCTGAGCAGCTTCTACAGCAGCTGGTGTG 660
Qy 1464 ATG-CCCCAGGTACTTCAGTATGTCAGTATGTCGTGCTGGGCTGGGCGGCTCCTGCT 1522
Db 661 ATGCCCCAGGTCTTCTACTAGCGGAGTATGTCGTGCTGGGCTGGAGGCTCCTGTT 720
Qy 1523 GCTGGTCCCTCATCTACCAAGTTGCGCAGCAGGAGAAATGCTTTTATTTGGAGTGG 1582
Db 721 TGCTGGTCCCATCT- GCACTGGCAGCAGGAGAAATGCTTTTGGTAGAGTGG 779
Qy 1583 TA--GTAAAAAGGCTCGCAGATAAGAGGCCATTCAGGCCCTACTCTGAGTCTCTGATG 1640
Db 780 TACGTGAAGAAAGGCTCCAGGATAGCAGGCCATTCAGGCCCTACTCTGAGTCTCTGTTG 839
Qy 1641 TCACAGCTGCGAAGGCGAGCTGTCAGAAAGCCAGCTGTAGGTCCCAA 1693
Db 840 TCCAGTTGCCAAGGGGCGGCTGGTCCAGAAAGCCAGGTATAGGGGCTGAA 892

RESULT 14

BQ877329 968 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT_8074145 NIH_MGC_102 Homo sapiens cdna clone IMAGE:6087067
DEFINITION 5', mRNA sequence.

ACCESSION
VERSION BQ877329.1 GI:22269337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 968)
TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov

Tissue Procurement: ATCC

cdna Library Preparation: Rubin Laboratory
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2323 row: a column: 20

High quality sequence stop: 728.

Location/Qualifiers

1. 968

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/clone="IMAGE:6087067"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 102"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cdna made by oligo-dt priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCAGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.9%; Score 624.8; DB 5; Length 968;
Best Local Similarity 79.0%; Pred. No. 9.2e-155;
Matches 743; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 496 TGGAGCACCAGCCTTCATTTCCAGCGGACAGGTCCACGGCTTCAGAGTCACTACA 555

Db 4 TCGAGTACCGCACCCTTCAGTTCAGCCCTCCCAAGTCCACGGCTCGGAGCGACTACA 63

Qy 556 TTATCTGCTTAACATTTCTGCTTTGGGGGCGCAGTAATGATGGAGCAAGTCTGCAG 615

Db 64 TCGTATGCCCAACATCTCTGCTTTGGGTGCGGGGTGATGATGGAGAAATAGCCCATGA 123

Qy 616 GCCTGAAGCTGATGATGACCTTGGGGCTGGCCACCTTTGGGCCAGCGTSCCTTTATGAACC 675

Db 124 CCCTGAAGCTCATGATGACCTTGGCATTCACACCTCCGCGAAGCGTCTTCATGAACC 183

Qy 676 GAACAGTTGTGTGATCTCTGTGGGGCTATGAGATCCCTTCGTGAATTTATCAACAAAT 735

Db 184 GCATGTGGGTGATCATGTGGGGCTTACAAGGACCCCTTTGTAATCTCATCAACAAAT 243

Qy 736 ACTTACCAGACATGTTCCCATCAAGGGCAAGTTCCGCCCTGTTTGTGAGATGAACAACT 795

Db 244 ACTTTCAGGCATGTTCCCTTCAAGGACAAAGTTCCGATTTATTTGCTGAGCTCAACAACT 303

Qy 796 CAGACTCTGGGCTCTTCACTGTGTTCAAGGGCGTCCAGAACTTCAGCAAGATCCACCTCG 855

Db 304 CCGACTCTGGGCTCTTCAAGGGCGTCCAGAACTTCAGCAAGATCCACCTCG 363

Qy 856 TGGACAGATGGATGGGCTCAGCAAGTCAACTATCTGGCATTTCAAGAGTGCAGCAATGA 915

Db 364 TGGACAGTGGAAACGGGCTGAGCAAGGTTGACTTCTGGCATTCGATTCAGTGCAGCAATGA 423

Search completed: February 24, 2006, 02:49:14
Job time : 7298.62 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 18:01:48 ; Search time 308.759 Seconds
(without alignments)
10293.724 Million cell updates/sec

Title: US-08-765-108-3
Perfect score: 1788
Sequence: 1 GCCACTGACGGCTACTGC.....CTCTCAGCGGACAGTCGC 1788

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1788	100.0	1788	2	US-08-559-505-1
2	1788	100.0	1788	2	US-08-749-907-1
3	1788	100.0	1788	3	US-09-241-581B-3
4	1788	100.0	1788	3	US-08-265-428-3
5	1788	100.0	1788	3	US-09-385-799-1
6	1788	100.0	1788	6	PCT-US95-07721-3
7	1786	99.9	1825	3	US-08-890-980-3
8	1786	99.9	1825	3	US-08-890-979-3
9	1786	99.9	1825	3	US-09-032-894-3
10	1786	99.9	1825	3	US-09-031-626-3
11	1369.8	76.6	1785	2	US-08-559-505-3
12	1369.8	76.6	1785	2	US-08-749-907-3
13	1369.8	76.6	1785	3	US-09-241-581B-7
14	1369.8	76.6	1785	3	US-09-385-799-3
15	1369.8	76.6	1785	6	PCT-US95-07721-7
16	1139.4	63.7	2630	2	US-08-890-980-1
17	1139.4	63.7	2630	3	US-08-890-979-1
18	1139.4	63.7	2630	3	US-09-032-894-1
19	1139.4	63.7	2630	3	US-09-031-626-1
20	1136.2	63.5	2566	3	US-09-270-542-124
21	1136.2	63.5	2566	3	US-09-054-272-58
22	1136.2	63.5	2566	3	US-10-024-396-3
23	971	54.3	2595	3	US-09-949-016-2296
24	285	15.9	719	3	US-10-024-396-11

25 193.2 10.8 465 3 US-09-949-016-2027 Sequence 2027, Ap
26 189 10.6 485 3 US-10-024-396-12 Sequence 12, Appl
27 132.6 7.4 397 3 US-09-513-999C-2451 Sequence 2451, Ap
28 131.8 7.4 41322 3 US-10-024-396-13 Sequence 13, Appl
29 131.8 7.4 90472 3 US-09-949-016-14038 Sequence 14038, A
30 128.6 7.2 481 2 US-08-890-980-11 Sequence 11, Appl
31 128.6 7.2 481 3 US-08-890-979-11 Sequence 11, Appl
32 128.6 7.2 481 3 US-09-032-894-11 Sequence 11, Appl
33 128.6 7.2 481 3 US-09-031-626-11 Sequence 8, Appl
34 123 6.9 526 2 US-08-890-980-8 Sequence 8, Appl
35 123 6.9 526 3 US-08-890-979-8 Sequence 8, Appl
36 123 6.9 526 3 US-09-032-894-8 Sequence 8, Appl
37 123 6.9 526 3 US-09-031-626-8 Sequence 8, Appl
38 117.6 6.6 1002 2 US-08-890-980-5 Sequence 5, Appl
39 117.6 6.6 1002 3 US-08-890-979-5 Sequence 5, Appl
40 117.6 6.6 1002 3 US-09-032-894-5 Sequence 5, Appl
41 117.6 6.6 1002 3 US-09-031-626-5 Sequence 5, Appl
42 117 6.5 479 2 US-08-890-980-6 Sequence 6, Appl
43 117 6.5 479 3 US-08-890-979-6 Sequence 6, Appl
44 117 6.5 479 3 US-09-032-894-6 Sequence 6, Appl
45 117 6.5 479 3 US-09-031-626-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-559-505-1
; Sequence 1, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT1150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683
; OTHER INFORMATION: encode the amino acid sequence for the Hamster Scavenger Recept

Db 1201 ATGACACCTGTGTATCAGAGCGGCTTGTGGGTCTGAAACCTGACCCAAAGGGAGCAAT 1260
Qy 1261 CTTTGTCTCTTGACATCCATCCGCTCACTGGGATCCCCCATGAATCTTCTGTGAAGTTGC 1320
Db 1261 CTTTGTCTCTTGACATCCATCCGCTCACTGGGATCCCCCATGAATCTTCTGTGAAGTTGC 1320
Qy 1321 AGATAAGCTCTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCCG 1380
Db 1321 AGATAAGCTCTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCCCG 1380
Qy 1381 TGGTCTCTCCCATTTGCTGTGTTTGTAGCAGAGCGGTGCCATGGGCGGAGCCCTGGAACA 1440
Db 1381 TGGTCTCTCCCATTTGCTGTGTTTGTAGCAGAGCGGTGCCATGGGCGGAGCCCTGGAACA 1440
Qy 1441 CGTTCTACACGAGCTGTGTCTGTATGCCCCCAGGTACTTTCAGTATGTGCAATGTGCTTGC 1500
Db 1441 CGTTCTACACGAGCTGTGTCTGTATGCCCCCAGGTACTTTCAGTATGTGCAATGTGCTTGC 1500
Qy 1501 TGGGGCTGGGGGGCTCTCTGTCTGTGTGGTGGCCGTCATCTACAGTTGGCGCAGCAGAGA 1560
Db 1501 TGGGGCTGGGGGGCTCTCTGTCTGTGTGGTGGCCGTCATCTACAGTTGGCGCAGCAGAGA 1560
Qy 1561 AATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGATAGAGGSCCATTCAGG 1620
Db 1561 AATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGATAGAGGSCCATTCAGG 1620
Qy 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCAAGGGGCAACGGTGTGCAAGACCAAGC 1680
Db 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCAAGGGGCAACGGTGTGCAAGACCAAGC 1680
Qy 1681 TGTAGGCTGCCAAGACACACAGAGCCCCCAACCTGATAGCTTGTGTGAGCAGCCAT 1740
Db 1681 TGTAGGCTGCCAAGACACACAGAGCCCCCAACCTGATAGCTTGTGTGAGCAGCCAT 1740
Qy 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTGAGGACTCTCTCAGGGGACAGTCGC 1788
Db 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTTGGAGTCTCTCAGGGGACAGTCGC 1788

RESULT 4

US-08-265-428-3
; Sequence 3, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683 encode the amino
US-08-265-428-3

Query Match 100.0%; Score 1788; DB 3; Length 1788;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACCTGCAGGGCTACTGCTCCGGCCACTGCTGAGACTCACCTTGTGTAAGCTG 60
Db 1 GCCACCTGCAGGGCTACTGCTCCGGCCACTGCTGAGACTCACCTTGTGTAAGCTG 60
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Db 61 AGCTCTCGGCTTCTGTCTATCTCTGTGGCTCTGTGCTCTGTGCTCTCAATC 120
Qy 121 CTTGAGCCCCCGAGCCCCGGGCCGCAACACGCGACATGCGCGCAGCGCGCGCT 180
Db 121 CTTGAGCCCCCGAGCCCCGGGCCGCAACACGCGACATGCGCGCAGCGCGCGCT 180
Qy 181 GGTGGGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT 240
Db 181 GGTGGGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT 240
Qy 241 TCCTCGGTGATGCTCTGCTCATCAAAACAGCAGGTACTGGAAGATGTCGCGATAGACCCA 300
Db 241 TCCTCGGTGATGCTCTGCTCATCAAAACAGCAGGTACTGGAAGATGTCGCGATAGACCCA 300
Qy 301 GCAGCTGTCTCTTTGCAATGTGGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
Db 301 GCAGCTGTCTCTTTGCAATGTGGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
Qy 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGTGAGAACCCAGTATGCGGAGC 420
Db 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGTGAGAACCCAGTATGCGGAGC 420
Qy 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCCACATCACCTTCAATGACAAATG 480
Db 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCCACATCACCTTCAATGACAAATG 480
Qy 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCCAACGGCT 540
Db 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCCAACGGCT 540
Qy 541 CTGAGAGTACTACATTAATCTGCTTAACTTCTGCTTTGGGGGGCGCAATGATG 600
Db 541 CTGAGAGTACTACATTAATCTGCTTAACTTCTGCTTTGGGGGGCGCAATGATG 600
Qy 601 AGAGCAAGTCTGAGGCTCAAGCTGATGATGCTTGGGGCTGGCCACCTTGGGGCAGC 660
Db 601 AGAGCAAGTCTGAGGCTCAAGCTGATGATGCTTGGGGCTGGCCACCTTGGGGCAGC 660
Qy 661 GTGCTTTTATGAACCGAAACAGATTTGGTGGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Db 661 GTGCTTTTATGAACCGAAACAGATTTGGTGGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Qy 721 ATTTTATCAAAATATCTTACAGAGATGTTCCCATCAAGGGCAAGTTCGGCTGTTT 780
Db 721 ATTTTATCAAAATATCTTACAGAGATGTTCCCATCAAGGGCAAGTTCGGCTGTTT 780
Qy 781 TTGAGATGACAACTCAGACTCTGGGCTCTTCACTGTGTTTCAAGGGGCTCCAGACTTCA 840
Db 781 TTGAGATGACAACTCAGACTCTGGGCTCTTCACTGTGTTTCAAGGGGCTCCAGACTTCA 840
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Qy 901 AGCAGTGCACATGATCAATGGCACTTCGGGCGAGATGGGGACCACTTATGACACACCC 960
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Qy 961 AGTCCTCGCTGGGAATCTTTCAGTCCGGAAGCTGCAGGTCTATGAAGCTCACCTACCATG 1020
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Db 1021 ATTACAGGGGTGTTGAAGGCATCCCACTTATCGCTTTCACAGCCCTTAAACTTTGTTG 1080
Qy 1081 CCAATGGGTCTGTTTACCAACCCCAATGAAGGTTTCTGCGGTGCTTGAATCCGGCATTC 1140
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Qy 1141 AAAATGTCAGCACTTGAGGTTTGGTGACCCCTGTTTCTGTCACACCTTCACTTCTACA 1200
Db 1141 AAAATGTCAGCACTTGAGGTTTGGTGACCCCTGTTTCTGTCACACCTTCACTTCTACA 1200
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Db 1321 AGATAAGCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGAAGATCGAGCCCG 1380
Qy 1381 TGGTCTCTCCATCTGTTGTTGAGCAGAGCGGTGCTGAGGGCGGAGCCCTGAAACA 1440
Db 1381 TGGTCTCTCCATCTGTTGTTGAGCAGAGCGGTGCTGAGGGCGGAGCCCTGAAACA 1440
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RESULT 5

US-09-385-799-1

; Sequence 1, Application US/09385799

; Patent No. 6962688

; GENERAL INFORMATION:

; APPLICANT: Money Krieger, Attilio Rigotti, and Karen Kozarsky

; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

```
ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,799
FILING DATE: 30-Aug-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,907
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 156..1683
OTHER INFORMATION: /function= "Nucleotides 156 through 1683
encode the amino acid sequence for the Hamster Scavenger Receptor Class
B-1."
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-385-799-1
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Query Match 100.0%; Score 1788; DB 3; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACCTGCAGGGCTACTGCTGCTCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60
Db 1 GCCACCTGCAGGGCTACTGCTGCTCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60
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Db 61 AGCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCTTCTGTGCTGCTGCTGCTGCTGCT 120
Qy 121 CCTGAGCCCGGAGCCCGGCGGCACACCGGACATGGCGGACGCCGAGCGCGCGCT 180
Db 121 CCTGAGCCCGGAGCCCGGCGGCACACCGGACATGGCGGACGCCGAGCGCGCGCT 180
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Db 181 GGTGCGGCTGGGGCTGGGGCTGCTGTGGGCTGCTGTGCGCTGCTGTGCTGCTGCTGCTGCT 240
Qy 241 TCCTCGTGTGCTTCTGTCATCTGTCGCTCATCAAAACAGCAGGTACTGAAGATGTCGGATAGACCCCA 300
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Db 361 TCTTCGAGTGGTCAATCCAGCAGATCCTTAAGGGTGAAGCCAGTAGTGGGGAGC 420
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Db 421 GTGACCCCTATGTCTACAGGGAATTCAGACATAAGGCCAACATCACCTTTCAATGACAAATG 480
Qy 481 ATACTGTGTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCACGGCT 540
Db 481 ATACTGTGTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCACGGCT 540
Qy 541 CTGAGAGTGACTACATATATACCTGCTCAACATTTCTGTGCTTGGGGGGCGCAGTAATGATGG 600
Db 541 CTGAGAGTGACTACATATATACCTGCTCAACATTTCTGTGCTTGGGGGGCGCAGTAATGATGG 600
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Db 601 AGACCAAGTCTGACAGGCTGAAGCTGATGATGACCTTTGGGGCTGGCCACCTTTGGGGCCAGC 660
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Qy 721 ATTTTATCAACAAATACCTACAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTTG 780
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Qy 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGCGGACCATTCATGACACCC 960
Db 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGCGGACCATTCATGACACCC 960
Qy 961 AGTCCTCGCTGGAATCTTCACTCGGAAGCTCGAGTCTATGAAGTCACTACCTACCATTG 1020
Db 961 AGTCCTCGCTGGAATCTTCACTCGGAAGCTCGAGTCTATGAAGTCACTACCTACCATTG 1020
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Qy 1081 CCAATGGTCTGTTTACCCACCAATGAAGTCTTCTGCGCGTCTGAAATCCGGCATTC 1140
Db 1081 CCAATGGTCTGTTTACCCACCAATGAAGTCTTCTGCGCGTCTGAAATCCGGCATTC 1140
Qy 1141 AAAATGTCAGCACTTGCAAGTCTGAGTCCACCTGTTTCTGTACACCCCTCACTTCTACA 1200
Db 1141 AAAATGTCAGCACTTGCAAGTCTGAGTCCACCTGTTTCTGTACACCCCTCACTTCTACA 1200
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Db 1201 ATGCAAGCCCTGCTATCAGAACCTGTTGGGTCTGAACCCCTGACCCCAAGGAGCATTC 1260
Qy 1261 CTTTGTCTCTGACATCAATCCGGTCTACTGGATCCCATGAATCTGTTGTGAGTTGC 1320
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Qy 1321 AGATAAGCCTTACATCAAGCTCTCAAGGCAATGGGCAACAGCAAGATCGAGCCG 1380
Db 1321 AGATAAGCCTTACATCAAGCTCTCAAGGCAATGGGCAACAGCAAGATCGAGCCG 1380
Qy 1381 TGGTCTCTCCATCTGCTGTGTTTGAAGCAGAGCGGTGCGATGGGGGGCGAGCCCTGAACA 1440
Db 1381 TGGTCTCTCCATCTGCTGTGTTTGAAGCAGAGCGGTGCGATGGGGGGCGAGCCCTGAACA 1440
Qy 1441 CGTTCCTACAGCAGCTGGTGTGATGCCCAAGGTACTTCAAGTATGTCAGTATGTCGTCG 1500

Db 1441 CGTTCCTACAGCAGCTGGTGTGATGCCCGCAGGTACTTCAAGTATGTCAGTATGTCGTCG 1500
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Db 1501 TGGGGCTGGGGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGAGAGGCCATTCAGG 1620
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Db 1621 CCTACTCTGAGTCTCTGATGTCACAGTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
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Db 1681 TGAGGGTCCCAAGACACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1741 CGAGCCCTACACCCCGCTTCTTGAAGTCTCTCTGAGCGGACAGTCGC 1788
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RESULT 6

PCT-US95-07721-3
; Sequence 3, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Fabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through
; OTHER INFORMATION: 1683 encode the amino acid sequence for
; OTHER INFORMATION: the Hamster Scavenger Receptor Class
; OTHER INFORMATION: B-1."
PCT-US95-07721-3

Query Match

100.0%; Score 1788; DB 6; Length 1788;

RESULT 8

US-08-890-979-3
; Sequence 3, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 156..1682
US-08-890-979-3

Query Match 99.9%; Score 1786; DB 3; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCACCTGCAGGGCTACTGCTCGCGCCACTGCCTGAGACTCACCTTCTGGAACGTG	60
DB	1	GCACCTGCAGGGCTACTGCTCGCGCCACTGCCTGAGACTCACCTTCTGGAACGTG	60
QY	61	AGCCTCGGCTTCTGCTATCTCTGTGGCTCTGTGGCTTCTGTGCTGCCCTTCAGTC	120
DB	61	AGCCTCGGCTTCTGCTATCTCTGTGGCTCTGTGGCTTCTGTGCTGCCCTTCAGTC	120
QY	121	CCTGAGCCCCGAGCCCGGCGCGCACGCGGACATGGCGCGGAGCGCGCGCT	180
DB	121	CCTGAGCCCCGAGCCCGGCGCGCACGCGGACATGGCGCGGAGCGCGCGCT	180
QY	181	GGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT	240
DB	181	GGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT	240
QY	241	TCCTCGTGATGCCCTCGCTCATCAACAGCAGGTACTGAAGAATGTCGCGATAGACCCCA	300
DB	241	TCCTCGTGATGCCCTCGCTCATCAACAGCAGGTACTGAAGAATGTCGCGATAGACCCCA	300
QY	301	GCAGCTGTCTTGTGCAATGGAGAGATCCCTGTACCTTCTACTTGTCCGTCTACT	360
DB	301	GCAGCTGTCTTGTGCAATGGAGAGATCCCTGTACCTTCTACTTGTCCGTCTACT	360

QY	361	TCCTCGAGGTGTCATCCAGCGAGATCCTAAAGGGTGAGAGCCAGTAGTCGGGAGC	420
DB	361	TCCTCGAGGTGTCATCCAGCGAGATCCTAAAGGGTGAGAGCCAGTAGTCGGGAGC	420
QY	421	GTGACCCCTATGCTACAGGGAATTCAGACATAAGGCCAAACATCACCTTCAATGACAATG	480
DB	421	GTGACCCCTATGCTACAGGGAATTCAGACATAAGGCCAAACATCACCTTCAATGACAATG	480
QY	481	ATATCTGTCTCTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCACGGCT	540
DB	481	ATATCTGTCTCTTGTGGAGCACCGCAGCTCCATTTCCAGCCGGACAGGTCCACGGCT	540
QY	541	CTGAGAGTCACTACATTACTATCTGCTTGTGCTTGTGGGGCGCAGTAATGATGG	600
DB	541	CTGAGAGTCACTACATTACTATCTGCTTGTGCTTGTGGGGCGCAGTAATGATGG	600
QY	601	AGAGCAAGTCTGAGGCCCTGAAGCTGATGATGACCTTGGGGCTGGCCACTTGGGGCAGC	660
DB	601	AGAGCAAGTCTGAGGCCCTGAAGCTGATGATGACCTTGGGGCTGGCCACTTGGGGCAGC	660
QY	661	GTGCTCTTATGAACCGACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA	720
DB	661	GTGCTCTTATGAACCGACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA	720
QY	721	ATTTTATCAACAATACTTACAGACATGTTCCCATCAAGGGCAAGTTTCGGCTCTTTTG	780
DB	721	ATTTTATCAACAATACTTACAGACATGTTCCCATCAAGGGCAAGTTTCGGCTCTTTTG	780
QY	781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTCCAGAACTTCA	840
DB	781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTCCAGAACTTCA	840
QY	841	GCAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGCTCACTACTGCGATTCAG	900
DB	841	GCAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGCTCACTACTGCGATTCAG	900
QY	901	AGCAGTGCACATGATCAATGCGACTTCCGGGCGAGATGTGGGCAACCATTCATGACACCC	960
DB	901	AGCAGTGCACATGATCAATGCGACTTCCGGGCGAGATGTGGGCAACCATTCATGACACCC	960
QY	961	AGTCTCGCTGGAAATTCCTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTACATG	1020
DB	961	AGTCTCGCTGGAAATTCCTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTACATG	1020
QY	1021	ATTCAGGGGTGTTGAAGGCATCCCACTATCGCTTTCAGCCCTTAAACCTTTCTTTG	1080
DB	1021	ATTCAGGGGTGTTGAAGGCATCCCACTATCGCTTTCAGCCCTTAAACCTTTCTTTG	1080
QY	1081	CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTTGAATCCGGCATTC	1140
DB	1081	CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTTGAATCCGGCATTC	1140
QY	1141	AAAATGTACAGCTTGCAGGTTTGGTGCACCCCTGTTCTGTCAACCTTCATTTTACA	1200
DB	1141	AAAATGTACAGCTTGCAGGTTTGGTGCACCCCTGTTCTGTCAACCTTCATTTTACA	1200
QY	1201	ATGCAGACCTGTGCTATCAGAACCCGTTCTGGGCTGTAACCTTGACCCCAAGGAGCAT	1260
DB	1201	ATGCAGACCTGTGCTATCAGAACCCGTTCTGGGCTGTAACCTTGACCCCAAGGAGCAT	1260
QY	1261	CTTTGTTCTTGCATCTCCATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAGTTGC	1320
DB	1261	CTTTGTTCTTGCATCTCCATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAGTTGC	1320
QY	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCG	1380
DB	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCG	1380
QY	1381	TGCTCTCCATTCGTGTGTTGACAGAGCGGTGCCATGGGCGGAGCCCTCAACA	1440
DB	1381	TGCTCTCCATTCGTGTGTTGACAGAGCGGTGCCATGGGCGGAGCCCTCAACA	1440
QY	1441	CGTTCTACAGCGAGCTGGTGTGATGCCCGAGGTACTTTCAGTATGTGCAATGTGTGTGC	1500

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1501 TGGGGCTGGGCGGCTCTCTGCTGCTGGTGGTCCCGTCACTACCAAGTTGCGCAGCCAGGAGA 1560
1501 TGGGGCTGGGCGGCTCTCTGCTGCTGGTGGTCCCGTCACTACCAAGTTGCGCAGCCAGGAGA 1560
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1681 TGAGGGTCCCAAGACACACAGGAGCCCCCCCCAAGCTGATAGTCTGCTCAGACCAAGCCAT 1740
1681 TGAGGGTCCCAAGACACACAGGAGCCCCCCCCAAGCTGATAGTCTGCTCAGACCAAGCCAT 1740
1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC 1786
1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC 1786

RESULT 10
US-09-031-626-3
; Sequence 3, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031.626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)

US-09-031-626-3
Query Match 99.9%; Score 1786; DB 3; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGGCTACTGCTGCTCCGSCCACTGCTGAGACTCACCTGCTGGAAGCTG 60
DB 1 GCCACCTGCAGGGCTACTGCTGCTCCGSCCACTGCTGAGACTCACCTGCTGGAAGCTG 60
QY 61 AGCCTCGGCTTCTGCTATCTCTGTGGCTCTGTGCTTCTGTGCTGCTGCTGCTGCTGCTG 120
DB 61 AGCCTCGGCTTCTGCTATCTCTGTGGCTCTGTGCTTCTGTGCTGCTGCTGCTGCTGCTG 120
QY 121 CTTGAGCCCGGAGCCCGGCGGACACGCGGACATGGGCGGAGCGCGCGCT 180
DB 121 CTTGAGCCCGGAGCCCGGCGGCGGACACGCGGACATGGGCGGAGCGCGCGCT 180
QY 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240
DB 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240
QY 241 TCCTCGTATGATCCCTCGCTCATCAACAGCAGGTAATGTCCGATAGACCCCA 300

DB 241 TCCTCGTATGATCCCTCGCTCATCAACAGCAGGTAATGTCCGATAGACCCCA 300
QY 301 GCAGCCTGCTCTTTCGAATGTGGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGCTACT 360
DB 301 GCAGCCTGCTCTTTCGAATGTGGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGCTACT 360
QY 361 TCTTCAGGTGGTCAATCCAGCGAGATCCTTAAAGGCTGAGAAGCCAGTAGTGGGGAGC 420
DB 361 TCTTCAGGTGGTCAATCCAGCGAGATCCTTAAAGGCTGAGAAGCCAGTAGTGGGGAGC 420
QY 421 GTGGAGCCCTATGTCTACAGGGAATTCAGACATAAGGCCAAATCATCCTTCAATGACAATG 480
DB 421 GTGGAGCCCTATGTCTACAGGGAATTCAGACATAAGGCCAAATCATCCTTCAATGACAATG 480
QY 481 ATACTGTGTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAGTCCTCCAGCGCT 540
DB 481 ATACTGTGTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAGTCCTCCAGCGCT 540
QY 541 CTGAGAGTGACTACATTAATTAATCTGCTTAAATCTTGTCTTGGGGGCGCAGTAATGATGG 600
DB 541 CTGAGAGTGACTACATTAATTAATCTGCTTAAATCTTGTCTTGGGGGCGCAGTAATGATGG 600
QY 601 AGAGCAAGTCTGAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACTTGGGGCAGC 660
DB 601 AGAGCAAGTCTGAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACTTGGGGCAGC 660
QY 661 GTGCCCTTATGAACGAAACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
DB 661 GTGCCCTTATGAACGAAACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
QY 721 ATTTATCAACAAATTAATTAATCTGCTTAAAGGCTGGAAGTTCGGGCTGTTTG 780
DB 721 ATTTATCAACAAATTAATTAATCTGCTTAAAGGCTGGAAGTTCGGGCTGTTTG 780
QY 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTCAGGGGCTGCAAACTTCA 840
DB 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTCAGGGGCTGCAAACTTCA 840
QY 841 GCNAGATCCACCTGGTGGGACAGATGGAATGGGCTCAGCAAGTCACTACTGSCATTCAG 900
DB 841 GCNAGATCCACCTGGTGGGACAGATGGAATGGGCTCAGCAAGTCACTACTGSCATTCAG 900
QY 901 AGCAGTGCAACATGATCAATGGCCTTCCGGGCGAGATGTGGGCAACCATTCATGACACCCC 960
DB 901 AGCAGTGCAACATGATCAATGGCCTTCCGGGCGAGATGTGGGCAACCATTCATGACACCCC 960
QY 961 AGTCCTCGCTGGAAATTTCTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACATG 1020
DB 961 AGTCCTCGCTGGAAATTTCTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACATG 1020
QY 1021 ATTCAGGGGTGTTTGAAGGATCCCACTATCGCTTTCAGCGCCCTTAAACCTTTGTTTG 1080
DB 1021 ATTCAGGGGTGTTTGAAGGATCCCACTATCGCTTTCAGCGCCCTTAAACCTTTGTTTG 1080
QY 1081 CCAATGGGCTGTTTACCCCAATGAAGGTTTCTGCGCGCTGCTTGAATCCGGCATTC 1140
DB 1081 CCAATGGGCTGTTTACCCCAATGAAGGTTTCTGCGCGCTGCTTGAATCCGGCATTC 1140
QY 1141 AAAATGTACGACTTCAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200
DB 1141 AAAATGTACGACTTCAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200
QY 1201 ATGCAGACCTGTGCTATCAGAGCGGTTCTGGGCTGTAACCTGACCCCAAGGAGCAT 1260
DB 1201 ATGCAGACCTGTGCTATCAGAGCGGTTCTGGGCTGTAACCTGACCCCAAGGAGCAT 1260
QY 1261 CTTTGTCTTGTGACATCCATCCGCTCACTGGGATCCCAATGAAGTCTTCTGTGAAGTTC 1320
DB 1261 CTTTGTCTTGTGACATCCATCCGCTCACTGGGATCCCAATGAAGTCTTCTGTGAAGTTC 1320
QY 1321 AGATAAGCCTCTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGAAAGATCGAGCCCG 1380
DB 1321 AGATAAGCCTCTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGAAAGATCGAGCCCG 1380

305	AGTCCGGGAGCGTGGACCCCTATGTCTACAGGGAGTTCCAGACAAAGGTCACACATCACCTTT	364
470	CAATGACAAATGATACTGTGTCTTGTGTGGAGCACCGCAGCGCTCCATTTCCAGCGCGACAG	529
365	CAATGACAAAGACACCGTGTCTTGTGTGGAGACCGCAGCGCTCCATTTCCAGCGCTGACAA	424
530	GTCCCACGGCTCTGAGAGTGACTACATATTATCTGCCTTAACATTTCTGTCTTGGGGGGCGC	589
425	GTCGCATGGGCTCAGAGAGTGACTACATTGTACTGCTTAACATCTCTGGTCTCTGGGGGGCTC	484
590	AGTAAATGATGGAGAGCAAGTCTGCAGCGCTGMACTGATGATGACCTTTGGGGCTGGCCAC	649
485	GATATTGATGGAGAGCAAGCTGTGAGCTCTGAAGCTGATGATGACCTTTGGCGTGTGTCAC	544
650	CTTGGGCCAGCGTCCCTTTATGAAACCAAGTGTGTGAGATCTCTGTGGGGCTATGAGGA	709
545	CATGGGCCAGCGTCTTTTATGAACCCGACAGTTGGTGAGATCTGTGGGGCTATGACGA	604
710	TCCCTTCGTGTAATTTTATCAACAAATACTTACACGACATGTTCCCATCAAGGGCAAGTT	769
605	TCCCTTCGTGCAATTTCTCAACAGTACTCCACAGCATGCTTCCCATAAAGGGCAAAATT	664
770	CGGCGCTGTTTGTGAGATGAACTCAGACTCTGGGCTCTTCACTGTGTGTTACGGGCGT	829
665	TGGCGCTGTTTGTGGGATGAACAACTCGAAATCTTGGGGTCTTCACTGCTTTCACGGGCGT	724
830	CCAGAACTTTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA	889
725	CCAGAACTTTCAGCAGGATCCATCTGGTGGACAAATGGAAACGACTCAGCAAGATCGATTTA	784
890	CTGCAATTCAGAGCAGTGCAACATGATCAATGGCACTTCCGGGCAGAGTGTGGGCACCATT	949
785	TTGGCAATTCAGAGCAGTGTAACATGATCAATGGGACTTCCGGGCAGAGTGTGGGCACCCCTT	844
950	CATGACACCCAGTCTCGCTGGAAATCTTCAGTCCGGAAGCTGCAAGTCTATGAAGCT	1009
845	CATGACACCCGAATCTCGCTGGAAATCTTTCAGCCCGGAGGCATGCAAGTCCATGAAGCT	904
1010	CACCTACCATGATTCAGGGGTGTTGAAGGATCCCACTATCGCTTCACAGCCCTTAA	1069
905	GACCTACAAACGAATCAAGGGGTGTTGAAGGCAATTCACAGTATCGCTTCAGGGCCCCGA	964
1070	AACCTTTGTTGGCCAATGGGTCTGTTTACCACCCCAATGAAGGTTTCTGCCCCGTCTTGA	1129
965	TACTCTGTTTGGCCAAAGGTCGCTACCCACCCCAACGAAGGCTTCTGCCCATGCGGAGA	1024
1130	ATCCGGCAATCAAAATGTGACGACTTGGAGGTTTGGTGCAACCCCTGTTTCTGTCAACACC	1189
1025	GTCGTGGCAATTCAGAAATGTGACACCTCGCAGGTTTGGTGGCGCTCTGTTCTCTCCACCC	1084
1190	TCACTTCTACAAATCGAGACCCGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACCC	1249
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1250	AAGGGAGCAATCTTTGTTTCTTGAATCCATCCGGTCACTGGGATCCCCATGAACCTGTC	1309
1145	AAAGGAGCAATTCCTTTGTTCTTAGACATCCATCCGCTCACTGGGATCCCCATGAACCTGTC	1204
1310	TGTGAAGTTTGAGATAGACCTCTTACATAAAGCTGTGAAGGGCAATTTGGGCATAACAGGAA	1369
1205	TGTGAAGATGCACTGAGACCTCTTACATCAATCTGTCAAGGGCATCGGGCAAAACAGGAA	1264
1370	GATCGAGCCGTGTCTCTCCATTTGCTGTGTTTGAACAGAGCGGTGCCATTTGGCGCGGA	1429
1265	GATCGAGCCAGTGTCTTCCCGTTGCTGTGTTTGCATCGAGAGCGGAGCAATTTGGGTGGCAA	1324
1430	GCCCTCTGAACAGTTTCTACAGCAGCTGGTCTGATGCCCCAGGTACTTCAGTATGTGCA	1489
1325	GCCCTCTGAGCAGTTTCTACAGCAGCTGGTGTCTGATGCCCCAGGTTCTTCTACTACGGCA	1384
1490	GTATGTGCTGTGGGCTGGCGGCCTCTCTGCTGTGTGTCCTGTCCTTACCAAGTTGCG	1549
1385	GTATGTGCTGTGGGCTTGGAGGCTCTCTGTGCTGGTGCCATCATCTGCCAATCTGCG	1444

Qy	1550	CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGAGGGCTCGCAGGATAGGA	1609
Db	1445	CAGCCAGGAGAAATGCTTTTGTTTTGGAGTGTAGTAAAGAGGGCTCCCAGGATAGGA	1504
Qy	1610	GGCCATTACGGCCTACTCTGAGTCTCTGATGTCCACAGCTGCCAAGGGCACGTCGTGCA	1669
Db	1505	GGCCATTACGGCCTACTCTCTGAGTCCCTGATGTCCACAGCTGCCAAGGGCACGTCGTGCA	1564
Qy	1670	AGAACCCAAAGCTGTAGGGTCCCAAGACACACAGAGCCCCCCCCAACTGTGATAGCTTGGTC	1729
Db	1565	AGAACCCAAAGCTATAGGCTCTGTAGACACTAATAGCCCCCCTGATAGCTTGGTC	1624
Qy	1730	AGACAGCCCATCCAGGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC	1786
Db	1625	AGACAGCCCAACCACTCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC	1681

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Query Match	76.6%	Score 1369.8;	DB 3;	Length 1785;
Best Local Similarity	88.6%	Pred. No. 0;		
Matches 1485;	Conservative	0; Mismatches	192;	Indels 0;
Gaps 0;				

Query Match 76.6%; Score 1369.8; DB 3; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; G

SEQUENCE CHARACTERISTICS:

LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577 /Function = "Nucleotides 51 through 1577 encode the amino acid sequence for the murine Scavenger Receptor Class B1."
OTHER INFORMATION: 1577 encode the amino acid sequence for the murine Scavenger Receptor Class B1."

PCT-US95-07721-7

Query Match 76.6%; Score 1369.8; DB 6; Length 1785;

Best Local Similarity 88.6%; Pred. No. 0;

Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY	110	CCCTTCAGTCCCTGAGCCCGGAGCCCGGGCGGCACACGCGGACATGGCGGCGAGCGC	169
DB	5	CTCCTTCAGTCCCTGAGCCCGGAGCCCTTCGCGCACGCGGACATGGCGGCGAGCTC	64
QY	170	CAGGGCGCGCTGGTGGCGGTGGGGCTGGGCGTCTGGGGCTGCTGTGCGCTGTGCTCGG	229
DB	65	CAGGGCGCGCTGGTGGCGGTGGGGCTGGGCGCTGGGGCTGCTGTGCTGTGCTCGGCTCGG	124
QY	230	TGTGGTATGATCCTCGTGTATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCCG	289
DB	125	CGTTGTATGATCCTCATGTGTGCTCTCCCTCATCAAGCAGCAGGTGTCTCAAGAATGTCCG	184
QY	290	CATAGACCCAGCAGCCTGTCTTGGCAATGTGGAGGAGATCCCTGTACCTTCTACTTT	349
DB	185	CATAGACCCAGCAGCCTGTCTTGGGATGTGGAGGAGATCCCGGTCTCTTCTACTTT	244
QY	350	GTCCGTCTACTTTTCAGGTGGTCAATCCAGCAGGATCCTAAAGGGTGAGAAGCCAGT	409
DB	245	GTCTGTCTACTTTTCGAAGTGTCAACCAACAGAGGTCTCTCAACGCGCAGGAGCCAGT	304
QY	410	AGTGGGAGCGGTGGACCCCTATGCTACAGGGAAATTCAGACATAAGGCCAAATACCTTT	469
DB	305	AGTCCGGAGCGTGGACCCCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACCTT	364
QY	470	CAATGCAATGATGACTGTGCTTGTGGAGCAGCGAGCTCCATTTCCAGCGGACAG	529
DB	365	CAATGCAACAGACACCGTGTCTTGTGGAGAACCGGAGCTCCATTTCCAGGCTTGACAA	424
QY	530	GTCCACCGCTCTGAGAGTGACTACATTAATGCTTACCTTAACTTCTGTCTTGGGGGCGC	589
DB	425	GTCCGATGGCTCAGAGATGACTACATTTGCTTACCTTAACTTCTGTCTTGGGGGCGTC	484
QY	590	AGTAATGATGGAGAGCAAGTCTGAGGCTCTGAAGCTGATGATGACCTTGGGGCTGGCCAC	649
DB	485	GATATTGATGGAGCAAGCTGTGAGCCTGAAGCTGATGACCTTGGCGCTGGTTCAC	544
QY	650	CTTGGGCCAGGTGCTTTATGAACCGAACAGATTGGTGAGATCTGTGGGGCTATGAGGA	709
DB	545	CATGGGCCAGGTGCTTTATGAACCGCACAGATTGGTGAGATCTGTGGGGCTATGACGA	604
QY	710	TCCCTTCGTGAATTTTATCAACAAATCTTACCAGACATGTTCCCATCAAGGGCAAGTT	769
DB	605	TCCCTTCGTGAATTTTCTCAACAGCTACCTCCCGACATGCTTCCCATCAAGGGCAAGTT	664
QY	770	CGGCTGTGTTGTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGCGT	829
DB	665	TGGCTGTGTTGTGGGATGAACAACTCGAATTTCTGGGGCTTTCACCTGTCTTACGGGCGT	724
QY	830	CCAGAACTTCAGCAGATCCACCTGGTGGACAGATGGAAATGGGCTCAGCAAGTCAACTTA	889
DB	725	CCAGAAATTCAGCAGGATTCATCTGGTGGACAAATGGAAACGGACTCAGCAAGATCGATTA	784

QY	890	CTGGCATTCAGAGCAGTGCACATGATCAATGGCACTTCCGGGCGAGATGTGGGCAACATT	949
DB	785	TTGGCATTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGCGAGATGTGGGCAACCTT	844
QY	950	CATGACACCCAGTCTCTGCTGGAATTTCTAGTCCGGAAGCTGCAGTCTCTATGAAGCT	1009
DB	845	CATGACACCCGAATCCTGCTGGAATTTCTAGCCTGGAGGATGCAGTCTCATGAAGCT	904
QY	1010	CACCTACCATGATTCAGGGGTGTTTGAAGGCATCCCACTATCGCTTCACAGCCCTTAA	1069
DB	905	GACCTACAACGAATCAAGGGTGTTTGAAGGCATTTCCACGTATCGCTTCAGGCCCTCGA	964
QY	1070	AATCTTTGTTGCAATGGGTCTGTTTACCCCAATGAAGTTTCTGCCGCTGCTTGA	1129
DB	965	TACTCTGTTTGCACACGGGTCTGTTACCCCAACGAAGGCTTCTGCCCATGCCGAGA	1024
QY	1130	ATCCGGCATTTCAAAATGTGAGCCTGTGAGGTTTGGTGACCCCTGTGTTCTGTCAACCC	1189
DB	1025	GTCTGGCATTTCAAAATGTGAGCCTGTGAGGTTTGGTGACCCCTGTGTTCTCTCCACCC	1084
QY	1190	TCACCTTTACAATGACAGCCCTGTGCTATCAGAAGCGTCTCTGGGTCTGAACCTGACCC	1249
DB	1085	CCACITTTTACAACGCGACCCCTGTGTTGTGAGAAGCTGTTCTTGGTCTGAACCTTAAACC	1144
QY	1250	AAGGGAGCATTTCTTGTCTTGAACATCCATCCGCTCACTGGGATCCCATGAACCTGTTT	1309
DB	1145	AAGGGAGCATTTCTTGTCTTGAACATCCATCCGCTCACTGGGATCCCATGAACCTGTTT	1204
QY	1310	TGTGAAGTTGCAAGTAAGCTCTTAATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGAA	1369
DB	1205	TGTGAAGATGCAAGTGAAGCTCTTAATCAAAATCTGTCAAGGGCATTCGGGCAACAGGAA	1264
QY	1370	GATCAGACCCGTGCTCTCCATTTGCTGTGTTTGAAGAGAGCGGTGCCATGGGCGCGA	1429
DB	1265	GATCAGACCCGTGCTCTCCATTTGCTGTGTTTGAAGAGAGCGGTGCCATGGGCGCGA	1324
QY	1430	GCCCTTGAAACAGCTTCTACACGAGCTGTGCTGATGCCCCAGGTACTTTCAGTATGTGA	1489
DB	1325	GCCCTTGAGCAGCTTCTACACGAGCTGTGCTGATGCCCCAGGTACTTTCAGTATGTGA	1384
QY	1490	GTATGTGCTGTGGGCTGGGCGGCTCTCTGCTGTGTGTGCTGCTGCTATCTACAGTTGCG	1549
DB	1385	GTATGTGCTGTGGGCTGGGCGGCTCTCTGCTGTGTGTGCTGCTGCTATCTGCGCACTCG	1444
QY	1550	CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTTCGAGGATGAAGA	1609
DB	1445	CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTTCGAGGATGAAGA	1504
QY	1610	GGCCATTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAAGGTGCTGCA	1669
DB	1505	GGCCATTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAAGGTGCTGCA	1564
QY	1670	AGAGCCAAAGTGTAGGTTCCCAAGACACAGAGACCCCTCCCAACCTGATAGCTTGGTC	1729
DB	1565	AGAGCCAAAGTGTAGGTTCCCAAGACACATTAAGCCCTCCCAACCTGATAGCTTGGTC	1624
QY	1730	AGACAGGCTTCCAGCCCTTACACCCGCTTCTTGAAGTCTCTCTCAGCGGACAGTC	1786
DB	1625	AGACAGGCTTCCAGGCTTCTTGAAGTCTCTCTCAGCGGACAGTC	1681

Search completed: February 23, 2006, 18:13:43

Job time : 310.759 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1788	100.0	1788	3	US-09-148-012-1	Sequence 1, Appli
2	1788	100.0	1788	6	US-10-178-611-1	Sequence 1, Appli
3	1788	100.0	1788	6	US-10-164-863-1	Sequence 1, Appli
4	1788	100.0	1788	7	US-10-706-073-1	Sequence 1, Appli
5	1788	100.0	1788	9	US-10-933-037-1	Sequence 1, Appli
6	1786	99.9	1825	3	US-09-779-152-3	Sequence 3, Appli
7	1786	99.9	1825	5	US-10-023-610-3	Sequence 3, Appli
8	1786	99.9	1825	7	US-10-212-848-3	Sequence 3, Appli
9	1441.2	80.6	2496	7	US-10-322-281-564	Sequence 564, App
10	1413	79.0	2497	7	US-10-152-319A-1909	Sequence 1909, Ap
11	1369.8	76.6	1785	3	US-09-148-012-3	Sequence 3, Appli
12	1369.8	76.6	1785	6	US-10-178-611-3	Sequence 3, Appli
13	1369.8	76.6	1785	6	US-10-164-863-3	Sequence 3, Appli
14	1369.8	76.6	1785	7	US-10-706-073-3	Sequence 3, Appli
15	1369.8	76.6	1785	9	US-10-933-037-3	Sequence 3, Appli
16	1243.8	69.6	1607	3	US-09-882-948A-285	Sequence 285, App
17	1243.8	69.6	1607	8	US-10-807-114-285	Sequence 285, App
18	1139.4	63.7	2630	3	US-09-779-152-1	Sequence 1, Appli
19	1139.4	63.7	2630	5	US-10-023-610-1	Sequence 1, Appli
20	1139.4	63.7	2630	7	US-10-212-848-1	Sequence 1, Appli
21	1137.8	63.6	2558	7	US-10-276-774-1032	Sequence 1032, Ap
22	1136.2	63.5	2566	6	US-10-024-396-3	Sequence 3, Appli
23	1136.2	63.5	2566	7	US-10-648-593-90	Sequence 90, Appl

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 156..1683
OTHER INFORMATION: /function= "Nucleotides 156 through 1683
encode the amino acid sequence for the Hamster Scavenger Receptor Class
B-I."
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-178-611-1

Query Match 100.0%; Score 1788; DB 6; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCGAGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTGCTGGAAGCTG 60
DB 1 GCCACCTGCGAGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTGCTGGAAGCTG 60
QY 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CTTGAGCCCGCGAGCCCGGCGCCGACACGCGGACATGCGCGGAGCGCGCGCGCT 180
DB 121 CTTGAGCCCGCGAGCCCGGCGCCGACACGCGGACATGCGCGGAGCGCGCGCGCT 180
QY 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
DB 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
QY 241 TCCTCGTGATGCTCGCTCATCAAAACAGCAGGCTACTGAAGATGTCGGCATAGACCCCA 300
DB 241 TCCTCGTGATGCTCGCTCATCAAAACAGCAGGCTACTGAAGATGTCGGCATAGACCCCA 300
QY 301 GCAGCTGTCTCTTTGCAATGTGGAAGAGATCCCTGTACCTTCTACTGTGCGTCTACT 360
DB 301 GCAGCTGTCTCTTTGCAATGTGGAAGAGATCCCTGTACCTTCTACTGTGCGTCTACT 360
QY 361 TCTTCGAGGTGCTCAATCCCGAGGAGATCTTAAGGCTGAGACCCAGTAGTGGCGGAGC 420
DB 361 TCTTCGAGGTGCTCAATCCCGAGGAGATCTTAAGGCTGAGACCCAGTAGTGGCGGAGC 420
QY 421 GTGACCTATGCTACAGGGAATTCAGACATAGGCAACATCACCTTCAATGACAAATG 480
DB 421 GTGACCTATGCTACAGGGAATTCAGACATAGGCAACATCACCTTCAATGACAAATG 480
QY 481 ATACTGTGTCTTTGTGGAGCACCGCAGCTTCCATTTCCAGCGGACAGGTCCCAAGGCT 540
DB 481 ATACTGTGTCTTTGTGGAGCACCGCAGCTTCCATTTCCAGCGGACAGGTCCCAAGGCT 540
QY 541 CTGAGAGTACTATATCTGCTTAACATCTGCTTGGGCTGGGCTGGGCTGGGCTGGGCT 600
DB 541 CTGAGAGTACTATATCTGCTTAACATCTGCTTGGGCTGGGCTGGGCTGGGCTGGGCT 600
QY 601 AGAGCAAGTCTGAGGCTGAAGCTGATGATGACCTTTGGGCTGGGCTGGGCTGGGCT 660
DB 601 AGAGCAAGTCTGAGGCTGAAGCTGATGATGACCTTTGGGCTGGGCTGGGCTGGGCT 660
QY 661 GTGCTTTTATGAACCGAACAGTGTGGTGGAGATCTGTGGGCTATGAGGATCCCTTCG 720
DB 661 GTGCTTTTATGAACCGAACAGTGTGGTGGAGATCTGTGGGCTATGAGGATCCCTTCG 720
QY 721 ATTTTATCAACAAATACCTACAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTTTG 780
DB 721 ATTTTATCAACAAATACCTACAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTTTG 780
QY 781 TTGAGATGAACAACTCAGACTCTGGCTTCTCACTGTGTTACGGGCTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACTCAGACTCTGGCTTCTCACTGTGTTACGGGCTCCAGAACTTCA 840
QY 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG 900

RESULT 3

US-10-164-863-1

; Sequence 1, Application US/10164863

; Publication No. US20030232879A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Monty

; APPLICANT: Miettinen, Helena

; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY

; FILE REFERENCE: MIT 9094

841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGTCATTTCAG 900
QY
901 AGCAGTGCACATGATCAATGGCACTTCGGGGCAGATGTGGGCACCATTCATGACACCCC 960
DB
901 AGCAGTGCACATGATCAATGGCACTTCGGGGCAGATGTGGGCACCATTCATGACACCCC 960
QY
961 AGTCTCTGCTGGAAATTTCTTCAGTCCGGAAGCCTGCGAGGTCTATGAAGCTCACCTACCATG 1020
DB
961 AGTCTCTGCTGGAAATTTCTTCAGTCCGGAAGCCTGCGAGGTCTATGAAGCTCACCTACCATG 1020
QY
1021 ATTTCAGGGTGTGTTGAAGGATCCCACTATCGCTTCACAGCCCTTAAACCTTTGTTTG 1080
DB
1021 ATTTCAGGGTGTGTTGAAGGATCCCACTATCGCTTCACAGCCCTTAAACCTTTGTTTG 1080
QY
1081 CCAATGGGCTGTGTTTACCAACCAATGAAGTTCCTGCGGCTGCTTGAATCGGGCATTC 1140
DB
1081 CCAATGGGCTGTGTTTACCAACCAATGAAGTTCCTGCGGCTGCTTGAATCGGGCATTC 1140
QY
1141 AAAATGTGACACTTCGAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200
DB
1141 AAAATGTGACACTTCGAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200
QY
1201 ATGACAGCCCTGTGCTATCAGAAAGCCGTTCTGGGCTGTAACCCCTGACCCCAAGGAGCAT 1260
DB
1201 ATGACAGCCCTGTGCTATCAGAAAGCCGTTCTGGGCTGTAACCCCTGACCCCAAGGAGCAT 1260
QY
1261 CTTTGTCTTGTGACATCCATCCGCTCACTGGGATCCCAATGAAGTTCCTGTCTGCAAGTTGC 1320
DB
1261 CTTTGTCTTGTGACATCCATCCGCTCACTGGGATCCCAATGAAGTTCCTGTCTGCAAGTTGC 1320
QY
1321 AGATAAGCCCTTACATCAAAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
DB
1321 AGATAAGCCCTTACATCAAAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
QY
1381 TGTCTCTCCATTCGCTGTGTTGAGCAGAGCGGTGCCATGCGGCGGCGAGCCCTGGAACA 1440
DB
1381 TGTCTCTCCATTCGCTGTGTTGAGCAGAGCGGTGCCATGCGGCGGCGAGCCCTGGAACA 1440
QY
1441 CGTTCTACAGCAGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB
1441 CGTTCTACAGCAGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY
1501 TGGGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB
1501 TGGGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY
1561 AATGCTTTTATTTTGGAGTGTGTTAAAGGCTCGCAGGATAGAGGCGCATTCAGG 1620
DB
1561 AATGCTTTTATTTTGGAGTGTGTTAAAGGCTCGCAGGATAGAGGCGCATTCAGG 1620
QY
1621 CCTACTCTGAGTCTGATGTCACAGCTGCCAAGGCGCGGCTGTCAGAGAGCCAGC 1680
DB
1621 CCTACTCTGAGTCTGATGTCACAGCTGCCAAGGCGCGGCTGTCAGAGAGCCAGC 1680
QY
1681 TGTAGGCTCCAAAGACACACAGGAGCCCGCCCAACCTGATGCTTGTGTCAGACAGCAT 1740
DB
1681 TGTAGGCTCCAAAGACACACAGGAGCCCGCCCAACCTGATGCTTGTGTCAGACAGCAT 1740
QY
1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTCTCAGCGGACAGTCCG 1788
DB
1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTCTCAGCGGACAGTCCG 1788

; Sequence 1, Application US/10706073
; Publication No. US20040077526A1

GENERAL INFORMATION:

; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction

; FILE REFERENCE: MIT8299

; CURRENT APPLICATION NUMBER: US/10706,073

; PRIOR FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: 09/148,012

; PRIOR FILING DATE: 1998-10-04

; PRIOR APPLICATION NUMBER: 60/057,943

; PRIOR FILING DATE: 1997-09-05

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1788

; TYPE: DNA

; ORGANISM: Hamster

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (156)..(1683)

; OTHER INFORMATION: Encodes amino acid sequence for the Hamster

; OTHER INFORMATION: Scavenger Receptor Class B-1

US-10-706-073-1

Query Match 100.0%; Score 1788; DB 7; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCACCTGCGAGGCTACTGCTGCTCCGGCCACCTGCTGAGACTCACCTTGTGGAAGCTG 60
Db	1	GCACCTGCGAGGCTACTGCTGCTCCGGCCACCTGCTGAGACTCACCTTGTGGAAGCTG 60
Qy	61	AGCTCGGCTTCTGTCATCTCTGGGCTCTGTCGCTTCTGTCGCTCCCTTTCAGTC 120
Db	61	AGCTCGGCTTCTGTCATCTCTGGGCTCTGTCGCTTCTGTCGCTCCCTTTCAGTC 120
Qy	121	CCTGAGCCCGCGAGCCCGGCGCGCACACGCGGACATGGGCGGCGAGCGCGCGCGCT 180
Db	121	CCTGAGCCCGCGAGCCCGGCGCGCACACGCGGACATGGGCGGCGAGCGCGCGCGCT 180
Qy	181	GGGTGGCGGTGGGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTG 240
Db	181	GGGTGGCGGTGGGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTG 240
Qy	241	TCCTCGTGATGCTGCTGCTCATCAACAGCAGGCTGCTGAGAGATGTCGATAGACCCCA 300
Db	241	TCCTCGTGATGCTGCTGCTCATCAACAGCAGGCTGCTGAGAGATGTCGATAGACCCCA 300
Qy	301	GCAGCTGCTCTTGGCAATGGAGAGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
Db	301	GCAGCTGCTCTTGGCAATGGAGAGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
Qy	361	TCCTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAGAGCCAGTATGCGGAGC 420
Db	361	TCCTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAGAGCCAGTATGCGGAGC 420
Qy	421	GTGACCCCTATGCTACAGGGAATTCAGACATAGAGCCCAATCACCTTCAATGACAAATG 480
Db	421	GTGACCCCTATGCTACAGGGAATTCAGACATAGAGCCCAATCACCTTCAATGACAAATG 480
Qy	481	ATACCTGTGCTCTTGTGGAGCAGCGAGCTTCCATTTCCAGCCGGAAGGCTCCACGGCT 540
Db	481	ATACCTGTGCTCTTGTGGAGCAGCGAGCTTCCATTTCCAGCCGGAAGGCTCCACGGCT 540
Qy	541	CTGAGAGTACTACATTAATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGAG 600
Db	541	CTGAGAGTACTACATTAATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGAG 600
Qy	601	AGAGCAAGTCTGAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db	601	AGAGCAAGTCTGAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660

Qy	661	GTCCCTTTATGAACCGAACAGTTGGTGGAGATCCTGTGGGCTATGAGGATCCCTTGGTGA 720
Db	661	GTCCCTTTATGAACCGAACAGTTGGTGGAGATCCTGTGGGCTATGAGGATCCCTTGGTGA 720
Qy	721	ATTTTATCAACAATATCTTACAGAGATGTTCCCAATCAAGGCAAGTTCCGCTGTTTG 780
Db	721	ATTTTATCAACAATATCTTACAGAGATGTTCCCAATCAAGGCAAGTTCCGCTGTTTG 780
Qy	781	TTGAGATGAACCACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCTCCAGAACTTCA 840
Db	781	TTGAGATGAACCACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCTCCAGAACTTCA 840
Qy	841	GCAAGATCCCACTGGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCAATTCAG 900
Db	841	GCAAGATCCCACTGGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCAATTCAG 900
Qy	901	AGCAGTGCAACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCACTTATGACACCCC 960
Db	901	AGCAGTGCAACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCACTTATGACACCCC 960
Qy	961	AGTCCCTCGCTGGAATCTTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACCATTG 1020
Db	961	AGTCCCTCGCTGGAATCTTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACCATTG 1020
Qy	1021	ATTGAGGGTGTGTTGAAGGATCCCACTATCGCTTTCAGCCCTTAAACTTTTGTGTTG 1080
Db	1021	ATTGAGGGTGTGTTGAAGGATCCCACTATCGCTTTCAGCCCTTAAACTTTTGTGTTG 1080
Qy	1081	CGAATGGTCTGTTTACCAACCAATGAAGTTTTCGCGCTGCTTGAATCCGGCAATTC 1140
Db	1081	CGAATGGTCTGTTTACCAACCAATGAAGTTTTCGCGCTGCTTGAATCCGGCAATTC 1140
Qy	1141	AAATGTGACAGCTTTCAGGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCGAG 1200
Db	1141	AAATGTGACAGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCGAG 1200
Qy	1201	ATGACAGACCTGTGCTATCAGAAAGCGCTTTCGGGTCTGAACCTTGAACCCCAAGGAGCAAT 1260
Db	1201	ATGACAGACCTGTGCTATCAGAAAGCGCTTTCGGGTCTGAACCTTGAACCCCAAGGAGCAAT 1260
Qy	1261	CTTTGTTCTTGAATCCTATCCGCTCACTGGGATCCCAATGAACTGTTGTGTAAGTTGC 1320
Db	1261	CTTTGTTCTTGAATCCTATCCGCTCACTGGGATCCCAATGAACTGTTGTGTAAGTTGC 1320
Qy	1321	AGATAGACCTTACATCAAGCTGTCAGGCAATTCGGGCAACAGGAGATCGAGCCCG 1380
Db	1321	AGATAGACCTTACATCAAGCTGTCAGGCAATTCGGGCAACAGGAGATCGAGCCCG 1380
Qy	1381	TGTCCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCTTGGGCTGAGCCCTTGAACA 1440
Db	1381	TGTCCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCTTGGGCTGAGCCCTTGAACA 1440
Qy	1441	CGTTCTACACGAGCTGTTGATGCCAGGATCTTCAAGTATGTCAGTATGTCGTCG 1500
Db	1441	CGTTCTACACGAGCTGTTGATGCCAGGATCTTCAAGTATGTCAGTATGTCGTCG 1500
Qy	1501	TGGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db	1501	TGGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy	1561	AATGCTCTTTTATTTTGGAGTGTGTAATAAGGCTTCCAGAGATAGAGGCGGCTTCAAG 1620
Db	1561	AATGCTCTTTTATTTTGGAGTGTGTAATAAGGCTTCCAGAGATAGAGGCGGCTTCAAG 1620
Qy	1621	CCTACTCTGAGTCTCTGATGTCACAGCTGCGCAAGGCAAGGCTGCTGCAAGAGCAAGC 1680
Db	1621	CCTACTCTGAGTCTCTGATGTCACAGCTGCGCAAGGCAAGGCTGCTGCAAGAGCAAGC 1680
Qy	1681	TGTAGGGTCCCAAGACACCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db	1681	TGTAGGGTCCCAAGACACCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740

Qy 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTGGC 1788
Db 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTGGC 1788

RESULT 5

US-10-933-037-1
; Sequence 1, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683
; encode the amino acid sequence for the Hamster Scavenger Receptor Class
; B-1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-933-037-1

Query Match 100.0%; Score 1788; DB 9; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCCTGAGACTCACCTTCTGGAAAGCTG 60
Db 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCCTGAGACTCACCTTCTGGAAAGCTG 60
Qy 61 AGCCTCGGCTTCTGATCTCTGTGGGCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 AGCCTCGGCTTCTGATCTCTGTGGGCTCTGTGGGCTCTGTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 CCTGAGCCCGGAGCCCGGCGCCGACACGCGACATGGCGGCGAGCGCCAGGCGCGGCT 180
Db 121 CCTGAGCCCGGAGCCCGGCGCCGACACGCGACATGGCGGCGAGCGCCAGGCGCGGCT 180
Qy 181 GGGTGGCGGTGGGCGTGGGCGTGGTGGGCTGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 240
Db 181 GGGTGGCGGTGGGCGTGGGCGTGGTGGGCTGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG

Db 181 GGGTGGCGGTGGGCGTGGGCGTGGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 240
Qy 241 TCCTCGTGTATGCTCGCTCGCTCATCAACAGCAGGTACTGAAGTATGTCGCATAGACCCCA 300
Db 241 TCCTCGTGTATGCTCGCTCGCTCATCAACAGCAGGTACTGAAGTATGTCGCATAGACCCCA 300
Qy 301 GCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTCTGACCTTCTACTTTGTCGGTCTACT 360
Db 301 GCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTCTGACCTTCTACTTTGTCGGTCTACT 360
Qy 361 TCTTCGAGGTGTCAATCCAGCAGATCTTAAAGGTGAGAACGAGTAGTTCGGGAGC 420
Db 361 TCTTCGAGGTGTCAATCCAGCAGATCTTAAAGGTGAGAACGAGTAGTTCGGGAGC 420
Qy 421 GTGGACCTTATCTCTACAGGGGATTCAGACATAAAGCCCAACATCACCTTCAATGACAA 480
Db 421 GTGGACCTTATCTCTACAGGGGATTCAGACATAAAGCCCAACATCACCTTCAATGACAA 480
Qy 481 ATACTGTGTCTTTTGTGGAGCACCGCAGCTCTCATTTCCAGCGGACAGGTCCACGGCT 540
Db 481 ATACTGTGTCTTTTGTGGAGCACCGCAGCTCTCATTTCCAGCGGACAGGTCCACGGCT 540
Qy 541 CTGAGAGTGACTACATATATATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAATG 600
Db 541 CTGAGAGTGACTACATATATATCTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAATG 600
Qy 601 AGAGCAAGTCTCAGGCGCTGAGCTGATGATCACCTTGGGGCTGGCCACCTTTGGGCGAG 660
Db 601 AGAGCAAGTCTCAGGCGCTGAGCTGATGATCACCTTGGGGCTGGCCACCTTTGGGCGAG 660
Qy 661 GTGCGCTTATGAACCGAACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Db 661 GTGCGCTTATGAACCGAACAGTTGGTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA 720
Qy 721 ATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTTCGGCTTTTG 780
Db 721 ATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTTCGGCTTTTG 780
Qy 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCGTCCAGAACTTCA 840
Db 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCGTCCAGAACTTCA 840
Qy 841 GCAAGATCCACCTGTGGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGATTCA 900
Db 841 GCAAGATCCACCTGTGGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGATTCA 900
Qy 901 AGCAGTGCAACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACATTCATGACACCC 960
Db 901 AGCAGTGCAACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACATTCATGACACCC 960
Qy 961 AGTCTCTGCTGGAATTTCTCAGTCCGAGAGCTCGAGGTCTATGAGCTCACCTACCAG 1020
Db 961 AGTCTCTGCTGGAATTTCTCAGTCCGAGAGCTCGAGGTCTATGAGCTCACCTACCAG 1020
Qy 1021 ATTTCAGGGGTGTTTGAAGGCATCCCCACCTATCGCTTTCACAGCCCCATAAACTTTCT 1080
Db 1021 ATTTCAGGGGTGTTTGAAGGCATCCCCACCTATCGCTTTCACAGCCCCATAAACTTTCT 1080
Qy 1081 CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTGCTTGAATCCGGCATTC 1140
Db 1081 CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTGCTTGAATCCGGCATTC 1140
Qy 1141 AAAATGTGACACTTTCAGGTTTGGTGACCCCTGTTTCTGTCTCACACCTTCACTTCTACA 1200
Db 1141 AAAATGTGACACTTTCAGGTTTGGTGACCCCTGTTTCTGTCTCACACCTTCACTTCTACA 1200
Qy 1201 ATGACAGACCTTGTCTATCAGAAAGCGGTTCTGGGTCTGAACCTTGACCCCAAGGAGCAT 1260
Db 1201 ATGACAGACCTTGTCTATCAGAAAGCGGTTCTGGGTCTGAACCTTGACCCCAAGGAGCAT 1260
Qy 1261 CTTTGTCTTGTGACATCCATCCCGGTCACTGGGATCCCATGAACTGTTCTGTGAAAGTTGC 1320
Db 1261 CTTTGTCTTGTGACATCCATCCCGGTCACTGGGATCCCATGAACTGTTCTGTGAAAGTTGC 1320

Qy 1321 AGATAAGCTCTACATCAAGCTGTCAAGGGCATTTGGGCAAAAGGGAAGATGAGCCCG 1380
Db 1321 AGATAAGCTCTACATCAAGCTGTCAAGGGCATTTGGGCAAAAGGGAAGATGAGCCCG 1380
Qy 1381 TGGTCTCCCAATCTGCTGTTTCAGACAGAGCGGTGCGCATGGGGCGGAGCCCTGAACA 1440
Db 1381 TGGTCTCCCAATCTGCTGTTTCAGACAGAGCGGTGCGCATGGGGCGGAGCCCTGAACA 1440
Qy 1441 CGTTCTACAGCAGCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 1441 CGTTCTACAGCAGCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Qy 1501 TGGGGCTGGGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 TGGGGCTGGGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTGCGAGGATGAGGAGGAGGAGGAGG 1620
Db 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTGCGAGGATGAGGAGGAGGAGGAGG 1620
Qy 1621 CCTACTCTGAGTCTCTGATGTACAGCTGCGAAGGGCAGGGTCTGCGAAGAGCCCAAGC 1680
Db 1621 CCTACTCTGAGTCTCTGATGTACAGCTGCGAAGGGCAGGGTCTGCGAAGAGCCCAAGC 1680
Qy 1681 TGTAGGTTCCAAAGACACCAAGAGCCCCCCCCAACCTGATAGTGTGTCAGACAGCCAT 1740
Db 1681 TGTAGGTTCCAAAGACACCAAGAGCCCCCCCCAACCTGATAGTGTGTCAGACAGCCAT 1740
Qy 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCG 1788
Db 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCG 1788

RESULT 6
US-09-779-152-3
; Sequence 3, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; FILE REFERENCE: CARDIOVASCULAR DISORDERS
; CURRENT APPLICATION NUMBER: US/09/779,152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)

US-09-779-152-3
Query Match 99.9%; Score 1786; DB 3; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACCTGCGAGGGTACTGCTGCTCGGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 1 GCCACCTGCGAGGGTACTGCTGCTCGGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Qy 61 AGCTTCGCTCTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 AGCTTCGCTCTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 CCTGAGCCCGGAGCCCGGGCCGACACGCGGACATGCGGCGGAGCGCGGCGGCGCT 180

Db 121 CCTGAGCCCGGAGCCCGGGCCGACACGCGGACATGCGCGGAGCGCGCGCGCGCT 180
Qy 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGG 240
Db 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGG 240
Qy 241 TCCTCTGATGTCCTTCGCTCATCAAAAGAGGATGCTGAAGATGTCGCGCATAGACCCCA 300
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Qy 301 GCAGCTGTCCTTTGCAATGTCGAAGGATGCTGACCTTACCTTCTACTTGTGCTGCTACT 360
Db 301 GCAGCTGTCCTTTGCAATGTCGAAGGATGCTGACCTTACCTTCTACTTGTGCTGCTACT 360
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Qy 421 GTGGAACCTATGCTACAGGGAATCAGACATTAAGGCCAAATCATCCTTCAATGACAATG 480
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Qy 1020 AGTCCTCGCTGGAATCTTTCAGTCCGGAAGCTGTCAGAGTCTATGAAGCTCACCTACCATG 1020
Db 1020 AGTCCTCGCTGGAATCTTTCAGTCCGGAAGCTGTCAGAGTCTATGAAGCTCACCTACCATG 1020
Qy 1080 ATTTCAGGGGTGTTGAAAGCATCCCACTATGCTGTCAGCCCTTCAAGCCCTTAAACCTTTG 1080
Db 1080 ATTTCAGGGGTGTTGAAAGCATCCCACTATGCTGTCAGCCCTTCAAGCCCTTAAACCTTTG 1080
Qy 1140 CCNATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGGCTGCTTGAATCGGCAATTC 1140
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Qy 1200 AAAATGTCAGACTTTCAGGTTTGGTGACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
Db 1200 AAAATGTCAGACTTTCAGGTTTGGTGACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
Qy 1260 ATGTCAGACCTTGTGCTATCAGAGCGGCTTCTGGGCTGTAACCTTGACCCCAAGGAGCAT 1260

1141 AAAATGTCAGACCTTGAGGTTGGTGACCCCTGTTTCTGTGTACACCCCTCACTTCTACA 1200
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1201 ATGCAGACCTTGCTCTATCAGAAGCCGTTCTGGGTCTGAACCTTGACCCCAAGGGAGCAAT 1260
1261 CTTTGTTCCTTGACATCATCCGCTCACTGGGATPCCCATGAATCTGTGTGAAGTTGC 1320
1261 CTTTGTTCCTTGACATCATCCGCTCACTGGGATPCCCATGAATCTGTGTGAAGTTGC 1320
1321 AGATAAGCCTCTACATCAAGCTGTCAAGGGCATTTGGGGCAAAAGGAGATGAGAGCCCG 1380
1321 AGATAAGCCTCTACATCAAGCTGTCAAGGGCATTTGGGGCAAAAGGAGATGAGAGCCCG 1380
1381 TGGTCCCTCCATTCGCTGTGTTTGTAGCAGAGCGGTGCGCATGGGGCGGAGCCCTGAACA 1440
1381 TGGTCCCTCCATTCGCTGTGTTTGTAGCAGAGCGGTGCGCATGGGGCGGAGCCCTGAACA 1440
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1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC 1786
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RESULT 8

US-10-212-848-3
; Sequence 3, Application US/10212848
; Publication No. US2004002325A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: MM-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)
US-10-212-848-3

Query Match 99.9%; Score 1786; DB 7; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GCCACCTGCAGGGGCTACTGTGCTCCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60

1 GCCACCTGCAGGGGCTACTGTGCTCCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60
61 AGCCTCGGCTTCTGTCTCATCTCTGTGCGCTCTGTGCGCTTCTGTGCGTGTCCCTTCAGTC 120
61 AGCCTCGGCTTCTGTCTCATCTCTGTGCGCTCTGTGCGCTTCTGTGCGTGTCCCTTCAGTC 120
121 CTTGAGCCCCCGAGAGCCCGGGCCGACACGCGGACATGGGGCGGACGCGGCGGCGCT 180
121 CTTGAGCCCCCGAGAGCCCGGGCCGACACGCGGACATGGGGCGGACGCGGCGGCGCT 180
181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGTGTGCGCTGTGTGCGTGTGCGTGTGTTATGA 240
181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGTGTGCGCTGTGTGCGTGTGCGTGTGTTATGA 240
241 TCTCTGTGATGCCCTCGCTCATCAAAACAGCAGTACTCTGAAGAATGTCCGATAGACCCCA 300
241 TCTCTGTGATGCCCTCGCTCATCAAAACAGCAGTACTCTGAAGAATGTCCGATAGACCCCA 300
301 GCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
301 GCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
361 TCTTCAGGTGTGTCATCCAGCGGATCCTTAAAGGGTGAGAGCCAGTAGTGGGGAGC 420
361 TCTTCAGGTGTGTCATCCAGCGGATCCTTAAAGGGTGAGAGCCAGTAGTGGGGAGC 420
421 GTGGACCTCTATGTCTACAGGGAATTCAGACATCAAGGCCCAACATCATCTTCAATGACAATG 480
421 GTGGACCTCTATGTCTACAGGGAATTCAGACATCAAGGCCCAACATCATCTTCAATGACAATG 480
481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCTCATTTTCAGCCGCGACAGTCCCAAGGCT 540
481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCTCATTTTCAGCCGCGACAGTCCCAAGGCT 540
541 CTGAGAGTGACTATACATTAATCTGCTTAAACATCTGTGCTTTGGGGGGCGCAGTAATGATG 600
541 CTGAGAGTGACTATACATTAATCTGCTTAAACATCTGTGCTTTGGGGGGCGCAGTAATGATG 600
601 AGAGCAAGTCTGCGAGCCCTGAAAGCTGATGATGACCTTTGGGGGCTGGCCACTTGGGGCCAGC 660
601 AGAGCAAGTCTGCGAGCCCTGAAAGCTGATGATGACCTTTGGGGGCTGGCCACTTGGGGCCAGC 660
661 GTGCTTTTATGAACCGAACAGATGTGTGAGATCTGTGGGGCTATGAGGATCCCTTCTGTGA 720
661 GTGCTTTTATGAACCGAACAGATGTGTGAGATCTGTGGGGCTATGAGGATCCCTTCTGTGA 720
721 ATTTTATCAAAATACTTACAGACATGTTCCTCCATCAAGGGCAAGTTCGGGCTGTGTTG 780
721 ATTTTATCAAAATACTTACAGACATGTTCCTCCATCAAGGGCAAGTTCGGGCTGTGTTG 780
781 TTGAGATGAACTCACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
781 TTGAGATGAACTCACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
841 GCAAGATCCACCTGTGGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCACTTCAG 900
841 GCAAGATCCACCTGTGGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCACTTCAG 900
901 AGCAGTGCACATGATCAATGACATTTCCGGGCGAGATGTGGGCAACATTCATGACACCCC 960
901 AGCAGTGCACATGATCAATGACATTTCCGGGCGAGATGTGGGCAACATTCATGACACCCC 960
961 AGTCCTCGCTGGGAATCTTTCAGTCCGGAAGCTGAGGCTCTATGAAGCTCACCTACCATG 1020
961 AGTCCTCGCTGGGAATCTTTCAGTCCGGAAGCTGAGGCTCTATGAAGCTCACCTACCATG 1020
1021 ATTCAGGGGTGTTTGAAGGATCCCCACCTATCGCTTTCAGCGCCCTAAACCTTTGTTG 1080
1021 ATTCAGGGGTGTTTGAAGGATCCCCACCTATCGCTTTCAGCGCCCTAAACCTTTGTTG 1080
1081 CCAATGGGTCTGTGTTTACCACCAATGAAGGTTTCTGCGCGCTTGAATCGGCACTTC 1140

781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGCGTCCAGAACTTCA 840
828 TTGGGATGAGACTGAGTCTGGCGTCTTACCGTCTTACAGGTGTCAGAAATTTCA 887
841 GCAAGATCCACCTGGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTAGTGCATTCAG 900
888 GCAAGATCCATCTGGTGGATGGAACGGCTCAGCGAGGTCAACTATTGGCAATTCGG 947
901 AGCAGTGCAACATGATCAATGSCACTTCCGGGCGAGATGTTGGGCAACATTCAGACACCC 960
948 AACAGTGCAACATGATCAATGGTACTGCCGGGCGAGATGTTGGGCAACATTCAGACACCC 1007
961 AGTCCTCGCTGGAAATCTTTCAGTCCGGAAGCTGCGAGGTCTATGAAGCTCACCTACCATG 1020
1008 AATCCTCACTGGAAATCTTTCAGCCGAGAGCTGCGAGTCTATGAAGCTCACCTACCATG 1067
1021 ATTACAGGGGTGTTGAAGGATCCCACTATCGCTTTCAGAGCCCTTAAACTTTGTTG 1080
1068 AATCAAGGGTGTTCGAAGGATCCCACTATCGCTTTCAGAGCCCTTAAACTTTGTTG 1127
1081 CCAATGGTCTGTTTACCCCACTCAATGAAGGTCTTCCCGCTGCTTGAATCCGCAATTC 1140
1128 CCAAGGGTCCGTCTACCCCACTCAATGAAGGTCTTCCCGCTGCTGCGAGTCCGCAATTC 1187
1141 AAAATGTCAGCACTTGCAGGTGTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
1188 AGAATGTCAGCACTTGCAGGTGTTGGTGCACCCCTGTTTCTTCCAGCCCACTTCTACA 1247
1201 ATGCAAGCTGCTGATATCAAGAGCGGTCTGGGTCTGAACCTCTGACCCCAAGGAGCAAT 1260
1248 ATGCTGACCCCGTCTGTGAGAAGCTGTTCTGGTCTGAACCTCTGACCCCAAGGAGCAAT 1307
1261 CTTTGTCTTGCATCATCATCCGCTCACTGGGATCCCACTGTAAGTCTTCTGTAAGTTC 1320
1308 CTTTGTCTTGCATCATCATCCGCTCACTGGGATCCCACTGTAAGTCTTCTGTAAGTTC 1367
1321 AGATAAGCTCTACATCAAGAGCTGTCAGGAGCTTGGGCAACAGGAGAGATCGAGCCCG 1380
1368 AGCTGAGTCTGTACATCAATCCGTCAAGGCGCTGCGGCAACAGGAGAGATCGAGCCAG 1427
1381 TGGTCTCCCACTGCTGTGTTGAGCAGAGCGGTGCTGAGGCGGCGAGCCCTTGAACA 1440
1428 TAGTCTGCTGCTGCTGTTGAAACAGAGCGGATGATGGGTGGCAAGACCTTGAACA 1487
1441 CGTCTACAGCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
1488 CGTCTACAGCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1547
1501 TGGGCTGCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1548 TGGGCTTGGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1607
1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGCTCGCAGGATTAAGGAGCCATTCAGG 1620
1608 AATGCTTTTATTTTGGAGTGGTAGTAAAGGCTCGCAGGATTAAGGAGCCATTCAGG 1667
1621 CCTACTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
1668 CCTACTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1727
1681 TGTAGGCTCCCAAGAGACACCAAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 1740
1728 TGTAGGCTCCCAAGAGACACCAAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 1787
1741 CCAGCCCTTACACCCCGCTTTCTTGGAGTCTCTCTCAGCGGACA 1783
1788 CCAGTCCCTACACCCCGCTTTCTGAGGACTCTCTCAGCGGACA 1830

RESULT 11

US-09-148-012-3

; Sequence 3, Application US/09148012

; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT/150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (51)..(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine
; OTHER INFORMATION: Scavenger Receptor Class BI
; US-09-148-012-3

Query Match 76.6%; Score 1369.8; DB 3; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 110 CCCCTTCAGTCCCTGAGCCCGCGGAGCCCGCCGACACGCGGACATGGCGGCGAGCCG 169
DB 5 CTCCTTCAGGTCTGAGCCCGGAGAGCCCTTCCGCGCACGCGGACATGGCGGCGAGTCC 64
QY 170 CAGGCGCGCTGGGTGGCGGTGGGCGTGGGCGTGGTGGGCGTGGTGGGCGTGGTGGG 229
DB 65 CAGGCGCGCTGGGTGGCGGTGGGCGTGGGCGTGGTGGGCGTGGTGGGCGTGGTGGG 124
QY 230 TGTGTTATGATCTCTGCTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGATGTCG 289
DB 125 CGTTGTGATGATCTCTGCTGATGCCCTCGCTCATCAAGCAGCAGGTGCTCAAGATGTCG 184
QY 290 CATAGACCCAGCAGCTGCTGCTTGGCATGTGGAGGAGATCCCTGTACCCCTTCTACTTT 349
DB 185 CATAGACCCAGCAGCTGCTGCTTGGGATGTGGAGGAGATCCCGGCTCCCTTCTACTTT 244
QY 350 GTCCGCTACTTCTTCGAGTGTGTCAATCCAGCAGAGATCTTAAAGGGTGAGAAGCCAGT 409
DB 245 GTCTGTACTTCTTTCGAAGTGTCAACCCAAACAGAGTCTCTCAAGCGCAGAGCCAGT 304
QY 410 AGTGGGAGCGGTGGAGCCCTTGTCTACAGGGAATTCAGACATTAAGGCCAAATCACTT 469
DB 305 AGTCCGGAGCGGTGGAGCCCTTGTCTACAGGAGTTCAGACAAAGGTCAACATCACTT 364
QY 470 CAATGCAATGATGATGCTGCTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAG 529
DB 365 CAATGCAACAGCACCGTGTCTTGTGGAGAACCGCAGCTCCATTTCCAGCGCTGACAA 424
QY 530 GTCCCAAGCTCTGAGAGTGAATACATTAATATATGCTTAACATTTCTGCTCTTGGGGGCGC 589
DB 425 GTCCGATGCTCAGAGTGAATACATTAATATATGCTTAACATTTCTGCTCTTGGGGGCGC 484
QY 590 AGTAATGATGGAGAGCAAGTCTGAGGCTGAGAGCTGAGATGAGACCTTGGGGGTGGCCAC 649
DB 485 GATATTGATGGAGAGCAAGCTGTGAGCCTGTAAGCTGATGATGATGATGATGATGATGATG 544
QY 650 CTTGGGCGAGCTGCTCTTATGAACCGAAGTGTGGTGAATCTTGGGGCTTATGAGGA 709
DB 545 CATGGGCGAGCTGCTCTTATGAACCGCAGTGTGGTGAATCTTGGGGCTTATGAGGA 604
QY 710 TCCCTTCGTGAATTTTATCAAAATACATTAATATATGCTTAACATTTCTGCTCTTGGGGGCGC 769
DB 605 TCCCTTCGTGAATTTTCTCAACAGTACCTCCAGACATGCTTCCATTAAGGGCAATTT 664
QY 770 CGGCTCTGTTGTTGAGATCAACCACTCAGACTCTGGGCTCTTCACTGTGTTCAAGGGCGT 829

Db 665 TGGCTGTTTGGGATGAACAACTCGAATCTGGGGTCTTCACTGTCTTTCAGCGCGT 724
Qy 830 CCAGAACTTCAGCAAGATCCACTGGTGGAGAGATGGAATGGGCTCAGCAAGGTCAACTA 889
Db 725 CCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGAACGAGCTCAGCAAGATCGATTA 784
Qy 890 CTGGCAATTCAGCAGGATGAACATGATCAATGGCACTTCGGGAGAGATGGGGACCAATT 949
Db 785 TTGGCAATTCAGCAGGATGAACATGATCAATGGCACTTCGGGAGAGATGGGGACCAATT 844
Qy 950 CATGACACCCAGTCTCGCTGGAAATCTTCAGTCCGGAAGCCCTGCGAGGTCTATGAAGCT 1009
Db 845 CATGACACCCAGTCTCGCTGGAAATCTTCAGTCCGGAAGCCCTGCGAGGTCTATGAAGCT 904
Qy 1010 CACTACATGATTCAGGGGTGTTGAAGGATCCCAACCTATCGCTTCACAGCCCTTAA 1069
Db 905 GACCTACAAAGATCAAGGGGTGTTGAAGGATCCCAACCTATCGCTTCACAGCCCTTAA 964
Qy 1070 AACTTTGTTGGCAATGGTCTGTTTACCCCAATGAAGGTTCCTGCGGTGCTTGA 1129
Db 965 TACTCTGTTTGGCAACGGGTCCGTCTACCCCAATGAAGGTTCCTGCGGTGCTTGA 1024
Qy 1130 ATCCGGCAATTCAGAAATGTCAGCACTTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1189
Db 1025 GTCTGGCAATTCAGAAATGTCAGCACTTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1084
Qy 1190 TCATCTTCAAAATGTCAGCACTTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1249
Db 1085 CCATTTTACAAAGCCAGCTGTTGTCAGAGCTGTTCTGTTCTGTACACCC 1144
Qy 1250 AAGGAGATCTTGTGTTCTGATCAATCCATTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1309
Db 1145 AAGGAGATCTTGTGTTCTGATCAATCCATTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1204
Qy 1310 TGTGAAGTTCAGATAGCTCTTACATCAAGCTTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1369
Db 1205 TGTGAAGTTCAGATAGCTCTTACATCAAGCTTCAGGTTTGGTGCACCCCTGTTCTGTACACCC 1264
Qy 1370 GATCAGCCCGTGTCTCCATTCGTTGTTGAGCAGAGCGGTGCTTACATTCAGGTTGCG 1429
Db 1265 GATCAGCCCGTGTCTCCATTCGTTGTTGAGCAGAGCGGTGCTTACATTCAGGTTGCG 1324
Qy 1430 GCGCTGAAACAGCTTCAGCAGAGCTGTTGATGCGCCAGGATCTTCAATGATGCA 1489
Db 1325 GCGCTGAAACAGCTTCAGCAGAGCTGTTGATGCGCCAGGATCTTCAATGATGCA 1384
Qy 1490 GTATGCTCTGCGGCTGCGGCGCTCTGCTGCTGCGGCTCTTACATTCAGGTTGCG 1549
Db 1385 GTATGCTCTGCGGCTGCGGCGCTCTGCTGCTGCGGCTCTTACATTCAGGTTGCG 1444
Qy 1550 CAGCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGCAGGATAGGA 1609
Db 1445 CAGCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGCAGGATAGGA 1504
Qy 1610 GGCAATTCAGGCTTCTGATGCTCTGATGCTACAGCTGCGCAGGAGCTGCTGCA 1669
Db 1505 GGCAATTCAGGCTTCTGATGCTCTGATGCTACAGCTGCGCAGGAGCTGCTGCA 1564
Qy 1670 AGAAGCCAGCTGATGAGGTTCAGAGACACCAAGAGCCCGCCCACTGATGATGCTGCT 1729
Db 1565 AGAAGCCAGCTGATGAGGTTCAGAGACACCAAGAGCCCGCCCACTGATGATGCTGCT 1624
Qy 1730 AGACCCAGCTTACAGCCCTTACAGCCCTTCTGAGGACTCTCTCAGCGGAGATC 1786
Db 1625 AGACCCAGCTTACAGCCCTTCTGAGGACTCTCTCAGCGGAGATC 1681

RESULT 12

US-10-178-611-3

; Sequence 3, Application US/10178611

; Publication No. US20030167475A1

; GENERAL INFORMATION:

; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky

; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; encode the amino acid sequence for the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-178-611-3

Query Match 76.6%; Score 1369.8; DB 6; Length 1785;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 110 CCCCTTCAGTCCCTGAGCCCGGAGCCCGGCGCCGACACGCGACATGGCGGCGCAGCGC 169
Db 5 CTCCTTCAGGTCTTCGAGCCCGGAGAGCCCTTCGCGCAGCGGACATGGCGGCGCAGCTC 64
Qy 170 CAGGGCGCGCTGGGTGGCGGTGGGGCTGGGGCTGCTGTGGGGCTGCTGTGGCTGCTCGG 229
Db 65 CAGGGCGCGCTGGGTGGCGGTGGGGCTGGGGCTGCTGTGGGGCTGCTGTGGCTGCTCGG 124
Qy 230 TGTGGTTATGATCTCTGTGATGCGCTCGCTCATCAAAACAGCAGGATGAGGATGTCG 289
Db 125 CGTTGTGATGATCTCTCATGTTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTC 184
Qy 290 CATAGACCCAGCAGCTGCTCTTTCGAAATGCGAAGGAGATCCCTGACCTTCTACTT 349
Db 185 CATAGACCCAGCAGCTGCTCTTTCGAAATGCGAAGGAGATCCCTGACCTTCTACTT 244
Qy 350 GTCCGCTTACTTCTTCGAGGTGCTCAATCCAGCGAGATCCTAAAGGGTGAGAGCCAGT 409
Db 245 GTCTGTCTACTTCTTCGAGGTGCTCAACCAACAGAGGTCTCTCAACGCGCAGAGCCAGT 304
Qy 410 AGTGGCGGAGCGGTGAGCCCTTATGCTACAGGGAATTCAGACATGAAGCCCAACATCAGCTT 469
Db 305 AGTGGCGGAGCGGTGAGCCCTTATGCTACAGGGAATTCAGACATGAAGCCCAACATCAGCTT 364

QY 470 CAATGACATGATACTGTGTCTCTTTGTGGAGCACCGCAGCCTCAATTTCCAGCCGACAG 529
DB 365 CAATGACACGACACCGGTCTCTGTGGAGAACCGCAGCCTCAATTTCCAGCCTGACAA 424
QY 530 GTCCACCGCTCTGAGAGTGAATACATTAATATGCTTAACTATCTGCTTTGGGGGCGC 589
DB 425 GTCCGCTGCTCAGAGAGTGAATACATTAATATGCTTAACTATCTGCTTTGGGGGCGC 484
QY 590 AGTAATGATGGAGCAGTCTGAGGCTGAGCTGATGATGATGATGATGATGATGATGATGAT 649
DB 485 GATATGATGGAGCAGCCTGTGAGCCTGAGCTGATGATGATGATGATGATGATGATGATGAT 544
QY 650 CTTGGGCGACGCTGCTTATGAAACGACAGTTGGTGAGATCTGTTGGGGCTATGAGGA 709
DB 545 CATGGGCGACGCTGCTTATGAAACGACAGTTGGTGAGATCTGTTGGGGCTATGAGGA 604
QY 710 TCCCTTCGTGAATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTT 769
DB 605 TCCCTTCGTGCAATTTCTCAACAGTACCTCCAGACATGCTTTCCCATAAAGGGCAAAAT 664
QY 770 CGGCTGTTTGTGAGATGAACTCAGACTCTGGCTCTTCACTGTGTTACGGGCGT 829
DB 665 TGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGCTCTTCACTGTCTTCACTGGGCGT 724
QY 830 CCAAGACTTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA 889
DB 725 CCAGATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCGAATTA 784
QY 890 CTGGCATTCAGAGCAGTGAACATGATCAATGGCACTTCGGGCGAGATGTGGGCACCAAT 949
DB 785 TTGGCAATTCAGAGCAGTGAACATGATCAATGGCACTTCGGGCGAGATGTGGGCACCCAT 844
QY 950 CATGACACCCAGTCTCGCTGGAAATCTTTCAGTTCGGGAAGCCTGCAAGGTCTATGAAGCT 1009
DB 845 CATGACACCCGAAATCTCGCTGGAAATCTTTCAGCCTGGAGGATGCAAGGTCTTCAAGCT 904
QY 1010 CACTCATCATGATTTCAGGGGTGTTTGAAGGCATCCACCATCTGCTTTCACACCCCTTAA 1069
DB 905 GACTCAACAGATCAAGGGGTGTTTGAAGGCATCCACCATCTGCTTTCAGGGCCCGGA 964
QY 1070 AACTTTGTTTCCCAATGGGTCTGTTTACCCACCAATGAAGGTCTTTCGCCGTGCTTGA 1129
DB 965 TACTCTGTTTCCCAACGGGTCTGTTTACCCACCAATGAAGGTCTTTCGCCGTGCTTGA 1024
QY 1130 ATCCGCAATTCAAAATGTCAGACTTGCAGGTTTGTGCAACCTGTTTCTGTCAACCC 1189
DB 1025 GTCTGGCAATTCAGAAATGTCAGCCTGTCAGGTTTGTGCGCCTCTGTTTCTCTCCACCC 1084
QY 1190 TCATTTCTCAATGTCAGACCTCTGTCTATCAGAAAGCCGTTCTGSETCTGAACCCCTGACCC 1249
DB 1085 CCATTTTTCAGCCGACCTCTGTTTGTGAGAAAGCTGTTCTTGGTCTGAACCCCTTACCC 1144
QY 1250 AAGGGAGCATTTCTTTTCTTACATCCATCCGCTCACTGGGATCCCATGAATGTTCT 1309
DB 1145 AAGGAGCATTTCTTTTCTTACATCCATCCGCTCACTGGGATCCCATGAATGTTCT 1204
QY 1310 TGTGAAGTTGAGATGAAGCCTCTATCATCAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAA 1369
DB 1205 TGTGAAGATGAGTGAAGCCTCTATCATCAAAATCTGTCAAGGGCATTTGGGCAAAACAGGGAA 1264
QY 1370 GATCGACCCGTGCTCTCCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGGGCGCGA 1429
DB 1265 GATCGACCCAGTGTCTCTGCGTTGCTGTGTTGAGCAGAGCGGTGCCATGGGCGCGA 1324
QY 1430 GCCCTTGAACACAGTTCTTACACGAGCTGGTGTGATGCCCGCAGGTACTTCAGTATGTGCA 1489
DB 1325 GCCCTTGAACACAGTTCTTACACGAGCTGGTGTGATGCCCGCAGGTACTTCAGTATGTGCA 1384
QY 1490 GTATGCTGCTGGGGCTTGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
DB 1385 GTATGCTGCTGGGGCTTGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444

QY 1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCCGAGGATAAGGA 1609
DB 1445 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCCGAGGATAAGGA 1504
QY 1610 GGCCATTCAGGCTACTCTGAGTCTCTGATGTACAGCTGCCAAGGGCAACGGTGTGCA 1669
DB 1505 GGCCATTCAGGCTACTCTGAGTCTCTGATGTACAGCTGCCAAGGGCAACGGTGTGCA 1564
QY 1670 AGAAGCCAGCTGTAGGTCCCAAGACACACAGAGCCGCCCAACCTCATAGCTTGGTC 1729
DB 1565 AGAAGCCAGCTGTAGGTCCCAAGACACACATAGAGCCGCCCAACCTCATAGCTTGGTC 1624
QY 1730 AGAAGCCAGCTGTAGGTCCCAAGACACACCTTCTGAGGACTCTCTCAGCGGACAGTC 1786
DB 1625 AGAAGCCAGCTGTAGGTCCCAAGACACACCTTCTGAGGACTCTCTCAGCGGACAGCC 1681

RESULT 13

US-10-164-863-3
; Sequence 3, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)..(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine Scavenger Receptor
; OTHER INFORMATION: Class B1
US-10-164-863-3

Query Match 76.6%; Score 1389.8; DB 6; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 110 CCGCTTCAGTCCCTGAGCCCGCGAGCCCGCGGCGCACACGCGGACATGGGGGCGAGCG 169
DB 5 CTCCTTCAGTCCCTGAGCCCGCGAGCCCGCGGCGCACACGCGGACATGGGGGCGAGCTC 64
QY 170 CAGGGCGCGCTGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 229
DB 65 CAGGGCGCGCTGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 124
QY 230 TGTGGTTATGATCCTCGTGATGCCCTCGCTCATCAAAACAGCAGGTAAGTAATGTCG 289
DB 125 CGTTGTGATGATCCTCATGTTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATGTCG 184
QY 290 CATAGACCCAGCAGCCTGCTCTTTGCAATGTGGAGGAGATCCCTGTACCCCTTCTACTT 349
DB 185 CATAGACCCAGCAGCCTGCTCTTTGCAATGTGGAGGAGATCCCTGTACCCCTTCTACTT 244
QY 350 GTCGCTACTACTTCTTCGAGGTGGTCAATCCAGCGAGATCCCTAAAGGGTGAGAGCCAGT 409
DB 245 GTCGCTACTACTTCTTCGAGGTGGTCAATCCAGCGAGGTCCCTCAACGCGCAGAGCCAGT 304
QY 410 AGTGGGGAGCGGTGGAGCCCTATGTCTACAGGGAAATTCAGACATTAAGGCCAATCATCCTT 469
DB 305 AGTGGGGAGCGGTGGAGCCCTATGTCTACAGGGAGTTTACAGCAAAAGGTCAACATCATCCTT 364

QY 470 CAATGACAAATGATGCTCTTTGGAGCAGCGGAGCCTCATTTTCAGCCGAGCAG 529
DB 365 CAATGACAAACACACCGCTGCTTTGGAGAAACCGAGCCTCATTTTCAGCCGAGCAA 424
QY 530 GTCCACAGGCTCAGAGTACTATATATACCTGCTAAACATTTCTGGGGGGCGC 589
DB 425 GTCCATGGCTCAGAGAGTACTATATATACCTGCTAAACATTTCTGGGGGGCGC 484
QY 590 AGTAATGATGGAGAGCAAGCTCTGAGGCTGGAAGCTGATGATGACCTTTGGGGCTGGCCAC 649
DB 485 GATATTGATGGAGAGCAAGCTGAGGCTGGAAGCTGATGATGACCTTTGGGGCTGGCCAC 544
QY 650 CTTGGGCGAGCGTCTTATGAAACCGAAACGTTGGTGAAGATCTGTTGGGGCTATGAGGA 709
DB 545 CATGGGCGAGCGTCTTATGAAACCGCAAGTTGGTGAAGATCTGTTGGGGCTATGAGGA 604
QY 710 TCCCTTCGTGAATTTATCAAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTT 769
DB 605 TCCCTTCGTGAATTTCTCAACAGTACCTCCAGACATGTTCCCATTAAGGGCAAAAT 664
QY 770 CGGCTCTGTTTGGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGCGT 829
DB 665 TGGCTCTGTTTGGAGTGAACAACTCGAATTTCTGGGCTCTTCACTGTGTTACGGGCGT 724
QY 830 CCAGAACTTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA 889
DB 725 CCAGAAATTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGATCGATTA 784
QY 890 CTGGCAATTCAGAGCAGTCAACATGATCAATGACATTCGGGCGAGATGGGCAACCAT 949
DB 785 TTGGCAATTCAGAGCAGTCAACATGATCAATGACATTCGGGCGAGATGGGCAACCAT 844
QY 950 CATGACACCCAGTCTCGCTGGAAATCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCT 1009
DB 845 CATGACACCCAGTCTCGCTGGAAATCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCT 904
QY 1010 CACTCAATGATTCAGGGGTGTTGAAGGATCCCACTATCGCTTCACAGCCCTCA 1069
DB 905 GACCTCAACAGATCAAGGGGTGTTGAAGGATTCCTCCACAGTATCGCTTCACGGCCCCGA 964
QY 1070 AACTTTGTTGCCAATGGGCTGTTTACCCACCAATGAAGTTCCTGCGGCTGCTTGA 1129
DB 965 TACTCTGTTTGGCAACGGGCTCGCTACCCCAACCAAGAGGCTTCCTGCCCATCCGAGA 1024
QY 1130 ATCCGGCAATTCAAATGTGACACTGTGAGTGTGGTGCACCCCTGTTTCTGTACACACC 1189
DB 1025 GTCTGGCAATTCAGAAATGTGACACTGTGAGTGTGGTGCACCCCTGTTTCTTCCCAACC 1084
QY 1190 TCACCTTCTACAAATCAGACCTGTGCTATCAGAAAGCCGTTCTGGGCTGAACCCCTGACC 1249
DB 1085 CCACCTTTTACAAACCGGACCTGTGTTGTGAGAAAGCTGTTCTGGTCTGAACCCCTAACCC 1144
QY 1250 AAGGGAGCATCTTTGTTCTTGAATCATCCATCCGCTCACTGGGATCCCATGAATGTTTC 1309
DB 1145 AAGAGGAGCATCTTTGTTCTTGAATCATCCATCCGCTCACTGGGATCCCATGAATGTTTC 1204
QY 1310 TGTGAAGTGTGAGATAAGCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGAA 1369
DB 1205 TGTGAAGTGTGAGATAAGCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACAGGAA 1264
QY 1370 GATCGAGCCGTTGTTCTTCCATGCTGTGTTGAGCAGAGCGGTTGCCATTTGGGCGCGA 1429
DB 1265 GATCGAGCCGTTGTTCTTCCGTTGCTGTGTTTGAACAGAGCGGCAATTTGGGTTGCA 1324
QY 1430 GCCCTGAAACAGTCTTACAGCAGCTGGTGTGATGATGATGATGATGATGATGATGATGAT 1489
DB 1325 GCCCTGAGCAGCTTCTACAGCAGCTGGTGTGATGATGATGATGATGATGATGATGATGAT 1384
QY 1490 GTATGTGCTGTGGGCTGGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
DB 1385 GTATGTGCTGTGGGCTGGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1550 CAGCCAGGAGAAATGCTTTTTTATTTTGGAGTGGTGTAGTAAAGAGGCTCGCAGGATAAGGA 1609

DB 1445 CAGCCAGGAGAAATGCTTTTTTGTGGAGTGTAGTAAAGAGGCTCCAGGATAAGGA 1504
QY 1610 GGCCATTTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCAAGGGCACGGTGTGCA 1669
DB 1505 GGCCATTTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCAAGGGCACGGTGTGCA 1564
QY 1670 AGAAGCCAGCTGTAGGCTCCAAAGACACACAGAGCCCCCAACCTGATAGCTTGGTC 1729
DB 1565 AGAAGCCAGCTATAGGCTCTGAGACACTATAAGCCCCCAACCTGATAGCTTGGTC 1624
QY 1730 AGACCGCATTCAGCCCCCTACACCCCGCTTCTTGAAGCTCTCTCAGCGGACAGTC 1786
DB 1625 AGACCGCATTCAGCCCCCTACACCCCGCTTCTTGAAGCTCTCTCAGCGGACAGTC 1681
RESULT 14
US-10-706-073-3
; Sequence 3, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51)-(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine
; OTHER INFORMATION: Scavenger Receptor Class BI
US-10-706-073-3
Query Match 76.6%; Score 1369.8; DB 7; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 110 CCCCTTCAGTCCCTGAGCCCCCGAGCCCGGCGGCACACGCGGACATGCGGCGAGCGC 169
DB 5 CTCCTTCAGTCCCTGAGCCCCCGAGAGCCCTTCGCGCACGCGGACATGCGGCGAGCTC 64
QY 170 CAGGGCGGCTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 229
DB 65 CAGGGCGGCTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 124
QY 230 TGTGGTGTATGATCCTCGTGTATGCTCGCTCATCAAAACAGCAGTACTGAAGATGTCG 289
DB 125 CGTTGTATGATCCTCATGTGTGCTCCCTCATCAAGCAGCAGGTGCTCAAGATGTCG 184
QY 290 CATAGACCCCGAGCAGCTGTCTTTTGAATGTGGAAGGAGATCCCTGTACCTTCTACTT 349
DB 185 CATAGACCCCGAGCAGCTGTCTTTTGAATGTGGAAGGAGATCCCTGTCTCTTCTACTT 244
QY 350 GTCCGTCTACTTCTTGAAGTGTCTAATCCAGCAGATCTTAAGGGTGAGAGCCAGT 409
DB 245 GTCTGTCTACTTCTTGAAGTGTCTAATCCAGCAGATCTTAAGGGTGAGAGCCAGT 304
QY 410 AGTGGCGGAGCGGAGCCCTTATCTGTACAGGGATTTACAGACATAAGCCAAACATCACTT 469
DB 305 AGTGGCGGAGCGGAGCCCTTATCTGTACAGGGATTTACAGACATAAGCCAAACATCACTT 364
QY 470 CAATGACAAATGATGCTGTGCTCTTTTGTGGAGCAGCCGAGCCTCCATTTTCCAGCGGACAG 529

Db 65 CAGGCGCGCTGGGTGGCCCTTTGGGGTTGGGGCCCTCGGGCTGCTGTTGCTGGCGCTCGG 124
Qy TGTGTTTATGATCTCGTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCCG 289
Db 125 CGTTGTATGATCTCATGTTGGCTCCCTCATCAGCAGCAGGTGTCAAGAAATGTCCG 184
Qy 290 CATAGACCCAGCAGCCTGTCTTTGCAATGTGAAAGAGATCCCTGTACCTTTCTACTT 349
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Qy 350 GTCCGCTACTCTTCGAGGTGTCAATCCAGCAGATCCTAAAGGGTGAAGCCAGT 409
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Qy 410 AGTCGGGAGCGTGGACCTATGTCTACAGGGAATTCAGACATAAAGCCCAACATCACCTT 469
Db 305 AGTCGGGAGCGTGGACCTATGTCTACAGGGAATTCAGACATAAAGCCCAACATCACCTT 364
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Qy 530 GTCCCAAGGCTCAGAGTGAATATGATGCTGCTAACTTCTGCTTTGGGGGGCGC 589
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Qy 590 AGTAATGATGAGAGCAAGTCTGAGCGCTCAAGCTGATGATGACCTTTGGGGCTGGCCAC 649
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Qy 650 CTTGGGCGAGCGTCTTTATGAAACCGAACAAGTTGGTGAATCCTGTGGGGCTATGAGGA 709
Db 545 CATGGGCGAGCGTCTTTATGAAACCGAACAAGTTGGTGAATCCTGTGGGGCTATGAGGA 604
Qy 710 TCCCTTCGTGAATTTATCAACAATTTACTTACAGACATGTTCCCATCAAGGGCAAGTT 769
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Qy 770 CGGCTCTTTGTTGAGATGAACACTCAGACTCTGGGCTCTTCACTGTTCTGAGGGCGT 829
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Qy 830 CCAGAACTTCAGCAAGATCCACCTGTTGAGAGATGGAATGGGCTCAGCAAGGTCAACTA 889
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Job time : 1479.74 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 18:13:56 ; Search time 549.461 Seconds
(without alignments)
6938.932 Million cell updates/sec

Title: US-08-765-108-3

Perfect score: 1788

Sequence: 1 GCCACCTGAGGGCTACTGC.....CTCTCAGCGGACAGTCGC 1788

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1788	100.0	1788	12	US-11-128-061-1074
2	1788	100.0	1788	12	US-11-128-049-1074
3	1424.6	79.7	2497	12	US-11-136-527-2943
4	1255.8	70.2	1531	9	US-11-222-745-3
5	1137.8	63.6	2569	9	US-10-821-234-66
6	1136.2	63.5	2566	9	US-11-072-175-90
7	1136.2	63.5	2566	12	US-11-055-309A-11
8	1061.2	59.4	1530	9	US-11-222-745-8
9	623.4	34.9	1400	12	US-11-136-527-7039
10	600	33.6	600	12	US-11-128-061-4716
11	600	33.6	600	12	US-11-128-049-4716
12	172.6	9.7	2076	12	US-11-136-527-1803
13	132.6	7.4	1400	12	US-11-136-527-5899
14	70.6	3.9	2216	8	US-10-909-125-1747
15	65	3.6	506	6	US-09-925-065A-51554
16	63	3.5	2675	12	US-11-136-527-2950
17	59.4	3.3	645	6	US-09-925-065A-675492
18	52.2	2.9	1910	12	US-11-128-061-1101
19	52.2	2.9	1910	12	US-11-128-049-1101
20	46.2	2.6	2718	6	US-09-925-065A-701020

c	21	45.2	2.5	610	6	US-09-925-065A-869021	Sequence 869021,
c	22	45.2	2.5	610	6	US-09-925-065A-869022	Sequence 869022,
c	23	44	2.5	496	12	US-11-128-061-2632	Sequence 2632, Ap
c	24	44	2.5	496	12	US-11-128-061-2632	Sequence 2632, Ap
c	25	44	2.5	496	12	US-11-128-049-2632	Sequence 2632, Ap
c	26	44	2.5	496	12	US-11-128-049-2674	Sequence 2674, Ap
c	27	43	2.3	2024	12	US-11-004-762-21	Sequence 21, Appl
c	28	41.4	2.3	2828	12	US-11-004-762-22	Sequence 22, Appl
c	29	40.8	2.3	3370	9	US-11-072-512-338	Sequence 338, Appl
c	30	40.2	2.2	23187	9	US-11-236-198-1	Sequence 1, Appli
c	31	39.6	2.2	9474	12	US-11-052-554A-526	Sequence 526, App
c	32	39.2	2.2	1109	8	US-10-955-054A-56	Sequence 56, Appl
c	33	39.2	2.2	2870	12	US-11-169-041-63	Sequence 63, Appl
c	34	38.6	2.2	833	8	US-10-750-185-56670	Sequence 56670, A
c	35	38.6	2.2	833	8	US-10-750-623-56670	Sequence 56670, A
c	36	38.2	2.1	630	6	US-09-925-065A-475014	Sequence 475014,
c	37	37.4	2.1	5300	12	US-11-000-688-563	Sequence 563, App
c	38	37.4	2.1	6615	12	US-11-052-554A-518	Sequence 518, App
c	39	37.2	2.1	2240	12	US-11-064-769-18	Sequence 18, Appl
c	40	37.2	2.1	7944	8	US-10-821-234-451	Sequence 451, App
c	41	37	2.1	1322	6	US-09-925-065A-673557	Sequence 673557,
c	42	37	2.1	1397	6	US-09-925-065A-704019	Sequence 704019,
c	43	36.8	2.1	2644	12	US-11-136-527-2717	Sequence 2717, Ap
c	44	36.6	2.0	347	6	US-09-925-065A-489729	Sequence 489729,
c	45	36.6	2.0	347	6	US-09-925-065A-489730	Sequence 489730,

ALIGNMENTS

RESULT 1

US-11-128-061-1074
; Sequence 1074, Application US/11/128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1074
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-1074

Query Match	100.0%	Score 1788;	DB 12;	Length 1788;
Best Local Similarity	100.0%	Pred. No. 0;		
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			Indels	0;
			Gaps	0;
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Qy	61	AGCTCGGCTTCTGTCATCTCTGTGCGCTCTGTGCGCTCTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTG	120	
Db	61	AGCTCGGCTTCTGTCATCTCTGTGCGCTCTGTGCGCTCTGTGCGCTCTGTGCTGCTGCTGCTGCTGCTG	120	
Qy	121	CTTGAGCCCGGAGCCCGGGCCGCGACGCGGACATGGCGCGAGCCGCGAGCCGCGCGCTT	180	
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Db 121 GCTCAAGAATGTCCGATAGACCCAGCAGCCTGTCTCTTTGCAATGTGGAAGAGATCCC 180
Qy 335 TGTACCCCTTCTACTGTCCGTCTACTTCTTCGAGGTGGTCAATCCAGCGAGATCCTAAA 394
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Qy 575 GGTCTTTGGGGGCGCAGTGAATGATGAGAGCAAGTCTGCAGGCTCTGAAGCTGATGATG 634
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Qy 695 GTGGGCTGAGAGTCCCTTGTGTAATTTTCAACAAATATCTTACAGACAGTGTCC 754
Db 541 GTGGGCTGAGAGTCCCTTGTGTAATTTTCAACAAATATCTTACAGACAGTGTCC 600
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Qy 815 TGTGTTTCAAGGCGTCCAGAACTTCAAGAGATCTCACTGGTGCACAGATGAATGGGT 874
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Qy 875 CAGCAAGGTCAACTTCTGCGATTTCAAGAGATCTCACTGGTGCAGATGAATGGGT 934
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Db 1141 CCCCATGAATGTTGTGAGTTGAGATTAAGCTCTTACATCAAGAGCTGTCAAGGCGAT 1200

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Qy 1415 TGGCATGGGCGGAGGCCCTCTGAACACAGTTCTACAGCAGCTGGTGTGATGATGATGATG 1474
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Qy 1475 ACTTCAGTATGTGCAATGTGCTGCTGGGCTGGGCGCTCTCTCTGCTGCTGCTGCTGCTG 1534
Db 1321 TCTTCTAGTGGCAGTATGTGCTGCTGGGCTGGGCGCTCTCTCTGCTGCTGCTGCTGCTG 1380
Qy 1535 CATCTACCAAGTTTGGCAGCAGCAGGAAATGCTTTTTTATTTTGGAGTGGTAGTAAAAAGGG 1594
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Qy 1655 GGGCAGCGTGTGCAAGAGCCAAAGCTGTAG 1685
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RESULT 5

US-10-821-234-66/c
; Sequence 66, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 66
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-66

Query Match 63.6%; Score 1137.8; DB 8; Length 2569;
Best Local Similarity 80.1%; Pred. No. 1.1e-307;
Matches 1337; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

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721 AGCAAGTTCACCTTCCGATTCAGATTCAGTCAAGTCAATGATCAATGGCACTTCGGGCA 780
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996 AGGTCTATGAAGTCACTACCTACATGATTCAGGGGTGTTTCAAGGCACTCCCACTATCGC 1055
841 CGATCCATGAAGTATGATCAAGAGTCAAGGGTGTGAGGATCCCACTATCGC 900
1056 TTCACAGCCCTTAAACTTTGTTTGGCAATGGGTGTTTACCCCAATGAAGGTTTC 1115
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1021 TTTCTCTCCATCTCACTTCTCAAGCCGACCCGGTTCGAGAGCGGTGACTGGC 1080
1236 CTGAACCTTGACCAAGGGAGCATTTCTTTGTTCTTGAATCCATCCGCTCACTGGGATC 1295
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1141 CCATGAATCTGTTGTAAGTTCAGATGAAGCTCTTACATGAATCTGTCAGAGCAAT 1200
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1416 GCCATGGGGCGGAGCCCTTGAACACAGCTTCTACAGCAGCTGTGTGCTGATGCCCAAGTA 1475
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1476 CTTCACTATGTCAGTATGCTGTGGGCTGGGGCTCTCTGCTGTGTGCTGCTGCTGCTG 1535
1321 ATGCACTATGCCAGTACGTCCTCTGGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTG 1380
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1656 GGCACGGTGTGCAAGAGCAAGCTGTAG 1685
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US-11-136-527-7039

; Sequence 7039, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7039
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-7039

Query Match 34.9%; Score 623.4; DB 12; Length 1400;

Best Local Similarity 89.6%; Pred. No. 5.7e-164;

Matches 657; Conservative 10; Mismatches 66; Indels 0; Gaps 0;

QY 1051 ATCGCTTACAGCCCTTAAACTTTGTTTGGCAATGGGTCTGTTACCCACCCCAATGAAG 1110
Db 1 ATCGCTTACAGCCCTTAAACTTTGTTTGGCAATGGGTCTGTTACCCACCCCAATGAAG 60
QY 1111 GTTTCGCGCTGCTTGAATCCGGCATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 1170
Db 61 GTTTCGCGCTGCTTGAATCCGGCATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 120
QY 1171 CCCTGTTTCTGTACACCTCTCACTTCTCAATTCGCAATTCGCAATTCGCAATTCGCA 1230
Db 121 CCCTGTTTCTCTCCAGCCCACTTCTCAATTCGCAATTCGCAATTCGCAATTCGCA 180
QY 1231 TGGGTCTGAACCTTGAACCAAGGAGCATTTCTTGTTCCTTGACATTCATCCCGTCACTG 1290
Db 181 TTGGTCTGAACCTTGAACCAAGGAGCATTTCTTGTTCCTTGACATTCATCCCGTCACTG 240
QY 1291 GGATCCCAATGAATCTGTTCCGTAAGATGAGTGTGTATCAKAAATCCGTCAGAG 1350
Db 241 GGATCCCAATGAATCTGTTCCGTAAGATGAGTGTGTATCAKAAATCCGTCAGAG 300
QY 1351 GCATTTGGGCAACAGAGGAGATCGAGCCCGTGTCTCCCATTTGCTGTGTGTTGAGCAGA 1410
Db 301 GCGTGGGCAACAGAGGAGATCGAGCCAGTAGTCTGCAATTTGCTGTGTGTTGAGCAGA 360
QY 1411 GCGGTGCCATGGGCGGAGCCCTTGAAACAGTTCACAGCAGCTGTGTGATGCGCCC 1470
Db 361 GCGGTGATGATGGGTGGCAAGACCTTGAAACAGTTCACAGCAGCTGTGTGATGCGCCC 420
QY 1471 AGGTACTTCAAGTATGTCAGTATGTCGTGGGCTGGGCGGCTCTGCTGCTGCTGCTG 1530
Db 421 ARGTTCTTCACTACGCGCAGTATGTCGTGGGCTGGGCGGCTCTGCTGCTGCTGCTG 480
QY 1531 CCGTCACTACCAAGTTCGCGCAGCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAA 1590
Db 481 CCATCAATTTACCACTGCGCGCAGCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAA 540
QY 1591 AGGGCTCGCAGGATTAAGAGGCAATTCAGGCTTCTCTGAGTCTCTGATGTCTACAGCTG 1650
Db 541 AGGGCTCGCAGGATTAAGAGGCAATTCAGGCTTCTCTGAGTCTCTGATGTCTACAGCTG 600
QY 1651 CCAAGGCAAGGCTGTGCAAGAGCCAGCTGTAGGTCCTCAAGACACACGAGCCCCC 1710
Db 601 CCAAGGCAAGGCTGTGCAAGAGCCAGCTGTAGGTCCTCAAGACACACGAGCCCCC 660
QY 1711 CCAACTGTAGTGTGTCAGACAGCCATTCAGCCCTTACACCCCGCTTCTTGTAGACT 1770
Db 661 CCAACTGTAGTGTGTCAGACAGCCATTCAGCCCTTACACCCCGCTTCTTGTAGACT 720
QY 1771 CTCTCAGCGGACA 1783
|||||

Db 721 CTCTCAGCGGACA 733

RESULT 10

US-11-128-061-4716
; Sequence 4716, Application US/11128061
; Publication No. US2006003958A1

GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE OF INVENTION: TO MONITOR GENE EXPRESSION

; FILE REFERENCE: 01997.027701

; CURRENT APPLICATION NUMBER: US/11/128,061

; PRIOR FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4716

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Cricetulus griseus

US-11-128-061-4716

Query Match 33.6%; Score 600; DB 12; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.5e-157;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1189	CTC	ACTTCTTACAATG	CAGACCCCTG	TGCTATC	AGAAGCCG	TTCTGGGTCT	GAAACCCCTG	AGCC	1248	
Db	1	CTC	ACTTCTTACAATG	CAGACCCCTG	TGCTATC	AGAAGCCG	TTCTGGGTCT	GAAACCCCTG	AGCC	60	
QY	1249	CA	AGGAGGATCTT	TGTTCTT	GACATCC	ATCCGGT	CACTGGGAT	CCCCATG	AACTGTT	1308	
Db	61	CA	AGGAGGATCTT	TGTTCTT	GACATCC	ATCCGGT	CACTGGGAT	CCCCATG	AACTGTT	120	
QY	1309	CTG	TGAAGTTG	CAGATAAG	CTCTAC	ATCAAG	CTGTCA	AGGCGCAT	TGGGCAAC	AGGGA 1368	
Db	121	CTG	TGAAGTTG	CAGATAAG	CTCTAC	ATCAAG	CTGTCA	AGGCGCAT	TGGGCAAC	AGGGA 180	
QY	1369	AG	ATCGAGCCCG	TGGTCT	CTCCCAT	TGCTGTG	TTTGAG	CAGACGGT	GCATGGGCGG	1428	
Db	181	AG	ATCGAGCCCG	TGGTCT	CTCCCAT	TGCTGTG	TTTGAG	CAGACGGT	GCATGGGCGG	240	
QY	1429	AG	CCCTGAA	CAGCTT	CTAC	AGCAGT	GGTGTG	TGATG	CCCCCAGG	TACTTCAGTATGTC 1488	
Db	241	AG	CCCTGAA	CAGCTT	CTAC	AGCAGT	GGTGTG	TGATG	CCCCCAGG	TACTTCAGTATGTC 300	
QY	1489	AG	TATGTG	CTGTGG	GGCTC	CTCTG	CTGTG	CCGTC	ATCTAC	CAGTTGC 1548	
Db	301	AG	TATGTG	CTGTGG	GGCTC	CTCTG	CTGTG	CCGTC	ATCTAC	CAGTTGC 360	
QY	1549	GC	AGCCAGG	AGAAATG	CTTTT	TATTTT	TGGAGT	GGTAGT	AAAAAGG	CTCCAGGATAAGG 1608	
Db	361	GC	AGCCAGG	AGAAATG	CTTTT	TATTTT	TGGAGT	GGTAGT	AAAAAGG	CTCCAGGATAAGG 420	
QY	1609	AG	GCATTC	CAGGCT	ACTCT	GAGT	CTCTG	ATGTC	ACAGT	GCACGGGACCGGTGTC 1668	
Db	421	AG	GCATTC	CAGGCT	ACTCT	GAGT	CTCTG	ATGTC	ACAGT	GCACGGGACCGGTGTC 480	
QY	1669	A	AGAGCC	CAAGCT	GTAG	GGTCCC	AAAG	CACAC	CAGG	CCCCCCTC	ATAGTTGTT 1728
Db	481	A	AGAGCC	CAAGCT	GTAG	GGTCCC	AAAG	CACAC	CAGG	CCCCCCTC	ATAGTTGTT 540
QY	1729	C	AGAC	CCATC	CAGCC	CTTAC	CCCCG	CTTCT	TGAG	GA	CTCTCTCAGCGGACAGTGC 1788

Db 541 CAGACCAGCCATCCAGCCCTACACCCGCTTCTTGGAGTCTCTCTCAGCGGACAGTGC 600

RESULT 11

US-11-128-049-4716

; Sequence 4716, Application US/11128049

; Publication No. US20060010513A1

GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

; FILE OF INVENTION: MAKING AND USING SAME

; FILE REFERENCE: 01997.027700

; CURRENT APPLICATION NUMBER: US/11/128,049

; PRIOR FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4716

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Cricetulus griseus

US-11-128-049-4716

Query Match 33.6%; Score 600; DB 12; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.5e-157;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1189	CTC	ACTTCTTACAATG	CAGACCCCTG	TGCTATC	AGAAGCCG	TTCTGGGTCT	GAAACCCCTG	AGCC	1248	
Db	1	CTC	ACTTCTTACAATG	CAGACCCCTG	TGCTATC	AGAAGCCG	TTCTGGGTCT	GAAACCCCTG	AGCC	60	
QY	1249	CA	AGGAGGATCTT	TGTTCTT	GACATCC	ATCCGGT	CACTGGGAT	CCCCATG	AACTGTT	1308	
Db	61	CA	AGGAGGATCTT	TGTTCTT	GACATCC	ATCCGGT	CACTGGGAT	CCCCATG	AACTGTT	120	
QY	1309	CTG	TGAAGTTG	CAGATAAG	CTCTAC	ATCAAG	CTGTCA	AGGCGCAT	TGGGCAAC	AGGGA 1368	
Db	121	CTG	TGAAGTTG	CAGATAAG	CTCTAC	ATCAAG	CTGTCA	AGGCGCAT	TGGGCAAC	AGGGA 180	
QY	1369	AG	ATCGAGCCCG	TGGTCT	CTCCCAT	TGCTGTG	TTTGAG	CAGACGGT	GCATGGGCGG	1428	
Db	181	AG	ATCGAGCCCG	TGGTCT	CTCCCAT	TGCTGTG	TTTGAG	CAGACGGT	GCATGGGCGG	240	
QY	1429	AG	CCCTGAA	CAGCTT	CTAC	AGCAGT	GGTGTG	TGATG	CCCCCAGG	TACTTCAGTATGTC 1488	
Db	241	AG	CCCTGAA	CAGCTT	CTAC	AGCAGT	GGTGTG	TGATG	CCCCCAGG	TACTTCAGTATGTC 300	
QY	1489	AG	TATGTG	CTGTGG	GGCTC	CTCTG	CTGTG	CCGTC	ATCTAC	CAGTTGC 1548	
Db	301	AG	TATGTG	CTGTGG	GGCTC	CTCTG	CTGTG	CCGTC	ATCTAC	CAGTTGC 360	
QY	1549	GC	AGCCAGG	AGAAATG	CTTTT	TATTTT	TGGAGT	GGTAGT	AAAAAGG	CTCCAGGATAAGG 1608	
Db	361	GC	AGCCAGG	AGAAATG	CTTTT	TATTTT	TGGAGT	GGTAGT	AAAAAGG	CTCCAGGATAAGG 420	
QY	1609	AG	GCATTC	CAGGCT	ACTCT	GAGT	CTCTG	ATGTC	ACAGT	GCACGGGACCGGTGTC 1668	
Db	421	AG	GCATTC	CAGGCT	ACTCT	GAGT	CTCTG	ATGTC	ACAGT	GCACGGGACCGGTGTC 480	
QY	1669	A	AGAGCC	CAAGCT	GTAG	GGTCCC	AAAG	CACAC	CAGG	CCCCCCTC	ATAGTTGTT 1728
Db	481	A	AGAGCC	CAAGCT	GTAG	GGTCCC	AAAG	CACAC	CAGG	CCCCCCTC	ATAGTTGTT 540
QY	1729	C	AGAC	CCATC	CAGCC	CTTAC	CCCCG	CTTCT	TGAG	GA	CTCTCTCAGCGGACAGTGC 1788

Db 1544 CAGAGTCA 1552

RESULT 15

US-09-925-065A-515554
 ; Sequence 515554, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 515554
 ; LENGTH: 506
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-515554

Query Match 3.6%; Score 65; DB 6; Length 506;
 Best Local Similarity 76.2%; Pred. No. 4.9e-08;
 Matches 80; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1684 AGGGTCCCAAGACACACAGCCGCCCTGAGCTGATAGCTGGTCAGACGACCCATCCA 1743
 Db 384 AGGGTCTGAGGACACCGTGAGCCAGCCAGGCTGGCGCTGGGGCTGACCGGCCCCCA 443
 QY 1744 GCCCTACACCCCGCTTCTTGGAGCTCTCTCAGCGGACAGTCGC 1788
 Db 444 GCCCTACACCCCGCTTCTCCCGACTCTCCCGAGGACAGCCCC 488

Search completed: February 23, 2006, 18:46:01
 Job time : 552.461 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:34:44 ; Search time 152 Seconds
(without alignments)
1471.341 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2881
Sequence: 1 MGSSARWVAVGLGVGVL.....YSESLMSPAAGTGVQRAKL 509

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	2 AAR88465	Aar88465 Hamster s
2	2681	100.0	509	2 AAW93574	Aaw93574 Hamster s
3	2681	100.0	509	2 AAY44019	Aay44019 Hamster s
4	2681	100.0	509	5 ABG33056	Abg33056 Hamster s
5	2681	100.0	509	5 AAE21523	Aae21523 Hamster s
6	2681	100.0	509	6 ABO27241	Abc27241 Human sca
7	2681	100.0	509	8 ADJ46121	Adj46121 Human sca
8	2681	100.0	509	8 ADJ53335	Adj53335 Hamster s
9	2681	100.0	509	8 ADU51467	Adu51467 Hamster s
10	2525	94.2	509	9 AEB03938	Aeb03938 Hamster s
11	2453	91.5	509	8 ADU51468	Adu51468 Mouse sca
12	2447	91.3	509	2 AAW93575	Aaw93575 Mouse sca
13	2447	91.3	509	2 AAY44020	Aay44020 Mouse sca
14	2447	91.3	509	5 ABB57092	Abb57092 Mouse isc
15	2447	91.3	509	5 AAE21525	Aae21525 Murine sc
16	2447	91.3	509	8 ADJ53337	Adj53337 Murine SR
17	2447	91.3	509	9 ADZ13455	Adz13455 Murine ca
18	2447	91.3	509	9 AEB03940	Aeb03940 Murine ca
19	2447	91.3	519	8 ABO84950	Abc84950 Murine ca
20	2447	91.3	519	8 ADR67033	Adr67033 Mouse can
21	2444	91.2	509	8 ADU51466	Adu51466 Rat scave
22	2444	91.2	510	7 ADE56446	Ade56446 Rat Prote
23	2444	91.2	510	7 ADE56442	Ade56442 Rat Prote
24	2430	90.6	509	7 ADE55241	Ade55241 Rat Prote

25	2244	83.7	509	6 ABO27240	Abc27240 Human sca
26	2244	83.7	509	8 ADJ46119	Adj46119 Human sca
27	2244	83.7	509	9 ADZ13464	Adz13464 Human can
28	2244	83.7	509	9 ADZ13458	Adz13458 Human can
29	2244	83.7	514	9 ADZ13466	Adz13466 Human can
30	2237	83.4	509	2 AAW97900	Aaw97900 Human SR-
31	2237	83.4	532	4 ABB12012	Abb12012 Human SR-
32	2237	83.4	532	7 ADE09273	Ade09273 Novel pro
33	2236	83.4	509	2 AAY49573	Aay49573 Human CLA
34	2236	83.4	509	6 AAO31106	Aao31106 Human CD3
35	2236	83.4	509	8 ADL61295	Adl61295 Human sca
36	2236	83.4	510	7 ADE56448	Ade56448 Human Pro
37	2236	83.4	510	7 ADE56444	Ade56444 Human Pro
38	2234	83.3	506	9 ADZ13453	Adz13453 Murine ca
39	2227	83.1	509	2 AAW97899	Aaw97899 Human SR-
40	2203	82.2	509	7 ADE40210	Ade40210 Human NOV
41	2117	79.0	481	7 ADE08291	Ade08291 Novel pro
42	2112.5	78.8	537	4 ABG22317	Abg22317 Novel hum
43	2086.5	77.1	552	6 ABR62035	Abr62035 Human SR-
44	2066.5	77.1	552	7 ADE55243	Ade55243 Human Pro
45	2066.5	77.1	552	8 ADP23287	Adp23287 PRO polyp

ALIGNMENTS

RESULT 1

AAAR88465	AAAR88465	standard; protein; 509 AA.
XX	AC	AAAR88465;
XX	XX	
DT	29-MAR-1996	(first entry)
DE	XX	Hamster scavenger receptor class B-I.
XX	KW	Scavenger receptor class BI; HaSR-BI; low density lipoprotein;
KW	KW	atherosclerosis; CHO; Chinese hamster ovary; lipoprotein receptor;
KW	KW	cholesterol.
XX	XX	
OS	Cricetulus sp.	
XX	XX	
FH	Key	Location/Qualifiers
FT	Domain	9..32
FT	Disulfide-bond	/label= Putative_transmembrane_domain
FT	Disulfide-bond	21..470
FT	Disulfide-bond	/note= "the cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulphide linkages"
FT	Modified-site	102..104
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	108..110
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	173..175
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	212..214
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	227..229
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	255..257
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	310..312
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	330..332
FT	Modified-site	/label= N-glycosylation_site
FT	Modified-site	383..385
FT	Modified-site	/label= N-glycosylation_site
FT	Domain	440..464
FT	Domain	/label= Putative_transmembrane_domain
XX	XX	
FN	W09600288-A2.	
XX	XX	
PD	04-JAN-1996.	

XX 19-JUN-1995; 95WO-US007721.
 XX 23-JUN-1994; 94US-00265428.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Krieger M, Acton SL, Pearson AM, Rigotti A;
 XX WPI; 1996-068872/07.
 XX N-PSDB; AAT10116.
 XX Class BI and CI scavenger receptor proteins - used to develop products
 PT for treating or preventing atherosclerosis, fat uptake by adipocyte(s)
 PT and immune disorders.
 XX Claim 5; Page 57-58; 84pp; English.
 XX A new hamster class B-I scavenger receptor, hasR-BI (AAR88465),
 CC selectively binds to low density lipoprotein (LDL) and to acetylated LDL.
 CC It was obtd. by expression of a cDNA clone (AAT10116) isolated from an
 CC expression library prepd. from CHO line Var-261 mRNA. hasR-BI is used to
 CC screen for cpds. that alter binding of scavenger receptor proteins to LDL
 CC or modified lipoprotein, to remove LDL from patient blood, to inhibit
 CC uptake of lipoprotein or lipids by adipocytes, to develop anti-
 CC atherosclerosis drugs, to treat some immune disorders and to raise
 CC diagnostic or therapeutic antibodies
 XX
 XX Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
 QY 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 DB 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSES DYIILPNILVLGGAVNMESKSAKGLKMLMTLGLATLGQAFMNRVTGCEIL 180
 DB 121 FQDRSHGSES DYIILPNILVLGGAVNMESKSAKGLKMLMTLGLATLGQAFMNRVTGCEIL 180
 QY 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 DB 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 QY 241 SKVNYWHSEQCNNINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 DB 241 SKVNYWHSEQCNNINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
 DB 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
 QY 361 LNPDPRHSFLDHPVTGIPMNC SVKQLISLYIKAVKGIGQTKIEPVVLP LLLWPFQSG 420
 DB 361 LNPDPRHSFLDHPVTGIPMNC SVKQLISLYIKAVKGIGQTKIEPVVLP LLLWPFQSG 420
 QY 421 AMGGEPLNTFYTLVMPQVLYQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 DB 421 AMGGEPLNTFYTLVMPQVLYQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 QY 481 SQDKAALQAYSESLSMPAAKGTVLQEAKL 509
 DB 481 SQDKAALQAYSESLSMPAAKGTVLQEAKL 509

ID AAW93574 standard; protein; 509 AA.
 XX AAW93574;
 XX 17-JUN-1999 (first entry)
 XX Hamster scavenger receptor class B-I protein.
 XX Scavenger receptor class B type I; hamster; steroid production; HDL;
 KW cholesterol; cholesteryl ester transport; high-density lipoprotein;
 KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;
 KW treatment; disorder; overproduction; underproduction; menopause;
 KW breast cancer; prostate cancer; endometriosis; fibroid tumour.
 XX Cricetulus griseus.
 XX WO9911288-A1.
 XX 11-MAR-1999.
 XX 04-SEP-1998; 98WO-US018463.
 XX 05-SEP-1997; 97US-0057943P.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Krieger M;
 XX WPI; 1999-204984/17.
 XX N-PSDB; AAX23403.
 XX Modification of steroid production in mammals - by administering
 PT modulator of SR-BI expression or activity.
 XX Disclosure; Page 79-80; 86pp; English.
 XX This invention describes a method for modifying steroid production in a
 CC mammal which comprises administering a compound that alters cholesterol
 CC or cholesteryl ester transport from high-density lipoprotein (HDL) or
 CC other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger
 CC receptor class B type I). This method is useful for female contraception,
 CC for treating disorders characterised by overproduction of steroids, for
 CC treating disorders characterised by underproduction of steroids,
 CC especially menopause, for treating disorders that can be treated by
 CC decreasing steroid production, especially breast cancer, prostate cancer,
 CC endometriosis or fibroid tumours
 XX
 XX Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
 QY 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 DB 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSES DYIILPNILVLGGAVNMESKSAKGLKMLMTLGLATLGQAFMNRVTGCEIL 180
 DB 121 FQDRSHGSES DYIILPNILVLGGAVNMESKSAKGLKMLMTLGLATLGQAFMNRVTGCEIL 180
 QY 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 DB 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 QY 241 SKVNYWHSEQCNNINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 DB 241 SKVNYWHSEQCNNINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300

QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIBPVVLPVLPLWFQSG 420
 Db 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIBPVVLPVLPLWFQSG 420
 QY 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLVPVVIYQLRSQEKCFLEWGSKKG 480
 Db 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLVPVVIYQLRSQEKCFLEWGSKKG 480
 QY 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509
 Db 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509

RESULT 3
 AAY44019
 ID AAY44019 standard; protein; 509 AA.
 XX AC AAY44019;
 XX XX
 DT 18-JAN-2000 (first entry)
 XX XX
 DE Hamster Scavenger receptor class BI protein.
 XX XX
 KW Hamster; scavenger receptor; modulation; cholesterol transport; lipid;
 KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;
 KW high density lipoprotein; ester; blood.
 XX OS Cricetulus sp.
 XX XX
 PN US5962322-A.
 XX XX
 PD 05-OCT-1999.
 XX XX
 PF 15-NOV-1996; 96US-00749907.
 XX XX
 PR 15-NOV-1996; 96US-00749907.
 XX XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (NASI) MASSACHUSETTS INST TECHNOLOGY.
 XX XX
 PI Krieger M, Rigotti A, Kozarsky K;
 XX XX
 DR WPI; 1999-589717/50.
 DR N-PSDB; AAZ30615.
 XX XX
 XX Modulating cholesterol transport for the control of cholesterol levels in
 PT blood.
 PT PT
 XX XX
 PS Disclosure; Col 21-24; 23pp; English.
 XX XX
 CC This sequence represents the hamster scavenger receptor class BI (SR-BI)
 CC which is used in a method of modulating cholesterol transport. The method
 CC comprises selectively altering the transport of lipid, cholesterol and/or
 CC lipoproteins (or their components) into and out of mammalian cells to
 CC alter plasma cholesterol levels, by administering a compound which alters
 CC the expression or activity of the SR-BI scavenger protein receptor. This
 CC alters the rate of clearance of the protein component of high density
 CC lipoprotein (HDL) as compared to the ester component of HDL. The method
 CC may be used to control cholesterol levels in the blood plasma of mammals
 XX XX
 SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSARARWAVGLGVVGLLCVAVLGVVMIWPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 Db 1 MGGSARARWAVGLGVVGLLCVAVLGVVMIWPSLIKQVVKVNRIDPSSLSFAMWKEIP 60

QY 61 VPFLSYVFEVNVNPSBILKGEKVPVVRGPPYVYRFRHKANITFNDNDTVSFVHRSLH 120
 Db 61 VPFLSYVFEVNVNPSBILKGEKVPVVRGPPYVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSSSDYIILPNILVLGAVNMESKAGLKMMTLGLATLQORAFMNRVTGEIL 180
 Db 121 FQDRSHGSSSDYIILPNILVLGAVNMESKAGLKMMTLGLATLQORAFMNRVTGEIL 180
 QY 181 WGYEDFPVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240
 Db 181 WGYEDFPVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240
 QY 241 SKVNYHSEOCNMINGTSGQMWAPFMTPOSSLBFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEOCNMINGTSGQMWAPFMTPOSSLBFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIBPVVLPVLPLWFQSG 420
 Db 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIBPVVLPVLPLWFQSG 420
 QY 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLVPVVIYQLRSQEKCFLEWGSKKG 480
 Db 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLVPVVIYQLRSQEKCFLEWGSKKG 480
 QY 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509
 Db 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509

RESULT 4
 ABG33056
 ID ABG33056 standard; protein; 509 AA.
 XX AC ABG33056;
 XX XX
 DT 20-NOV-2002 (first entry)
 XX XX
 DE Hamster scavenger receptor type B1 (haSR-B1).
 KW Hamster; scavenger receptor protein type B1; low density lipoprotein;
 KW LDL; cholesterol; endothelial; adipose; macrophage; lipoprotein receptor;
 KW receptor.
 XX OS Cricetulus griseus.
 XX XX
 PN US6429289-B1.
 XX XX
 PD 06-AUG-2002.
 XX XX
 PF 23-JUN-1994; 94US-00265428.
 XX XX
 PR 23-JUN-1994; 94US-00265428.
 XX XX
 PA (NASI) MASSACHUSETTS INST TECHNOLOGY.
 XX XX
 PI Krieger M, Acton SL, Pearson AM;
 XX XX
 DR WPI; 2002-689668/74.
 DR N-PSDB; ABS53744.
 XX XX
 PT New scavenger receptor protein type B1 useful for screening for drugs
 PT that inhibit the uptake of cholesterol in endothelial or adipose cells or
 PT macrophages.
 XX XX
 PS Claim 1; Col 29-32; 31pp; English.
 XX XX
 CC The present invention relates to a new scavenger receptor protein type B1
 CC which selectively binds to low density lipoprotein (LDL) and modified

CC lipoprotein with the characteristics of acetylated LDL. The invention is
 CC useful for screening for drugs that inhibit the uptake of cholesterol in
 CC endothelial or adipose cells or macrophages, and for screening for other
 CC lipoprotein receptors. The present amino acid sequence represents the
 CC hamster scavenger receptor protein type B1 (hasR-B1) of the invention
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFEVNVNPSILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Db 61 VPFYLSVYFEVNVNPSILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Qy 121 FQDRSHGSDYIIILPNILVLGGAVMMESKSLKLMMTLGLATLQRAFNMRTVGEIL 180
 Db 121 FQDRSHGSDYIIILPNILVLGGAVMMESKSLKLMMTLGLATLQRAFNMRTVGEIL 180
 Qy 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPDPRHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGQTKIPVVLPLLWEOQS 420
 Db 361 LNPDPRHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGQTKIPVVLPLLWEOQS 420
 Qy 421 AMGGEPLNTFYTLVLMQVQLVYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGEPLNTFYTLVLMQVQLVYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Qy 481 SQDKEATQAYSESLSMPAAKGTVLQEA 509
 Db 481 SQDKEATQAYSESLSMPAAKGTVLQEA 509
 RESULT 5
 AAE21523 standard; protein; 509 AA.
 AC AAE21523;
 XX
 XX 16-JUL-2002 (first entry)
 DT
 XX
 DE Hamster scavenger receptor type B-I (hasR-BI).
 XX
 KW Scavenger receptor protein type B1; low density lipoprotein; LDL;
 KW hamster; SR-BI.
 XX
 OS Cricetulus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 9..32
 FT /note= "Putative transmembrane domain"
 FT Modified-site 102..104
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 108..110
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 173..175
 FT /note= "Potential N-linked glycosylation site"

FT Modified-site 212..214
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 227..229
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 255..257
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 310..312
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 330..332
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 383..385
 FT /note= "Potential N-linked glycosylation site"
 FT Domain 440..464
 FT /note= "Putative transmembrane domain"
 XX
 PN US6350859-B1.
 XX
 XX 26-FEB-2002.
 PD
 XX
 XX 02-FEB-1999; 99US-00241581.
 PP
 XX
 XX 23-JUN-1994; 94US-00265428.
 PR
 XX 27-MAR-1997; 97US-00765108.
 PR
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Krieger M, Acton SL, Rigotti A;
 XX
 DR WPI; 2002-314680/35.
 DR N-PSDB; AAD33915.
 XX
 PT Antibody specific for scavenger receptor protein type B1 useful for
 PT detection, characterization or isolation of receptor proteins, as well
 PT inhibiting scavenger protein binding to low density lipoprotein.
 XX
 PS Claim 1; Col 33-36; 41pp; English.
 XX
 CC The invention relates to an antibody specific for scavenger receptor
 CC protein type B-I (SR-BI) derived from murine and hamster. Antibodies of
 CC the invention are useful for detection, characterization and isolation of
 CC receptor proteins and for inhibiting scavenger protein binding to low
 CC density lipoprotein (LDL). The present sequence is hamster (ha) SR-BI
 CC protein
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFEVNVNPSILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Db 61 VPFYLSVYFEVNVNPSILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Qy 121 FQDRSHGSDYIIILPNILVLGGAVMMESKSLKLMMTLGLATLQRAFNMRTVGEIL 180
 Db 121 FQDRSHGSDYIIILPNILVLGGAVMMESKSLKLMMTLGLATLQRAFNMRTVGEIL 180
 Qy 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFDHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIEPVVPLLWFQSG 420
Db 361 LNPDPREHSLFDHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIEPVVPLLWFQSG 420
Qy 421 AMGGEPLNTFTQVLMPQVLYVYVLLGLGGLLLVPVYIQLRSQKCFWWSGSKG 480
Db 421 AMGGEPLNTFTQVLMPQVLYVYVLLGLGGLLLVPVYIQLRSQKCFWWSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTGLVLEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTGLVLEAKL 509

RESULT 6

ABO27241
ID ABO27241 standard; protein; 509 AA.

XX AC ABO27241;

XX DT 10-SEP-2003 (first entry)

XX DE Human scavenger receptor BI, splice variant.

XX KW Human; receptor; scavenger receptor BI; SR-BI; cardiant; antilipemic;
KW high density lipoprotein; HDL; hormone replacement therapy;
KW postmenopausal female; cardiovascular disorder; coronary heart disease;
KW atherosclerosis; stroke; ischaemia; restenosis; congestive heart failure;
KW gangrene.

XX OS Homo sapiens.

XX PN US2003044782-A1.

XX PD 06-MAR-2003.

XX PF 08-FEB-2001; 2001US-00779152.

XX PR 10-JUL-1997; 97US-00890979.

XX PR 27-FEB-1998; 98US-00031626.

XX PA (ACTO/) ACTON S. L.

XX PA (MCCA/) MCCARTHY J. J.

XX PI Acton SL, McCarthy JJ;

XX DR WPI; 2003-503489/47.

XX DR N-PSDB; ACD44926.

PT Determining if a subject has or is at risk of developing abnormally low
PT high density lipoprotein level, involves determining identity of allelic
PT variant of polymorphic region of SR-BI gene of the subject.

PS Example 1; Fig 3; 84pp; English.

XX The invention relates to determining whether a subject has, or is at risk
XX of developing, an abnormally low high density lipoprotein (HDL) level,
XX involves determining the identity of the allelic variant of a polymorphic
XX region of the SR-BI (scavenger receptor BI) gene of the subject, and
XX comparing the allelic variant of the subject with allelic variants
XX associated with abnormally low HDL levels. Also included are a kit for
XX determining whether a subject has, or is at risk of developing, a low HDL
XX level (comprises a probe or primer which is capable of hybridizing to an
XX SR-BI gene, and thus identifying whether the SR-BI gene contains an
XX allelic variant of a polymorphic region which is associated with a low
XX HDL level) and predicting the effect of hormone replacement therapy on
XX the HDL level in a female subject (by identifying one or more allelic
XX variants of the SR-BI gene which are associated with abnormally low HDL
XX levels in females (especially postmenopausal females), thus predicting
XX the effect of hormone replacement therapy on the HDL level in the
XX subject). Also disclosed are methods of treating low HDL levels and
XX resulting cardiovascular disorders (e.g. coronary heart disease,
XX atherosclerosis, stroke, ischaemia, restenosis, congestive heart failure

CC and gangrene) by administering a compound that increases HDL levels, when
CC the subject has been identified as having the common allele at residue 41
CC of exon 8. The present sequence is a SR-BI protein
XX Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-262;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVVLLCAVLGVVMIIVMSLIIKQVILKNVRIDPSSISPAWKEIP 60
Db 1 MGSARARWAVAGLVGVVLLCAVLGVVMIIVMSLIIKQVILKNVRIDPSSISPAWKEIP 60

Qy 61 VPVLSVYFPEVNPSEILKGKPVVRERGPYVYRERPRKANTFNNDTVSFVHRSLH 120

Db 61 VPVLSVYFPEVNPSEILKGKPVVRERGPYVYRERPRKANTFNNDTVSFVHRSLH 120

Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180

Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180

Qy 181 WGYEDPEVNPSEILKGKPVVRERGPYVYRERPRKANTFNNDTVSFVHRSLH 240

Db 181 WGYEDPEVNPSEILKGKPVVRERGPYVYRERPRKANTFNNDTVSFVHRSLH 240

Qy 241 SKVNYHSEOCNMINGTSGQWAPFMTQSSLEFFSPSEACRSMKLTVDHSGVPEGIPTYR 300

Db 241 SKVNYHSEOCNMINGTSGQWAPFMTQSSLEFFSPSEACRSMKLTVDHSGVPEGIPTYR 300

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360

Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360

Qy 361 LNPDPREHSLFDHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIEPVVPLLWFQSG 420

Db 361 LNPDPREHSLFDHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIEPVVPLLWFQSG 420

Qy 421 AMGGEPLNTFTQVLMPQVLYVYVLLGLGGLLLVPVYIQLRSQKCFWWSGSKG 480

Db 421 AMGGEPLNTFTQVLMPQVLYVYVLLGLGGLLLVPVYIQLRSQKCFWWSGSKG 480

Qy 481 SODKEAIQAYSESLMSPAAGTGLVLEAKL 509

Db 481 SODKEAIQAYSESLMSPAAGTGLVLEAKL 509

RESULT 7

ADJ46121

ID ADJ46121 standard; protein; 509 AA.

XX AC ADJ46121;

XX DT 06-MAY-2004 (first entry)

XX DE Human scavenger receptor CD36L1 variant.

XX KW Human; receptor; scavenger receptor class B type 1; CD36L1; SNP;
XX single nucleotide polymorphism; coronary artery disease; atherosclerosis;
XX cardiovascular disease; myocardial infarction; stroke; gangrene;
XX high density lipoprotein; HDL; TG; triglyceride; diabetes; obesity;
XX metabolic disorder.

OS Homo sapiens.

XX PN US2004023225-A1.

XX PD 05-FEB-2004.

XX PF 05-AUG-2002; 2002US-00212848.

XX PR 05-AUG-2002; 2002US-00212848.

XX XX

PA (VITI-) VITIVITY INC.
XX
PI McCarthy J;
XX
XX WPI; 2004-224681/21.
DR N-PSDB; ADJ46120.
XX
XX
PT Determining the presence of abnormally high triglyceride (TG) level or
PT TG:high density lipoprotein cholesterol ratio comprises determining if
PT the subject has an allelic variant of a polymorphic region of the CD36L1
PT gene.
XX
XX Disclosure; SEQ ID NO 4; 80pp; English.
XX
XX The invention relates to determining whether a subject has, or is at risk
CC of developing, abnormally high triglyceride (TG) level or an abnormally
CC high TG:high density lipoprotein cholesterol (HDL-C) ratio, comprises
CC determining whether the subject has an allelic variant of a polymorphic
CC region of the CD36L1 gene (scavenger receptor class B type 1) that is
CC associated with abnormally high TG levels or TG:HDL-C ratios. Also
CC included are a method of diagnosing or aiding in the diagnosis of
CC abnormally high TG level or TG:HDL-C ratio in a subject, a method for
CC treating a subject having a disease or disorder associated with specific
CC allelic variants of a CD36L1 gene, a kit for determining whether a
CC subject has, or is at risk of developing, abnormally high TG level or an
CC abnormally high TG:HDL-C ratio (comprising a probe or primer capable of
CC hybridizing to a polymorphic region of a CD36L1 gene and identifying
CC whether the CD36L1 gene contains an allelic variant of a polymorphic
CC region associated with abnormally high TG level or TG:HDL-C ratio, and
CC instructions for use), a method for predicting the effect of hormone
CC replacement therapy on the TG level or TG:HDL-C ratio in a female
CC subject, a medical information system for assessing a subject's risk for
CC developing an abnormally high TG level or TG:HDL-C ratio (comprising
CC means for obtaining biological information from the individual to obtain
CC a CD36L1 genetic profile, means for representing the CD36L1 genetic
CC profile as digital molecular data, means for electronically processing
CC the CD36L1 digital genetic profile to generate a risk assessment report
CC for developing an abnormally high TG level or TG:HDL-C ratio and means
CC for displaying the risk assessment report on an output device, where the
CC presence of a polymorphic region of CD36L1 indicates an increased risk
CC for developing an abnormally high TG level or TG:HDL-C ratio), a
CC computerized method of providing medical advice to a subject, a method
CC for a health care provider to generate a personal health assessment
CC report for an individual and a method of assessing the health of an
CC individual. The composition and methods are useful for identifying risk
CC factors for abnormal lipid levels and their associated diseases and
CC disorders. These may be used for diagnosing, prognosing or treating
CC subjects having a disease or disorder associated with abnormal lipid
CC levels, such as vascular (e.g. coronary artery disease, atherosclerosis,
CC cardiovascular disease, myocardial infarction, stroke and gangrene) or
CC metabolic (e.g. diabetes or obesity) diseases or disorders. The present
CC sequence represents a human CD36L1 protein.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-262;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVGVLCAVLGVVILVWPSLIKQVILKNVRIDPSSLISFAMWKEIP 60
Db 1 MGSARARWAVGLGVGVLCAVLGVVILVWPSLIKQVILKNVRIDPSSLISFAMWKEIP 60
Qy 61 VPFLSVYFFVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFDNDTVSFVHRSLSH 120
Db 61 VPFLSVYFFVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFDNDTVSFVHRSLSH 120
Qy 121 FOPDRSHGSESDYIILPNILVLGAVVMESKAGLKMWTGLATLQORAFMNTVGEIL 180
Db 121 FOPDRSHGSESDYIILPNILVLGAVVMESKAGLKMWTGLATLQORAFMNTVGEIL 180
Qy 181 WGYEDPPFVNFKYLPDMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240

Db 181 WGYEDPPFVNFKYLPDMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYWHSQCNMNGTSGOMWAPMTPOSSLEFFSPEACRSKMLTYHDSGVPEGIPTYR 300
Db 241 SKVNYWHSQCNMNGTSGOMWAPMTPOSSLEFFSPEACRSKMLTYHDSGVPEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPPLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPPLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGGLLLLLLVPIYOLRSQEKCFLEWSSKKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGGLLLLLLVPIYOLRSQEKCFLEWSSKKG 480
Qy 481 SQDKBAIQAYSESLMSPAAKGTVLQBAKL 509
Db 481 SQDKBAIQAYSESLMSPAAKGTVLQBAKL 509
RESULT 8
ADJ53335
ID ADJ53335 standard; protein; 509 AA.
XX AC ADJ53335;
XX DT 06-MAY-2004 (first entry)
XX Hamster SR-BI scavenger receptor polypeptide.
XX Hamster; SR-BI; scavenger receptor; HDL receptor; lipid; cholesterol;
XX lipoprotein; bile acid; steroid hormone; vitamin A; atherosclerosis;
XX adipocyte fat uptake; endocrine disorder; antiarteriosclerotic; receptor;
XX scavenger receptor class BI.
XX Cricetinae gen. sp.
OS US2003167475-A1.
PN 04-SEP-2003.
XX 24-JUN-2002; 2002US-00178611.
XX 15-NOV-1996; 96US-00749907.
XX 30-AUG-1999; 99US-00385799.
XX (KOZA/) KOZARSKY K.
PA (RIGO/) RIGOTTI A.
PA (KRIE/) KRIEGER M.
XX Kozarsky K, Rigotti A, Krieger M;
XX WPI; 2004-246237/23.
DR N-PSDB; ADJ53334.
XX Screening for agents that influence lipid transport, useful e.g. for
PT treating or preventing atherosclerosis, based on modulation of the SR-BI
PT scavenger receptor.
XX Disclosure; SEQ ID NO 2; 22pp; English.
XX The invention relates to a method for screening compounds that alter
CC transport of lipids, cholesterol, lipoproteins or their components,
CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
CC homologue. The test compound is administered to an animal and cholesterol
CC or bile acid levels, production levels of steroid hormones or alterations
CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
CC hormones, bile acids and Vitamin A is measured. Agents that alter
CC transport of lipids, cholesterol or lipoproteins are potentially useful
CC for the treatment or prevention of atherosclerosis, fat uptake by

CC adipocytes and some endocrine disorders. This sequence represents the
 CC hamster SR-BI scavenger receptor of the invention.
 XX
 SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGGLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGGLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFFVNVNPSSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Db 61 VPFYLSVYFFVNVNPSSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Qy 121 FQDRSHGSESDYIIILPNILVLGVAVWMSKSGAGLMMTGLATLQORAFMNRVTGCEIL 180
 Db 121 FQDRSHGSESDYIIILPNILVLGVAVWMSKSGAGLMMTGLATLQORAFMNRVTGCEIL 180
 Qy 181 WGYEDPFFVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPFFVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEOCNMTNGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEOCNMTNGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPVLLWFEQSG 420
 Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPVLLWFEQSG 420
 Qy 421 AMGGEPLNTFTQVLVMPQVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGEPLNTFTQVLVMPQVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Qy 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
 Db 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509

RESULT 9

ADU51467
 ID ADU51467 standard; protein; 509 AA.
 XX
 AC
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Hamster scavenger receptor class B type I-related protein - SEQ ID 2.
 KW monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 KW SR-BI; spermatogenesis.
 XX Mesocricetus auratus.
 XX JP2004331633-A.
 XX 25-NOV-2004.
 XX 29-MAY-2003; 2003JP-00152800.
 XX 10-MAR-2003; 2003JP-00063407.
 XX (UYKA-) UNIV KANAZAWA TLO YG.
 XX WPI; 2004-810031/80.
 XX

PT Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
 PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 XX rat origin, useful for functional analysis of SR-BI.
 PS Disclosure; SEQ ID NO 2; 21pp; Japanese.

CC The invention comprises a monoclonal antibody that belongs to the mouse
 CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI
 CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a golden hamster SR-BI-related protein.

XX Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGGLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGGLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFFVNVNPSSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Db 61 VPFYLSVYFFVNVNPSSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 Qy 121 FQDRSHGSESDYIIILPNILVLGVAVWMSKSGAGLMMTGLATLQORAFMNRVTGCEIL 180
 Db 121 FQDRSHGSESDYIIILPNILVLGVAVWMSKSGAGLMMTGLATLQORAFMNRVTGCEIL 180
 Qy 181 WGYEDPFFVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPFFVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEOCNMTNGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEOCNMTNGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPVLLWFEQSG 420
 Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPVLLWFEQSG 420
 Qy 421 AMGGEPLNTFTQVLVMPQVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGEPLNTFTQVLVMPQVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
 Qy 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
 Db 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509

RESULT 10

AEB03938
 ID AEB03938 standard; protein; 509 AA.
 XX
 AC
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Hamster Scavenger Receptor Class B-1, SEQ ID 2.
 KW Antilipemic; transgenic animal; Scavenger Receptor Class B-1;
 KW high density lipoprotein receptor; cholesterol; lipid.
 XX Cricetulus griseus.
 OS
 XX US2005136005-A1.
 PN

XX PD 23-JUN-2005.
XX PF 02-SEP-2004; 2004US-00933037.
XX PR 23-JUN-1994; 94US-00265428.
XX PR 19-JUN-1995; 95MO-US007721.
XX PR 15-NOV-1996; 96US-00749507.
XX PR 27-MAR-1997; 97US-00765108.
XX PR 30-AUG-1999; 99US-00385799.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Kozareky K, Rigotti A, Krieger M;
XX WPI; 2005-457475/46.
XX DR N-PSDB; AEB03937, AEB03941.
XX
XX New genetically engineered mouse or derivative cells with inactivated SR-
XX BI gene expression or activity, useful as a model for designing drugs
XX PT that can modulate cholesterol transport.
XX
XX Disclosure; SEQ ID NO 2; 21pp; English.
XX
XX The present invention relates to a novel genetically engineered mouse, or
XX cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene
XX expression or SR-BI activity has been inactivated. SR-BI is a high
XX density lipoprotein (HDL) receptor. It was found that estrogen
XX downregulates SR-BI under conditions of upregulation of the low density
XX lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
XX adrenal membranes and other non-placental steroidogenic tissues from
XX animals treated with estrogen, but not in other non-placental non-
XX steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
XX tissue causes a decrease in blood cholesterol levels. The animal is
XX useful as a model for designing drugs that can modulate cholesterol
XX transport or that can stimulate or inhibit the binding to and lipid
XX movements mediated by SR-BI and redirect uptake and metabolism of lipids
XX and cholesterol by cells. The present sequence is a SR-BI, which was used
XX to illustrate the invention. Note: The SEQ ID 1 given in the sequence
XX listing (the sequence shown in AEB03937) is stated to be 1788 nucleotides
XX in length. However, there appears to be a 1 to 3 nucleotide deletion at
XX the end of each line of the sequence shown in the sequence listing.
XX corrected version of the sequence that is 1718 nucleotides in length. Therefore a
XX replace the missing nucleotides (the sequence shown in AEB03941). SEQ ID
XX 1 is stated to encode SEQ ID 2 (given in AEB03938). The SEQ ID 2 given in
XX the sequence listing also has a deletion of the final two letters of the
XX last amino acid residue given on each line of the sequence.
XX
XX Sequence 509 AA;
XX
XX Query Match 94.2%; Score 2525; DB 9; Length 509;
XX Best Local Similarity 95.5%; Pred. No. 2.5e-246;
XX Matches 486; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MGSARARWAVGVVGLICAVLGVVMIIVMPSLIKKOVLKVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGVVGLICAVLGVVMIIVMPSLIKKOVLKVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFFEVNPNSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFYLSVYFFEVNPNSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQPRDRSHGESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180
Db 121 FQPRDRSHGESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180
Qy 181 WGYEDDPFNFKYLPMPFPIKGFGLFVENNDSGLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGYEDDPFNFKYLPMPFPIKGFGLFVENNDSGLFTVFTGVQNFSKIHLVDRWNGX 240
Qy 241 SKVNYWHSEQCWNMTSGQWAPFWTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300

Db 241 SKVNYWHSEQCWNMTSGQWAPFWTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAXKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVSKLOISLYIKAVKIGIGOTGKIEPVVLPILLWPEQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVSKLOISLYIKAVKIGIGOTGKIEPVVLPILLWPEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVYIQLRSQEKCFPLFWSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVYIQLRSQEKCFPLFWSGSKG 480
Qy 481 SQDKEAIQAYSESLMSPAKAGTVLQEAKL 509
Db 481 SQDKEAIQAYSESLMSPAKAGTVLQEAKL 509
XX
XX RESULT 11
XX ADU51468
XX ID ADU51468 standard; protein; 509 AA.
XX AC ADU51468;
XX AC
XX 10-FEB-2005 (first entry)
XX DT
XX XX Mouse scavenger receptor class B type I-related protein - SEQ ID 3.
XX DE
XX XX monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
XX KW SR-BI; spermatogenesis.
XX KM
XX OS Mus musculus.
XX OS
XX JF2004331633-A.
XX PN
XX 25-NOV-2004.
XX PD
XX 29-MAY-2003; 2003JP-00152800.
XX PF
XX 10-MAR-2003; 2003JP-00063407.
XX PR
XX (UYKA-) UNIV KANAZAWA TLO YG.
XX PA
XX WPI; 2004-810031/80.
XX DR
XX Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
XX PT which specifically binds to scavenger receptor class B type I (SR-BI) of
XX rat origin, useful for functional analysis of SR-BI.
XX PT
XX Disclosure; SEQ ID NO 3; 21pp; Japanese.
XX PS
XX The invention comprises a monoclonal antibody that belongs to the mouse
XX CC IgG1/kappa subclass which specifically binds to scavenger receptor class
XX CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
XX CC is useful for the detection and analysis of SR-BI. The monoclonal
XX CC antibody of the invention is useful for analysing the influence of SR-BI
XX CC on spermatogenesis in testis. The present amino acid sequence represents
XX CC a mouse SR-BI-related protein.
XX CC
XX Sequence 509 AA;
XX
XX Query Match 91.5%; Score 2453; DB 8; Length 509;
XX Best Local Similarity 89.2%; Pred. No. 5e-239;
XX Matches 454; Conservative 35; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGSARARWAVGVVGLICAVLGVVMIIVMPSLIKKOVLKVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGVVGLICAVLGVVMIIVMPSLIKKOVLKVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFFEVNPNSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120

Db 61 VPFYLSVYFVFNPNVNEVLCQKPVRRERGYPVYRFRQKNITFNDNDTVSFVENRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
Qy 181 WGYEDDPFVFNKYLPMFPPIKGFGLFVFNWNSDGLFTVFTGVQNFSLHLDVNRNGL 240
Db 181 WGYDDPPVHFLNTYLPDMFPPIKGFGLFVFNWNSDGLFTVFTGVQNFSLHLDVNRNGL 240
Qy 241 SKVNYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSMKLTVDHSGVFGIPIYR 300
Db 241 SKIDYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSMKLTVDHSGVFGIPIYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKIGIGQTKIBPVVPLPLWFQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKIGIGQTKIBPVVPLPLWFQSG 420
Qy 421 AMGEPLNTFTQVLMPQVLYVLLGLGGLLLVPVLYQLRSOEKCFLFWSGSKG 480
Db 421 AMGKPLSTFTQVLMPQVLYVLLGLGGLLLVPVLYQLRSOEKCFLFWSGSKG 480
Qy 481 SQDKAIAQAYSESLSMSPAAGTGLQEA 509
Db 481 SQDKAIAQAYSESLSMSPAAGTGLQEA 509

RESULT 12

AAW93575
ID AAW93575 standard; protein; 509 AA.

AC AAW93575;

XX

DT 17-JUN-1999 (first entry)

DE Mouse scavenger receptor class B-1 protein.

XX Scavenger receptor class B type I; mouse; steroid production; HDL;
KW cholesterol; cholesteryl ester transport; high-density lipoprotein;
KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;
KW treatment; disorder; overproduction; underproduction; menopause;
KW breast cancer; prostate cancer; endometriosis; fibroid tumour.

XX Mus sp.

XX WO9911288-A1.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US018463.

XX 05-SEP-1997; 97US-0057943P.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M;

XX WPI; 1999-204984/17.

XX N-PSDB; AAX23404.

XX Modification of steroid production in mammals - by administering
PT modulator of SR-BI expression or activity.

XX Disclosure; Page 81-82; 86pp; English.

XX This invention describes a method for modifying steroid production in a
CC mammal which comprises administering a compound that alters cholesterol
CC or cholesteryl ester transport from high-density lipoprotein (HDL) or
CC other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger

CC receptor class B type I). This method is useful for female contraception,
CC for treating disorders characterised by overproduction of steroids, for
CC treating disorders characterised by underproduction of steroids,
CC especially menopause, for treating disorders that can be treated by
CC decreasing steroid production, especially breast cancer, prostate cancer,
CC endometriosis or fibroid tumours

XX Sequence 509 AA;

Query Match 91.3%; Score 2447; DB 2; Length 509;

Best Local Similarity 89.0%; Pred. No. 2e-238;

Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIILMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60

Db 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIILMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60

Qy 61 VPFYLSVYFVFNPNVNEVLCQKPVRRERGYPVYRFRQKNITFNDNDTVSFVENRSLH 120

Db 61 VPFYLSVYFVFNPNVNEVLCQKPVRRERGYPVYRFRQKNITFNDNDTVSFVENRSLH 120

Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180

Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180

Qy 181 WGYEDDPFVFNKYLPMFPPIKGFGLFVFNWNSDGLFTVFTGVQNFSLHLDVNRNGL 240

Db 181 WGYDDPPVHFLNTYLPDMFPPIKGFGLFVFNWNSDGLFTVFTGVQNFSLHLDVNRNGL 240

Qy 241 SKVNYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSMKLTVDHSGVFGIPIYR 300

Db 241 SKIDYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSMKLTVDHSGVFGIPIYR 300

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKIGIGQTKIBPVVPLPLWFQSG 420

Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKIGIGQTKIBPVVPLPLWFQSG 420

Qy 421 AMGEPLNTFTQVLMPQVLYVLLGLGGLLLVPVLYQLRSOEKCFLFWSGSKG 480

Db 421 AMGKPLSTFTQVLMPQVLYVLLGLGGLLLVPVLYQLRSOEKCFLFWSGSKG 480

Qy 481 SQDKAIAQAYSESLSMSPAAGTGLQEA 509

Db 481 SQDKAIAQAYSESLSMSPAAGTGLQEA 509

RESULT 13

AAAY44020

ID AAAY44020 standard; protein; 509 AA.

XX AAAY44020;

XX

DT 18-JAN-2000 (first entry)

DE Mouse Scavenger receptor class BI protein.

XX

XX Hamster; scavenger receptor; modulation; cholesterol transport; lipid;

XX lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;

XX high density lipoprotein; ester; blood.

XX Mus sp.

XX US95962322-A.

XX

XX 05-OCT-1999.

XX

XX 15-NOV-1996; 96US-00749907.

XX

XX 15-NOV-1996; 96US-00749907.

XX PR

XX (UYPE-) UNIV PENNSYLVANIA.
PA (WASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M, Rigotti A, Kozarsky K;
XX WPI; 1999-589717/50.
DR N-PSDB; AA230616.
XX
PT Modulating cholesterol transport for the control of cholesterol levels in
PT blood.
XX
PS Disclosure; Col 29-32; 23pp; English.
XX
CC This sequence represents the mouse scavenger receptor class BI (SR-BI)
CC which is used in a method of modulating cholesterol transport. The method
CC comprises selectively altering the transport of lipid, cholesterol and/or
CC lipoproteins (or their components) into and out of mammalian cells to
CC alter plasma cholesterol levels, by administering a compound which alters
CC the expression or activity of the SR-BI scavenger protein receptor. This
CC alters the rate of clearance of the protein component of high density
CC lipoprotein (HDL) as compared to the ester component of HDL. the method
CC may be used to control cholesterol levels in the blood plasma of mammals
XX
XX Sequence 509 AA;
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 2e-238;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGLGALGLLFAALGVVMIIVMPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPYLSVYFVFNVPNSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPYLSVYFVFNVPNEVLNGQKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLCGAVNMESKAGLKLMMTGLATLQORAFMNRVTGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKLMMTLALVTMGQAFMNRVTGEIL 180
QY 181 WGYEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPFPVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTGVQNFSRHLVDKWNGL 240
QY 241 SKVNYWHSEOCNMGTSQOMWAPFMTQSSLEFFSPSEACRSKMLTYVHDSGVEGIPYR 300
DB 241 SKIDYWHSEOCNMGTSQOMWAPFMTQSSLEFFSPSEACRSKMLTYNESRVFEGIPYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FTAPDTLUFANGSVYPPNEGFCPCRESGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360
QY 361 LNPDPREHSLPLDTHPTVTGIPMNCVSKLOISLYIKAVKGIGOTGKIBPVVLPILWFOQSG 420
DB 361 LNPDPKEHSLPLDTHPTVTGIPMNCVSKVQSLYIKSVKGIGOTGKIBPVVLPILWFOQSG 420
QY 421 AMGGEPLNTFTQLVLPQVLYQVYVLLGLGGLLLVPVYIQLRSQEKCFLWMSGKKG 480
DB 421 AMGKPLSTFTQLVLPQVLYQVYVLLGLGGLLLVPVYIQLRSQEKCFLWMSGKKG 480
QY 481 SODKEATQAYSESLSMAKGTVLOEAKL 509
DB 481 SODKEATQAYSESLSMAKGTVLOEAKL 509
RESULT 14
ABB57092
ID ABB57092 standard; protein; 509 AA.
XX
AC ABB57092;
XX

DT 07-MAR-2002 (first entry)
XX Mouse ischaemic condition related protein sequence SEQ ID NO:202.
DE
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease.
KW
XX Mus musculus.
OS
XX WO20018188-A2.
PN
XX 22-NOV-2001.
PD
XX 18-MAY-2001; 2001WO-JP004192.
PF
XX 18-MAY-2000; 2000JP-00145977.
PR
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
PA
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
PI
XX WPI; 2002-034733/04.
DR N-PSDB; AB199330.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
XX Claim 2; Page 576-579; 2690pp; English.
PS
XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (AB199202 to AB199912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
XX Sequence 509 AA;
Query Match 91.3%; Score 2447; DB 5; Length 509;
Best Local Similarity 89.0%; Pred. No. 2e-238;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGLGALGLLFAALGVVMIIVMPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPYLSVYFVFNVPNSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPYLSVYFVFNVPNEVLNGQKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLCGAVNMESKAGLKLMMTGLATLQORAFMNRVTGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKLMMTLALVTMGQAFMNRVTGEIL 180
QY 181 WGYEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPFPVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTGVQNFSRHLVDKWNGL 240
QY 241 SKVNYWHSEOCNMGTSQOMWAPFMTQSSLEFFSPSEACRSKMLTYVHDSGVEGIPYR 300
DB 241 SKIDYWHSEOCNMGTSQOMWAPFMTQSSLEFFSPSEACRSKMLTYNESRVFEGIPYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360

Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVLPLLMFEQSG 420
Db 361 LNPNKHEHSLFDLHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVLPLLMFEQSG 420
Qy 421 AMGGEPLNTFTQVLVMPQVLYQVYVLLGLGGLLLVPIIYQVRSQKCFPLFWGSKKG 480
Db 421 AMGKPLSTFTQVLVMPQVLYQVYVLLGLGGLLLVPIIYQVRSQKCFPLFWGSKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTQVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTQVLQEA 509

RESULT 15

AAE21525
ID AAE21525 standard; protein; 509 AA.

AC AAE21525;

DT 16-JUL-2002 (first entry)

DE Murine scavenger receptor type B-I (SR-BI).

KW Scavenger receptor protein type BI; low density lipoprotein; LDL; murine;
KW SR-BI.

OS Mus sp.

PN US6350859-B1.

PD 26-FEB-2002.

PF 02-FEB-1999; 99US-00241581.

PR 23-JUN-1994; 94US-00265428.

PR 27-MAR-1997; 97US-00765108.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Krieger M, Acton SL, Rigotti A;

DR WPI; 2002-314680/35.

DR N-PSDB; AAD33917.

PT Antibody specific for scavenger receptor protein type BI useful for
PT detection, characterization or isolation of receptor proteins, as well
PT inhibiting scavenger protein binding to low density lipoprotein.

PS Claim 1; Col 49-52; 41pp; English.

CC The invention relates to an antibody specific for scavenger receptor
CC protein type B-I (SR-BI) derived from murine and hamster. Antibodies of
CC the invention are useful for detection, characterisation and isolation of
CC receptor proteins and for inhibiting scavenger protein binding to low
CC density lipoprotein (LDL). The present sequence is murine SR-BI protein

SQ Sequence 509 AA;

Query Match 91.3%; Score 2447; -DB 5; Length 509;

Best Local Similarity 89.0%; Pred. No. 2e-238;

Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVGLLCVILGVNMLVPSLIKQVILKNVRIDPSSLSFAMWKEIP 60

Db 1 MGSRRARWALGILGALGLIFALGVNMLVPSLIKQVILKNVRIDPSSLSFGWKEIP 60

Qy 61 VPFFYLSVYFFEVNPNSEILKGEKVPVRERGYPVYRERHKNITFNDNDTVSFVHRSLH 120

Db 61 VPFFYLSVYFFEVNPNSEILKGEKVPVRERGYPVYRERHKNITFNDNDTVSFVHRSLH 120

Qy 121 FQDRSHGSSDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGAIL 180
Db 121 FQPKSHGSSDYIILPNILVLGGSILMESKPSVSLKLMTLALVTMGQRAFMRVTGAIL 180
Qy 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSTHLDVKNGL 240
Db 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGMNNSNSGVFTVFTGVQNFRIHLVDKNGL 240
Qy 241 SKVNYHSEQCNMINGTSGQWMAFPFMTPOSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKIDYHSEQCNMINGTSGQWMAFPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVLPLLMFEQSG 420
Db 361 LNPNKHEHSLFDLHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVLPLLMFEQSG 420
Qy 421 AMGGEPLNTFTQVLVMPQVLYQVYVLLGLGGLLLVPIIYQVRSQKCFPLFWGSKKG 480
Db 421 AMGKPLSTFTQVLVMPQVLYQVYVLLGLGGLLLVPIIYQVRSQKCFPLFWGSKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTQVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTQVLQEA 509

Search completed: February 23, 2006, 12:40:05
Job time : 156.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 12:40:25 ; Search time 26 Seconds
(without alignments)
1883.628 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2681
Sequence: 1 MGSSARWVAVGLGVVGLL.....YSSLSMPAAKGVTLQEA 509
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	1 A53920	scavenger receptor
2	2424	90.4	529	1 JC5533	scavenger receptor
3	2236	83.4	509	1 A48528	membrane glycoprot
4	752.5	28.1	478	1 A56325	lysosomal integral
5	739	27.6	478	2 JC5670	lysosomal membrane
6	738	27.5	478	1 JH0241	85K lysosomal memb
7	692	25.8	472	1 A54870	cell adhesion rece
8	678	25.3	472	2 I49590	CD36 antigen - mou
9	673	25.1	472	1 A47402	fatty acid binding
10	600	22.4	519	1 S38957	epithelial membran
11	597	22.3	457	1 S43137	D-CD36 protein - f
12	483	18.0	525	1 A59259	sensory neuron mem
13	481.5	18.0	534	2 T27054	hypothetical prote
14	412	15.4	536	2 T24000	hypothetical prote
15	377.5	14.1	531	2 T20763	hypothetical prote
16	369	13.8	590	2 T20537	hypothetical prote
17	353.5	13.2	552	2 T27424	hypothetical prote
18	344	12.8	562	2 T15396	hypothetical prote
19	113	4.2	901	2 T03726	capsid polypeptide
20	101	3.8	1589	2 T22668	hypothetical prote
21	100.5	3.7	557	2 T50788	ubiquitin specific
22	100.5	3.7	1573	2 T50113	3-dehydroquinase s
23	100	3.7	896	2 T07408	lipoxigenase (EC 1
24	99.5	3.7	451	2 F97230	probable maltodext
25	98.5	3.7	427	2 C87232	probable integral
26	98.5	3.7	448	2 T44869	probable membrane
27	98.5	3.7	3036	2 T18995	hypothetical prote
28	98	3.7	398	2 S74347	hypothetical prote
29	97	3.6	1026	2 T18220	chitin synthase (E

phospho-n-acetylmu
PTS system mannose
PTS system mannose
hypothetical prote
hypothetical prote
phosphotransferase
PTS system, mannos
htra-like serine p
pilin longus precu
probable nucleotid
uncharacterized pr
cellulose synthase
hypothetical prote
prostaglandin-endo
acetylornithine tr
viron protein - hu

30 96.5 3.6 361 2 E71664
31 95 3.5 303 2 AC1087
32 95 3.5 303 2 AB1451
33 94.5 3.5 756 2 C84682
34 94 3.5 828 2 G87584
35 93 3.5 303 2 C97304
36 93 3.5 303 2 C95033
37 92.5 3.5 433 2 H97199
38 92 3.4 238 2 I41148
39 92 3.4 369 2 S33518
40 92 3.4 2817 2 B97033
41 91.5 3.4 1081 2 T05351
42 91 3.4 350 2 C70561
43 91 3.4 603 2 JC5063
44 90.5 3.4 423 2 S61868
45 90 3.4 554 2 T41952

ALIGNMENTS

scavenger receptor SR-BI - Chinese hamster
N/Alternate names: CD36-related class B scavenger receptor
C/Species: Cricetulus griseus (Chinese hamster)
C/Date: 28-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: A53920
R/Acton, S.L.; Scherer, P.E.; Lodish, H.F.; Krieger, M.
J. Biol. Chem. 269, 21003-21009, 1994
A/Title: Expression cloning of SR-BI, a CD36-related class B scavenger receptor.
A/Reference number: A53920; MUID:94342261; PMID:7520436
A/Accession: A53920
A/Molecule type: mRNA
A/Residues: 1-509 <ACT>
A/Cross-references: UNIPROT:Q60417; UNIPARC:UPI00000E7766; GB:U11453; MID:9562021; PIDN:7
C/Function:
A/Description: mediates the endocytosis of modified lipoproteins such as oxidized or acet
C/Superfamily: lysosomal integral membrane protein II
C/Keywords: glycoprotein; transmembrane protein
F/2-8/Domain: intracellular #status predicted <CYT1>
F/9-33/Domain: transmembrane #status predicted <TM1>
F/34-442/Domain: extracellular #status predicted <EXT>
F/443-464/Domain: transmembrane #status predicted <TM2>
F/465-509/Domain: intracellular #status predicted <CYT2>
F/102,108,173,212,227,255,310,330/Binding site: carbohydrate (Asn) (covalent) #status pre


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Db 301 FVAPKTLFANGSIYPPNEGFCPCLESIGIONVSTCRFAPLSLPHFLNADPVLAEAVTG 360
Qy 361 LNPDPREHSLFDHPVTGIPMNCVSKLQISLYIKAVKIGQOTKIBPVVPLPILWPFQSG 420
Db 361 LHPNQEAHSLFDHPVTGIPMNCVSKLQISLYIKAVKIGQOTKIBPVVPLPILWFAESG 420
Qy 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLLPVYIQLRSEKCFELFWGSKKG 480
Db 421 AMEGTLLHTFTQVLMPKVMHYAQYVLLALGCVLLLPVPCIRSOEKCYLFWSSSKKG 480
Qy 481 SODKEALQAYSESLSMPAAKTVLQEAKL 509
Db 481 SKQKEALQAYSESLSMTAPKGSVLQEAKL 509

RESULT 4
A56525
Lysosomal integral membrane protein II - human
N;Alternate names: Igp85; Limp II; lysosomal membrane 85K sialoglycoprotein
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A56525; JQ1523
R;Calvo, D.; Dopazo, J.; Vega, M.A.
Genomics 25, 100-106, 1995
A;Title: The CD36, CLA-1 (CD36L1), and LIMPII (CD36L2) gene family: cellular distribution
A;Reference number: A56525; MUID:95293360; PMID:7539776
A;Accession: A56525
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-478 <CAL>
A;Cross-references: UNIPROT:Q14108; UNIPARC:UPI000017423A
R;Fujita, H.; Takata, Y.; Kono, A.; Tanaka, Y.; Takahashi, T.; Himeno, M.; Kato, K.
Biochem. Biophys. Res. Commun. 184, 604-611, 1992
A;Title: Isolation and sequencing of a cDNA clone encoding the 85KDa human lysosomal sial
A;Reference number: JQ1523; MUID:92246940; PMID:1374238
A;Accession: JQ1523
A;Molecule type: mRNA
A;Residues: 1-83,'E',85-478 <FUJ>
A;Cross-references: UNIPARC:UPI000032D38; GB:DL2676; NID:g219702; PIDN:BAA02177.1; PID:
A;Experimental source: PANCATEC islet
R;Sandoval, I.V.; Arredondo, J.J.; Alcalde, J.; Noriega, A.G.; Vandekerckhove, J.; Jimen
J. Biol. Chem. 269, 6622-6631, 1994
A;Title: The residues Leu(ile) (475)-Ile(Leu, Val, Ala) (476), contained in the extended c
some.
A;Reference number: A57905; MUID:94165051; PMID:7509809
A;Contents: annotation; sorting signal
C;Genetics:
A;Gene: GDB:CD36L2
A;Cross-references: GDB:383649
A;Map position: 4pter-4qter
C;Superfamily: lysosomal integral membrane protein II
C;Keywords: glycoprotein; lysosome; transmembrane protein
F;2-478/Product: lysosomal membrane 85K sialoglycoprotein #status predicted <LVS>
F;2-3/Domain: intracellular #status predicted <CYR1>
F;4-26/Domain: transmembrane #status predicted <TR1>
F;27-432/Domain: lysosomal luminal #status predicted <LLUM>
F;433-458/Domain: transmembrane #status predicted <TR2>
F;459-478/Domain: intracellular #status predicted <CYR2>
F;475-476/Region: endosomal/lysosomal sorting signal
F;45,68,105,206,224,249,304,325,412,430/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 28.1%; Score 752.5; DB 1; Length 478;
Best Local Similarity 33.9%; Pred. No. 3.2e-53;
Matches 162; Conservative 100; Mismatches 187; Indels 29; Gaps 9;

Qy 15 GVVGLLCAVLGVVMIL--VMPSLIKQVLKNVRIDPSSLSFAMWKEIPVPFYLVSVPFEV 72
Db 10 GTLSLLLVTSVTLVAVRFQKAVDQTIKNMVLQNGTKVFNSEWKPPLPVYIQTFYFN 69

A;Title: This protein is involved in sequestration of particular cytoplasmic proteins (
C;Superfamily: lysosomal integral membrane protein II
F;1-26/Domain: signal sequence #status predicted <SIG>
F;433-458/Domain: transmembrane #status predicted <TM>
F;474-475/Region: endosomal/lysosomal sorting signal

Query Match 27.6%; Score 739; DB 2; Length 478;
Best Local Similarity 32.9%; Pred. No. 4e-52;
Matches 158; Conservative 103; Mismatches 195; Indels 24; Gaps 9;

Qy 15 GVVGLLCAVLGVVMIL--VMPSLIKQVLKNVRIDPSSLSFAMWKEIPVPFYLVSVPFEV 72
Db 10 GTLSLLLVTSVTLVAVRFQKAVDQTIKNMVLQNGTKVFNSEWKPPLPVYIQTFYFN 69

Qy 73 VNPSEILKGEKPVVREPGVYVREFRHKANITFNDN-DTVSFVHEHSLHFPQDRSHGS 131
Db 70 TNPSEILQGEIPLLEBVGPTVYRELKANKIQQENGTTISAVTNKAYVFERQSVGDPN 129

Qy 132 -DYIILPNILVLGGAVNMESKSLGLMTLGLATLGQRAFPMNRTVGEILWGYEDPVPNF 190
Db 130 VDLIRTNIPLL--TVVDLAQLTLLRELIEAMKAYQKQLFVTHVHELLWGYKDEILSL 187

Qy 191 INKYLPMPEPIKGRGLFVEMNNSDSGLFTVTVGVQNFPSKIHLDVDRWGLSKVNYWHSEQ 250
Db 188 VHLFKPDVSP---NFGLFYERNGTNDGVEVFLTGEDYINLNFSKIIVEMNGKTSLDWMTTDT 244

Qy 251 CNMNGTSGQMAFPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYRFTAPKTLFAN 310
Db 245 CNMNGTSGDSFHLPLSKDEVLVLPFSDLCRSVHITFSSFENVEGLPAFRYKVPAILAN 304

Qy 311 GSVYPPNEGFC----PCLESIGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLGLNDPDR 366
Db 305 TS---ENAGFCIPEGNCLGSGVLNVISICKNGAPIIMSFPHFYQADRFVSAIEGMHNQ 361

Qy 367 EHSFLFDHPVTGIPMNCVSKLQISLYIKAVKIGQOTKIEPVVPLPILWFEQSGMGCEP 426
Db 362 DHETFVDINELTGIIILKAARFQINIYVKLDLDFVETGDIRTWVFPVYMLNESVHIDKET 421

Qy 427 LNTFTQLVMPQVLYQVYVLLGLGGLLLLPVYIQLRSEKCFELFWGSKGSDOK 484
Db 422 ASRL-KSMINTLLIITNPIIIMALGVFFGLV-----FTWLACKGQSSMDE 466

RESULT 5
JC5670
Lysosomal membrane 85K glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5670
R;Tabuchi, N.; Akasaki, K.; Sasaki, T.; Kanda, N.; Tsuji, H.
J. Biochem. 122, 756-763, 1997
A;Title: Identification and characterization of a major lysosomal membrane glycoprotein,
A;Reference number: JC5670; MUID:98060500; PMID:9399579
A;Accession: JC5670
A;Molecule type: mRNA
A;Residues: 1-478 <TAB>
A;Cross-references: UNIPROT:Q35114; UNIPARC:UPI0000231D6; GB:AB008553; NID:g2618485; PII
C;Comment: This protein is involved in sequestration of particular cytoplasmic proteins (
C;Superfamily: lysosomal integral membrane protein II
F;1-26/Domain: signal sequence #status predicted <SIG>
F;433-458/Domain: transmembrane #status predicted <TM>
F;474-475/Region: endosomal/lysosomal sorting signal

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A;Cross-references: UNIPARC:UPI0000174242
 R;Caimeil, B.; Parmentier, S.; Leung, L.L.; McGregor, J.L.
 Biochem. J. 279, 419-425, 1991
 A;Title: Separation of important new platelet glycoproteins (GP1a, GP1c, GP1c*, GP1a and
 A;Reference number: A56793; MUID:92061944; PMID:1953640
 A;Accession: D56793
 A;Molecule type: protein
 A;Residues: 2, 'X', '4', '6', 'X', '8-23 <CAT>
 A;Cross-references: UNIPARC:UPI0000174243
 A;Experimental source: platelet
 R;Greenwalt, D.E.; Watt, K.W.K.; So, O.Y.; Jiawani, N.
 Biochemistry 29, 7054-7059, 1990
 A;Title: PAS IV, an integral membrane protein of mammary epithelial cells, is related to
 A;Reference number: A35577; MUID:91027734; PMID:1699598
 A;Accession: A35577
 A;Molecule type: protein
 A;Residues: 'XX', '4', 'X', '6', 'X', '8-30 <GRE>
 A;Cross-references: UNIPARC:UPI0000174244
 A;Experimental source: milk fat globule membrane, lactating mammary tissue epithelial ce
 R;Wyller, B.; Davist, L.; Borkiewicz, H.; Bordet, J.C.; McGregor, J.L.
 Thromb. Haemost. 70, 500-505, 1993
 A;Title: Cloning of the cDNA encoding human platelet CD36: comparison to PCR amplified f
 A;Reference number: 159613; MUID:94082337; PMID:7505064
 A;Accession: 159613
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-43, 'R', '45-237', 'D', '239-472 <RES>
 A;Cross-references: UNIPARC:UPI0000168403; GB:S67532; NID:9456912; PIDN:AAD13993.1; PID:
 R;Tang, Y.; Taylor, K.T.; Sobiech, D.A.; Medved, E.S.; Lipsky, R.H.
 J. Biol. Chem. 269, 6011-6015, 1994
 A;Title: Identification of a human CD36 isoform produced by exon skipping. Conservation
 A;Reference number: A53212; MUID:94164961; PMID:7509795
 A;Accession: A53212
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-40, 144-169, 'ILNLSKSSSM', '170-185 <TA3>
 A;Cross-references: UNIPARC:UPI0000174245; GB:L06849
 C;Comment: This protein mediates the interaction of platelets with collagen and thrombos
 C;Genetics:
 A;Gene: GDB:CD36
 A;Cross-references: GDB:138800; OMIM:173510
 A;Map position: 7q11.2-7q11.2
 A;Introns: 40/3; 94/2; 143/3; 185/2
 C;Superfamily: lysosomal integral membrane protein II
 C;Keywords: alternative splicing; blocked amino end; cell adhesion; glycoprotein; lipop
 F;2-472/Product: cell adhesion receptor CD36 #status predicted <MAT>
 F;2-6/Domain: intracellular #status predicted <CYT>
 F;7-30/Domain: transmembrane #status predicted <TM>
 F;31-439/Domain: extracellular #status predicted <EXT>
 F;440-466/Domain: transmembrane #status predicted <TM2>
 F;467-472/Domain: intracellular #status predicted <CYT2>
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;3, 7, 464, 466/Binding site: palmitate (Cys) (covalent) #status predicted
 F;79, 102, 134, 163, 205, 220, 235, 247, 417/Binding site: carbonyl (Asn) (covalent) #status
 Query Match 25.8%; Score 692; DB 1; Length 472;
 Best Local Similarity 31.5%; Pred. No. 2.6e-48;
 Matches 144; Conservative 104; Mismatches 189; Indels 20; Gaps 8;
 QY 16 VVGLLCVAVGLVGMVLMVPSLIKKQVLRIDPSLSFAMWKEIPVPYLSVVFVFNVP 75
 DB 14 VIGAVLAVFGGILMPVGDMLTIKQVLEEGTIAFKNVKVTGTVEYRQFVIFDVQNP 73
 QY 76 SEILKGEKPV-VREGRPVYVR-EPRKANITFN-DNDTVSVEHRSLSHFOPDRSHGSESD 132
 DB 74 QEVNMSNSIQVKGQRPYTRVRFLAKENVTQDAEDNTVSFLQPNGAIFEPSLSVGTED 133
 QY 133 YIILPNILVGGVMMESKSGAGLKMMLTGLATLQGFAPNRTVGEILWGYDPPVFNFIN 192
 DB 134 NFTVLNLAFAASHYQNFQVQFQVQFQVQFQVQFQVQFQVQFQVQFQVQFQVQFQV 190
 QY 193 KYLPDMPPIKGFGLFVEMNNSDGLFTVFTVQVNFKSLHLVDRNGLSKVNYWHSEQC 252

DB 191 -----PYPTTTTGLFYPYNNATGAVVYFNGKDNISKVAIIDTYKGRNLSYWS-HCD 244
 QY 253 MINGTSGQWAPFMTPOSSLEFFSPACRSMKLTTHDSGVFEGIPTVYRTAPKTLFANGS 312
 DB 245 MINGTDAASPPFVEKQSVLQFFSSDICRSIYAVFESDVLNKGIPVYRFLVPSKAFASPV 304
 QY 313 VYPNEGFCP-----CLESIGQNVSTCRFGAPLFLSHPHFNADPVLSEAVLGLNPD 365
 DB 305 ENPDNYCFCTEKIISKNTSGVGLDISCKEGRDVIYSLPHFLYASPDVSEPIDGLNPE 364
 QY 366 REHSFLDIHPVTGIPMNCVKLOISLYIKAVKIGQGTGKIE-PVVLPLLWFEGSGAMGG 424
 DB 365 EHRTYLDIEPTFTGTLOFQAKRLQVNLVPSKIQVLRKLNKRNVIYVPIILWNLGTIGD 424
 QY 425 EPLNFTYQLVLMPOVLYQVYVLLGLGLLLVPVI 461
 DB 425 EKANMFRSQTGKINLLGLEMIILLSGVVMFVAFMI 461

RESULT 8

I49590

CD36 antigen - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49590

R;Endemann, G.; Stanton, L.W.; Madden, K.S.; Bryant, C.M.; White, R.T.; Protter, A.A.

J. Biol. Chem. 268, 11811-11816, 1993

A;Title: CD36 is a receptor for oxidized low density lipoprotein.

A;Reference number: I49590; MUID:93280144; PMID:7685021

A;Accession: I49590

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-472 <RES>

A;Cross-references: UNIPROT:Q08857; UNIPARC:UPI00000018D7; GB:L23108; NID:9567198; PIDN:?

C;Superfamily: lysosomal integral membrane protein II

Query Match 25.3%; Score 678; DB 2; Length 472;

Best Local Similarity 30.4%; Pred. No. 3.6e-47;

Matches 143; Conservative 102; Mismatches 178; Indels 48; Gaps 9;

QY 16 VVGLLCVAVGLVGMVLMVPSLIKKQVLRIDPSLSFAMWKEIPVPYLSVVFVFNVP 75

DB 14 VIGAVLAVFGGILMPVGDMLTIKQVLEEGTIAFKNVKVTGTVEYRQFVIFDVQNP 73

QY 76 SEILKGEKPV-VREGRPVYVR-EPRKANITFDND-TVSEHRSLSHFOPDRSHGSESD 132

DB 74 DVAKNSSKIKVQKQRPYTRVRYLAKENITQPEHTVSVFQPNGAIFEPSLSVGTEDD 133

QY 133 YIILPNILVGL-----GAVMMESKSGAGLKMMLTGLATLQGFAPNRTVGE 178

DB 134 NFTVLNLAFAAAAPHYQNSPVQVVLNLSLKSS-----MFQTRSLKE 177

QY 179 ILWGYDDPPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTVQVNFKSLHLVDRWN 238

DB 178 LLWGYKDPFLSLV-----PYPISTTVGVFPYNDTVGVYKVFNGKDNISKVAIESYK 231

QY 239 GLSKVNVVHSEQCQNMINGTSGQWAPFMTQSSLEFFSPACRSMKLTTHDSGVFEGIPT 298

DB 232 GKRLSYWPS-YCDMIMGNTDAASFPPPEKSRTLRFFSSDICRSIYAVFSEIDLKGPV 290

QY 299 YRTAPKTLFANGSVYPPNEGFCP-----CLESIGQNVSTCRFGAPLFLSHPHFNAD 351

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QY 352 PVLSEAVLGLNPDREHSLFLDIHPVTGIPMNCVKLOISLYIKAVKIGQGTGKIE-PV 410

DB 351 PDVSEPIEGHLPHNEDSHRYTLDVEPTGTLOFQAKRLQVNLVPSKIQVLRKLNKRNVI 410

QY 411 LPLLWFEQSGAMGEPINTFTYQLVLMPOVLYQVYVLLGLGLLLVPVI 461

DB 411 VPILWNLNETGTIGDEKAEKFTQVTGKIKLLGMVEMALLIGVVMFVAFMI 461

RESULT 9

A47402
fatty acid binding/transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: A47402
R:Abumrad, N.A.; El-Maghrabi, M.R.; Amri, E.Z.; Lopez, E.; Grimaldi, P.A.
J. Biol. Chem. 268, 17665-17668, 1993
A:Title: Cloning of a rat adipocyte membrane protein implicated in binding or transport
A:Reference number: A47402; MUID:93352566; PMID:7688729
A:Accession: A47402
A:Molecule type: mRNA
A:Residues: 1-472 <ABU>
A:Cross-references: UNIPROT:Q07969; UNIPARC:UPI0000155E68; GB:L19658; NID:G310112; PIDN:
C:Superfamily: lysosomal integral membrane protein II
C:Keywords: glycoprotein; transmembrane protein
F:2-6/Domain: intracellular #status predicted <CYT1>
F:7-30/Domain: transmembrane #status predicted <CYT1>
F:31-439/Domain: extracellular #status predicted <EXT>
F:440-466/Domain: transmembrane #status predicted <EXT>
F:467-472/Domain: intracellular #status predicted <CYT2>
F:79,102,134,205,220,235,247,417/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 25.1%; Score 673; DB 1; Length 472;
Best Local Similarity 31.0%; Pred. No. 9.2e-47;
Matches 146; Conservative 95; Mismatches 182; Indels 48; Gaps 9;
QY 16 VGLLCVAVGLVGMVILVMPSLIKQVLLKVRIDPSSLSFAMWKEIPVFFLSVYFVEVNP 75
DB 14 VIGAVLAVFGGILMPVGDLLIETKREIVLEEGTIAFKNVKRTGTITVYRQFVDFVQNP 73
QY 76 SEILKGKPV-VRRGKPVYR-BFRHKANITFEND--TVSFVHRSLHFOPDRSHGESD 132
DB 74 EVAKNSKIKVIRGPTTYRVLAKENITQPKSTVSVQPNGAIFPSLSVGTEND 133
QY 133 YIILPNLIVLG-----GAVMMESKAGLKLMMTLGLATLGLQAFMNRVTGE 178
DB 134 NFTVLNLAAVAAPHIYNTSFVQVGLNSLIKKSS-----MFTQSLKE 177
QY 179 ILWGYEDPFVNFINKYLPDMPIKGLFVEMNNSDGLFTVFTGVQNFSKHLVDWVN 238
DB 178 LLWGYKDPFFLSV-----PYPISTTVGVFPYNNVTVDGYSVNGKDNISKVAIIDTYK 231
QY 239 GLSKVNVHSEQCNMINGTSQWAPMTPOSSLRFPSPACRSMKLTTHDSGVFEGIPT 298
DB 232 GKRNLSWES-YCDMNGTDAASPPLGKSRTRLRFPSSDICHSIYAVFSEVNLKGIPIV 290
QY 299 YRFTAPKTLFANGSVYPPNFGFCP-----CLESIGQNVSTCRFGAPLFLSHPHFYNAD 351
DB 291 YRFVLPANAFASPLQPNPDNHCFCFTEKVISNNCTSYGVLDIGCKEKGKPVYNSLPHFLHAS 350
QY 352 PVLSEAVLGLNPDPREHSLFDTHPTVGIPMNCVSKLOISLYIKAVKGIQGTGKIB-PVV 410
DB 351 PDVSEPIEGLNPTDEHRTYLDVEPIGTFTLOFSKRLQVNLVKPARKIKALKNLKRPI 410
QY 411 LPLWFSQSGAMGGEPLNTFTVLVLMPOVLQVVOVVLGLGLLGLLVLVPI 461
DB 411 VPILMLNETGTIGDEKAMFNQVTKIKLGLVEMVLLGVGVVNFVAFMI 461

RESULT 10

S38957
epithelial membrane protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S38957
R:Hart, K.; Wilcox, M.
J. Mol. Biol. 234, 249-253, 1993
A:Title: A Drosophila gene encoding an epithelial membrane protein with homology to CD36
A:Reference number: S38957; MUID:94047068; PMID:7693949
A:Accession: S38957
A:Molecule type: mRNA
A:Residues: 1-519 <HAR>

A:Cross-references: UNIPROT:Q24336; UNIPARC:UPI00000774AD; EMBL:X73332; NID:G429163; PID:
C:Genetics:
A:Gene: FlyBase:emp
A:Cross-references: FlyBase:FBgn0010435
C:Superfamily: lysosomal integral membrane protein II
C:Keywords: transmembrane protein
F:2-19/Domain: intracellular #status predicted <CYT1>
F:20-39/Domain: transmembrane #status predicted <TM1>
F:460-482/Domain: transmembrane #status predicted <TM2>
F:483-519/Domain: intracellular #status predicted <CYT2>

Query Match 22.4%; Score 600; DB 1; Length 519;
Best Local Similarity 30.3%; Pred. No. 8.9e-41;
Matches 155; Conservative 88; Mismatches 224; Indels 44; Gaps 12;
QY 6 RARWAVGLGVVGLLCAVLGVVMILVMPSLIKQVLLKVRIDPSSLSFAMWKEIPVFFYL 65
DB 18 RKWWTI-----VVAALIIIGGIIVVACEFTVLIDAVVDRMVVALRPGAKTFGWAKAPVPEPI 74
QY 66 SVYFFEVNPSIL-KGEKPVVRRGPPVYRFRHKANITFENDNTVSFVHRSLHFQPD 124
DB 75 SLIYVNTVADDFLSNGSKAIIVDEGVPPYVSETWEKVNIVENDNGTLSYLRKIYSFRED 134
QY 125 RHGSESDYIILPNLIVLGAVMMESKAGLKLMMTLGLATLGLQAFMNRVTGEILWGYE 184
DB 135 LSVGPEDDVIVPNIPMLSATSQSKHAARFLRLAMASIMDILKIKPFVQVSVGQLLWGYE 194
QY 185 DPFVNFINKYLPDMPIKGL-----FGLFVEMNNSDGLFTVFTGVQNFSKHLVDWVN 239
DB 195 DPLL-----KLAKDVVPKEQLPYEFGLLYGKNGTSSDRVTNTVTDVDDIRRYGIDNFG 250
QY 240 LSKVNVHSEQCNMINGTSQWAPMTPOSSLRFPSPACRSMKLTTHDSGVFEG-IPT 298
DB 251 RTHLPHTWTDACNTLAGTDSIFPPHIDHRLVYDKDCLRLPLVFEKVTMSNEVFG 310
QY 299 YRFTAPKTLFANGSVYPPN-----GFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADP 352
DB 311 YRFTTRVGFRRCGQ--PPGQHVLLSRGKPCSPNGLFNVSLCOYDPSIMLSPPHFYLADE 368
QY 353 VLSEAVLGLNPDPRE-HSLFLDIHPVTGIPMNCVSKLOISLYIKAVKGIQGTGKIBPVVL 411
DB 369 SLRTQVEGISPPMKKEKHQFFFDVQPKMGTTLRVARIQINLAVSQVFDIKQVANFDDIIF 428
QY 412 LPLWFSQSGAMGGEPLNTFTVLV-----LMPQVLYQVVOVVLGLGLLGLLVLVPIYQLR- 465
DB 429 PILWFE-----GIDNLPDEVLTALMFAEQVPPKIRVALIVGLCALGVILLSTFTCLIRN 484
QY 466 SQEKCFLFWSGS-----KKGSDQKE 485
DB 485 SHRQSTLHLEGSNYLATAQVDMNKKQNKQ 515

RESULT 11

S43137
D-CD36 protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S43137; S43136
R:Franc, N.; Dimarq, J.; Hoffmann, J.; Lagueux, M.
submitted to the EMBL Data Library, March 1994
A:Description: d-CD36 : a second Drosophila gene related to the CD36 family of cell adhe
A:Reference number: S43136
A:Accession: S43137
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-457 <FRA>
A:Cross-references: UNIPROT:Q27367; UNIPARC:UPI000016BB39; EMBL:Z31583; NID:G468537; PID:
C:Genetics:
A:Gene: FlyBase:crouemort
A:Cross-references: FlyBase:FBgn0015924
C:Superfamily: lysosomal integral membrane protein II
Query Match 22.3%; Score 597; DB 1; Length 457;

Best Local Similarity 30.9%; Pred. No. 1.3e-40;
Matches 135; Conservative 84; Mismatches 198; Indels 20; Gaps 10;

QY 2 GGSARAWAVGLGVGLCAVLGVMLVMPSLIKQVLKQVKNVRIDPSSLSFAMKKEIPV 61
DB 7 GETORKVWV-FGLGSVFL---LGLIVFVPGIADNLVEDGLTKLGGTDAYSWLEAPI 62

QY 62 PFYLSVYFVEVNPSEILKGE-KPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 63 PLYLSFTYFNWNTNPDIRNPDIKENFVEMGPTFLKHKENYTFYDNATVAYYERTWF 122

QY 121 FQDRSHGSSDYIILPNILVLGAVMMESKAGLKLMTLGLATLQORAFMNTVGE-I 179
DB 123 FQDRSNGTLDDMWTAARATATVADEMRDQKIVKXIINFMLNHEGGKLYVTPVGEWI 182

QY 180 LWGYDEDFVNPINKPLPMPFIKKG-FGLFVEMNNS--DSGLFTVFTGVQVNFSLHVDLR 236
DB 183 FEGQDNITDFNLNFTTKIDIPYKRGWLADRNESITDGLFTIHTGTDIDISLGLTH 242

QY 237 WNLGSKVYNHSEOCNMINGTSQMWAPFMTQSSLEFFSEACRSKMLTVHDSGVFE-- 294
DB 243 WNGKAETGFYEM-PCGIWNGTGDGMFPFKMNVNDEITIFATDACRFNWL--RPRGTVENH 299

QY 295 GIPTYRTAPKTLFANGSVPPNNGFC-----PCLESGIQNVSTCFGAPFLSHSHFY 348
DB 300 GLTATKVGWTEETLDSGENYFNQACFCDEARFDECPKTVGVVECKACRDKAPIYSSPHFY 359

QY 349 NADPVLSEAVGLNPDPREHSLFDIHPVTGIPMNCVGLQISLYIKAVGIGTGKIEP 408
DB 360 LADQSYVDVAGMKPEKEHFFLAVEPTIGVPVQVHGRIQINMIERPDDEDDFDIYRGVQK 419

QY 409 VVLPFLWFQSGAMGGE 425
DB 420 VLMPMFWDQVLELSE 436

RESULT 12
A59259
sensory neuron membrane protein-1 - polyphemus moth
C:Species: Antherea polyphemus (polyphemus moth)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59259
R;Rogers, M.E.; Sun, M.; Lerner, M.R.; Vogt, R.G.
A:Title: Smp-1, a novel membrane protein of olfactory neurons of the silk moth Antherea
A:Reference number: A59259; MUID:97313452; PMID:916946
A:Accession: A59259
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Cross-references: UNIPROT:O02351; UNIPARC:UPI000007FD51; GB:U95026; NID:g2149911; PIDN
A:Experimental source: strain wild
C:Genetics:
A:Gene: SNMP1
C:Superfamily: lysosomal integral membrane protein II

Query Match 18.0%; Score 483; DB 2; Length 525;
Best Local Similarity 23.5%; Pred. No. 2.9e-31;
Matches 12; Conservative 108; Mismatches 229; Indels 76; Gaps 15;

QY 8 RWAVGLGVGLCAVLGVMLVMPSLIKQVLKQVKNVRIDPSSLSFAMKKEIPVFPYLS 66
DB 8 KYAAIGGVF-----VFGILIGWIPVVLKSKQIKEMALSKKTLDRQMKVFPALDFK 62

QY 67 YVFEVNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLHFPQDR 125
DB 63 VYIFNYTNVDIQRGAKPIVKEIGPYFPEWKEKVEVEDHEENDITTYKRLDVHFRPDL 122

QY 126 SHG--SESDYIILPNILVLGAVMMESKAGLKLMTLGLATLQORAFMNTVGEILWY 183
DB 123 SGPGLTGEEVLIIMPHLFILA-----MVATINREKPSMLNVKESINGIFDNP 169

QY 184 EDPFVN-----FIN---KYLPMDFPIKKG-----FGLFVEMN 212

DB 170 KDVFELRYKAMDIMFERGIIINCDRTFAPKAACTMKKDAVTGVIYBPNQFRESLFGTRN 229

QY 213 NS--DSGLFTVFTGVQVNFSLIKHLVDNRNGLSKVNYHSEOCNMINGTSQMWAPFMTQSS 271
DB 230 NTNPDVTVTKRGIKKIMDVGQVVALNGRQIDWR-DHCNBEFGTDTGVFPFLTYKDR 288

QY 272 LEFFSEACRSKMLTYHDSGVFEGIPTYRTAPKTLFANGSVVPPNNGFC-----PCLESG 327
DB 289 LQSFSPDLCHSFRAWQKTSYKGIKNTRYIANVGDPAND--PELQCFCDTDPDECLPKG 345

QY 328 IQNVSTCRFGAPFLSHPHFYNADPVLSEAVGLNPDPREHSLFDIHPVTGIPMNCVSK 387
DB 346 IMDIRKC-LKPMYVSLPHLEFLETDTSVTNQVKGILTPDPNEHGIADPEPLSGTLMDAKOR 404

QY 388 LQISLYIKAVKGIQGTGKIEPVLPLLPBQSGAMGGEPLNTFTQTLVLMPOVLQVQVY 447
DB 405 MQNLIKLRTRDKLTAIFKDLPSIVPCFWHVEGILLNKTFVKMLKHQLFIPKRVIGVRW 464

QY 448 LLGLGLLLLVPIYQLRSQEKCFLEWGS-----KKGSDQKBAIQAYSESLMSP 497
DB 465 MVSFGLIAVLAVMYHFKDN---IMGWAAKGESTTAKVNPEDGSGNEQRGVSVIGQDREPP 521

RESULT 13
T27054
hypothetical protein Y49E10.20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27054
R;Barlow, K.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z20303
A:Accession: T27054
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-534 <WIL>
A:Cross-references: UNIPROT:Q9XTT3; UNIPARC:UPI0000083B4E; EMBL:Z98866; PIDN:CAB11566.1;
A:Experimental source: clone Y49E10
C:Genetics:
A:Gene: CRSP:Y49E10.20
A:Map position: 3
A:Introns: 42/3; 105/2; 188/3; 231/3; 359/1; 440/2; 505/3
C:Superfamily: lysosomal integral membrane protein II

Query Match 18.0%; Score 481.5; DB 2; Length 534;
Best Local Similarity 27.7%; Pred. No. 4e-31;
Matches 150; Conservative 102; Mismatches 201; Indels 89; Gaps 23;

QY 16 VGLLCALVGLGVMLVMP--SLIKQVVLKQVKNVRIDPSSLSF-----AMWKEIPVP 62
DB 14 ILGLLAAGVLLIGIPDIRVNRQV-----IDQDFLGYTRDENGTEVFNAMTKSWLKP 68

QY 63 FY---LSVYFVEVNPSEILK-GEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHR 118
DB 69 LYANQLNIMFNVTNVDGILKRHEKNLHIGFVFEVQEKVYHVPADNDTVFYKNQK 128

QY 119 L-HFQDRS-----HGSSEDIILPNILV--LGAVMMESKAGLKLMTLGLATLQORAF 171
DB 129 LYHFNKNASCTCHDMK--VTIPNIVFQKLIDAADVTIFGVRIKFAIESVLKKNVSEAPY 186

QY 172 MNTVGEILW-GYEDFPVNFINK-----YLPDMFPIKGFGLFVEMNNSDGLFTVFTGV 225
DB 187 ITVKVSDALFDGEDFDIIVCKNKILQFLCETNSLQRRVGFYQNGTDDGIYEVDAGV 246

QY 226 QNFESKHLVDNRNGLSKV--NYHSEOCNMINGTSQMWAPFMTQSSLEFFSEACRS 283
DB 247 PPSKIGHLTYNNWNTNPEGTWDTKYARMINGTGQLFSPMLKREDRLTIFVFPQICRSI 306

QY 284 KLTYSGVFEGIPTYRTAPKTLFANGSVVPPNNGFC-----PCLES 326
DB 307 QMEYTKDVAVNGVPSRWYAPPLDLY--DPALPQNRFAFCNKNMGMPRYPDNTTVOIENCLPA 364

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:35:04 ; Search time 147.5 Seconds
(without alignments)
2434.671.Million cell updates/sec

Title: US-08-765-108-4

Perfect score: 2881

Sequence: 1 MGSGARARWAVGLGVVGLL.....YBSLMSPAKGTVLQBAKL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	1	Q60417 cricetus
2	2447	91.3	509	1	Q61009 mus musculus
3	2447	91.3	509	2	Q4FK30 mus musculus
4	2444	91.2	509	1	P87943 rattus norv
5	2430	90.6	509	2	Q88548 rattus norv
6	2424	90.4	509	2	Q6SR89 RAT
7	2260	84.3	509	2	Q6T8F1 TUPGB
8	2244	83.7	509	2	Q52L25 HUMAN
9	2227	83.1	509	2	Q6WIW9 RABIT
10	2215.5	82.6	506	2	Q6B417 RAT
11	2215	82.6	509	1	Q6B417 RAT
12	2158	80.5	509	1	Q6B417 RAT
13	2066.5	77.1	552	1	Q6B417 RAT
14	2066.5	77.1	552	1	Q6B417 RAT
15	2049	76.4	501	2	Q6WIW9 RABIT
16	1415.5	52.8	460	2	Q4S1T9 TETNG
17	1303	48.6	457	2	Q7Z1Y0 BRARE
18	797	29.7	2096	2	Q4S1T9 TETNG
19	772.5	28.8	532	2	Q64HW6 ONCNY
20	751.5	28.0	477	1	Q6B417 RAT
21	751.5	28.0	478	2	Q6B417 RAT
22	740	27.6	531	2	Q6JG88 BRARE
23	739	27.6	477	1	Q6B417 RAT
24	738	27.5	477	1	Q6B417 RAT
25	735	27.4	483	2	Q5XH33 XENLA
26	728	27.2	465	2	Q6DHCT BRARE
27	709.5	26.5	484	2	Q7Z1T6 XENLA
28	709	26.4	472	2	Q6BKES RAT
29	707.5	26.4	471	2	Q5Z1L8 CHICK
30	702	26.2	472	2	Q925W0 RAT
31	699	26.1	472	2	Q6IMX5 RAT

32	696	26.0	472	2	Q35754 RAT
33	692	25.8	471	1	CD36 HUMAN
34	688	25.7	522	2	Q7Q950 ANOGA
35	686	25.6	472	2	Q6J512 MACMU
36	686	25.6	472	2	Q4R6B4 MACFA
37	685	25.6	471	1	CD36 MESAU
38	683	25.5	460	2	Q4SAC1 TETNG
39	678	25.3	471	1	CD36 MOUSE
40	675	25.2	472	2	Q8C6Z4 MOUSE
41	673	25.1	471	1	CD36 RAT
42	657	24.5	471	1	CD36 BOVIN
43	649.5	24.2	601	2	Q8IGF0 DROME
44	647.5	24.2	520	2	Q7KVF1 DROME
45	647.5	24.2	551	2	Q9W0X0 DROME

ALIGNMENTS

RESULT 1

ID	SCRB1_CRIGR	STANDARD;	PRT;	509 AA.
AC	Q60417;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Scavenger receptor class B member 1 (SRB1) (SR-BI) (HaSR-BI).			
GN	Name=SCARB1;			
OS	Cricetulus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Cricetidae; Cricetinae; Cricetulus.			
OX	NCBI_TaxID=10029;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Ovarian carcinoma;			
RX	MEDLINE=94342261; PubMed=7520436;			
RA	Acton S.L., Scherer P.S., Lodish H.F., Krieger M.;			
RT	"Expression cloning of SR-BI, a CD36-related class B scavenger receptor."			
RL	J. Biol. Chem. 269:21003-21009(1994).			

CC - FUNCTION: Receptor for different ligands such as phospholipids, cholesterol ester, lipoproteins, phosphatidylserine and apoptotic cells. Probable receptor for HDL, located in particular region of the plasma membrane, called caveolae. Facilitates the flux of free and esterified cholesterol between the cell surface and extracellular donors and acceptors, such as HDL and to a lesser extent, apoB-containing lipoproteins and modified lipoproteins. Probably involved in the phagocytosis of apoptotic cells, via its phosphatidylserine binding activity (By similarity).

CC - SUBCELLULAR LOCATION: Integral membrane protein. Predominantly localized to cholesterol and sphingomyelin-enriched domains within the plasma membrane, called caveolae (By similarity).

CC - PTM: N-glycosylated (By similarity).

CC - SIMILARITY: Belongs to the CD36 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL: U11453; AAA61572.1; -; mRNA.

CC PIR: A53920; A53920.

CC InterPro: IPR002159; CD36.

CC InterPro: IPR005428; CD36 antigen.

CC PANTHER: PTHR11923; CD36; 1.

CC Pfam: PF01130; CD36; 1.

CC PRINTS: PR01610; CD36ANTIGEN.

CC PRINTS: PR01609; CD36FAMILY.

CC GlycoProtein; Receptor; Transmembrane.

CC TOPO_DOM 1 11 Cytoplasmic (Potential).

CC TRANSMEM 12 32 Potential.

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FT TOPO DOM 33 440 Extracellular (Potential).
FT TRANSMEM 441 461 Potential.
FT TOPO DOM 462 509 Cytoplasmic (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 509 AA; 56735 MW; 1A7C0F5F6CB61A17 CRC64;

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.7e-201;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSARARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQQLVKNVRIDPSSLSFAMWKEIP 60
Db 1 MGGSARARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQQLVKNVRIDPSSLSFAMWKEIP 60

Qy 61 VPFLSYVFFEVNPNSEILKGEKPVVRERGPYVYRPRHKNITFNDNTVSVFVHRSLH 120
Db 61 VPFLSYVFFEVNPNSEILKGEKPVVRERGPYVYRPRHKNITFNDNTVSVFVHRSLH 120

Qy 121 FQDRSHGSESDYIILPNILVILGAVNMESKAGLKLMTLGLATLGLQRAFMRRTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVILGAVNMESKAGLKLMTLGLATLGLQRAFMRRTVGEIL 180

Qy 181 WGYEDDPFVNFINKYLPDMFPIKGFGLFVEMNNSDSLFTVFTGVQNFSLHLDVRNGL 240
Db 181 WGYEDDPFVNFINKYLPDMFPIKGFGLFVEMNNSDSLFTVFTGVQNFSLHLDVRNGL 240

Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300

Qy 301 FTAPKTLFANGSVYPNPGFCPLGSIQNVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPNPGFCPLGSIQNVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFPQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFPQSG 420

Qy 421 AMGGEPLNTFTYQLVLMQVLYQVYVLLGLGGLLLLPVVIYQLRSQEKCFLFWGSKKG 480
Db 421 AMGGEPLNTFTYQLVLMQVLYQVYVLLGLGGLLLLPVVIYQLRSQEKCFLFWGSKKG 480

Qy 481 SODKEATQAYSESLMSPAAGTGVLOEAKL 509
Db 481 SODKEATQAYSESLMSPAAGTGVLOEAKL 509

```

RESULT 2

SCRB1_MOUSE STANDARD; PRT; 509 AA.

AC G61009; Q9CJW7;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Scavenger receptor class B member 1 (SRB1) (SR-BI).

GN Name=Scarb1; Synonyms=SRb1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96152374; PubMed=8560269;

RA Acton S., Rigotti A., Landschulz K.T., Xu S., Hobbs H.H., Krieger M.;

"Identification of scavenger receptor SR-BI as a high density lipoprotein receptor.";
Science 271:518-520(1996).
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L., Konoaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirose-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
[3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K., Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.M., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: Receptor for different ligands such as phospholipids, cholesterol ester, lipoproteins, phosphatidylserine and apoptotic cells. Probable receptor for HDL, located in particular region of the plasma membrane, called caveolae. Facilitates the flux of free and esterified cholesterol between the cell surface and extracellular donors and acceptors, such as HDL and to a lesser extent, apoB-containing lipoproteins and modified lipoproteins. Probably involved in the phagocytosis of apoptotic cells, via its phosphatidylserine binding activity (By similarity).
-1- SUBUNIT: The C-terminal region binds to PDZK1 (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly localized to cholesterol and sphingomyelin-enriched domains within the plasma membrane, called caveolae (By similarity).
-1- TISSUE SPECIFICITY: Expressed primarily in liver and nonplacental

steroidogenic tissues.
-!- PTM: N-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the CD36 family.

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EMBL; U37799; AAC52378.1; --; mRNA.
DR EMBL; AK010622; BAB27068.1; --; mRNA.
DR EMBL; AK028191; BAC25802.1; --; mRNA.
DR EMBL; AK033114; BAC28157.1; --; mRNA.
DR EMBL; BC004656; AA04656.1; --; mRNA.
DR Ensembl; ENSMUSG00000037936; Mus musculus.
DR MGI; MGI:893578; Scarb1.
DR GO; GO:0016599; C:cytosolic membrane; IDA.
DR GO; GO:0002399; C:integral to membrane of membrane fraction; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36 antigen.
DR PANTHER; PTHR11923; CD36; 1.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
DR Glycoprotein; Receptor; Transmembrane.
DR TOPO_DOM 1 11
FT Transmem 12 32
FT Potential 33 440
FT Extracellular (Potential). 441 461
FT Transmem 462 509
FT TOPO_DOM 102 102
FT CARBOHYD 108 108
FT CARBOHYD 116 116
FT CARBOHYD 173 173
FT CARBOHYD 212 212
FT CARBOHYD 227 227
FT CARBOHYD 255 255
FT CARBOHYD 288 288
FT CARBOHYD 310 310
FT CARBOHYD 330 330
FT CARBOHYD 383 383
FT CONFLICT 396 396
FT CONFLICT 468 509
SQ SEQUENCE 509 AA; 56754 MW; 5CFDD62DD6ECB1C CRC64;
L -> GPEDTTSPPNLIAMSDQPSPTPLLEDLSLQPTSS
EKCFLFWGSGKSGQDKAEIQAQVSESLMSPAAGTGLQAEK
S -> F (in Ref. 2; BAB27068).
AMA (in Ref. 2; BAB27068).
Query Match 91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 1.7e-182;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCVAVGVVMIIVMPSLIIKQOVLKNVRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGALGALGGLFAALGVVMIIVMPSLIIKQOVLKNVRIDPSSLSFAMWKEIP 60
QY 61 VPFLSYVFEVVPVNPSEILKGEKPVVRERGYPVYRFRHKNITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVFEVVPVNPSEILKGEKPVVRERGYPVYRFRHKNITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMMTLGLATLQORAFMNRVTGEIL 180
QY 181 WGYEDPFWNFINKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
DB 181 WGYDDPFWHFLNTYLPDMLPIKKGKGLFVGMNNSGVTFTVFTGVQNFSKIHLVDKRWGL 240
QY 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
QY 361 LNPNPKHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVLPLLPFQSG 420
DB 361 LNPNPKHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVLPLLPFQSG 420

RESULT 3

Q4FK30_MOUSE
ID Q4FK30_MOUSE PRELIMINARY; PRT; 509 AA.
AC Q4FK30;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Scarbi protein.
GN Name=Scarbi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Ebert L., Wuenstmann E., Schatten R., Henze S., Bohn E.,
RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
RA "Cloning of mouse full open reading frames in Gateway (R) system entry
RT vector (pDONR201).";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO10222; CAJ18430.1; --; mRNA.
SQ SEQUENCE 509 AA; 56754 MW; 5CFDD62DD6ECB1C CRC64;
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 1.7e-182;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCVAVGVVMIIVMPSLIIKQOVLKNVRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGALGALGGLFAALGVVMIIVMPSLIIKQOVLKNVRIDPSSLSFAMWKEIP 60
QY 61 VPFLSYVFEVVPVNPSEILKGEKPVVRERGYPVYRFRHKNITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVFEVVPVNPSEILKGEKPVVRERGYPVYRFRHKNITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMMTLGLATLQORAFMNRVTGEIL 180
QY 181 WGYEDPFWNFINKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
DB 181 WGYDDPFWHFLNTYLPDMLPIKKGKGLFVGMNNSGVTFTVFTGVQNFSKIHLVDKRWGL 240
QY 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
QY 361 LNPNPKHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVLPLLPFQSG 420
DB 361 LNPNPKHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVLPLLPFQSG 420

Qy	481	SODKEALQAYSESILMSPAAGTGVLOEAKL	509
Db	481	SODKEANQAYSESILMSPAAGTGVVQOEAKL	509
RESULT 6			
Q	QSR89	RAT	
ID	QSR89	RAT PRELIMINARY;	PRT; 509 AA.
AC	QSR89;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DB	Scavenger receptor class B type 1.		
GN	Name=Scarb1;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;		
RX	MEDLINE=99236778; PubMed=10221589; DOI=10.1385/ENDO.9:3:243;		
RA	McLean M.P., Sandhoff T.W.;		
RT	"Expression and hormonal regulation of the high-density lipoprotein		
RT	(HDL) receptor scavenger receptor class B type I messenger ribonucleic		
RT	acid in the rat ovary."		
RL	Endocrine 9:243-252(1998).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;		
RX	MEDLINE=20043932; PubMed=10579331; DOI=10.1210/en.140.12.5669;		
RA	Lopez D., McLean M.P.;		
RT	"Sterol regulatory element-binding protein-la binds to cis elements in		
RT	the promoter of the rat high density lipoprotein receptor SR-BI		
RT	gene."		
RL	Endocrinology 140:5669-5681(1999).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;		
RA	McLean M.P., Sandhoff T.W., Lopez D.;		
RL	Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AY451993; AAR18387.1; -; mRNA.		
DR	GO: GO:0016020; C:membrane; IEA.		
DR	GO: GO:0004872; F:receptor activity; IEA.		
DR	GO: GO:0007155; P:cell adhesion; IEA.		
DR	InterPro: IPR002159; CD36.		
DR	pfam: PF011130; CD36; 1.		
DR	PRINTS; PR01610; CD36ANTIGEN.		
DR	PRINTS; PR01609; CD36FAMILY.		
KW	Receptor.		
Q	SEQUENCE	509 AA; 56859 MW; EAA0A76ECD207706C CRC64;	
Query Match 90.4%; Score 2424; DB 2; Length 509;			
Best Local Similarity 88.4%; Pred. No. 1.1e-180;			
Matches 450; Conservative 31; Mismatches 28; Indels 0; Gaps 0;			
Qy	1	MGSARARWAVAGLVGVVGLLCVAVLGVMVILVMPSLIKQVVKVRIIDPSSLSFAMWKEIP	60
Db	1	MGVSSRARWALGLGVLLCAALGVIMLVPSLIKQVVKVRIIDPSSLSFGWKEIP	60
Qy	61	VPYLSVYFPEVNVNPSILKGEKPVVREPGYVYVREPRHKANITFDNDNTVSVFVHRSILH	120
Db	61	VPYLSVYFPEVNVNPSVLNGQKPVVREPGYVYVREPRQKNITFDNDNTVPYIENRSLR	120
Qy	121	FQDRSHGSSDYIILPNILVLGAVNMESKAGLKLMTTGLATLQORAFMNTVGEIL	180
Db	121	FQDRSGSSDYIILPNILVLGAVNMEDKPTSLKULMTLGLVTMQRAPMNTVGEIL	180
Qy	181	WGVEDPFPVNPINKYLPDMFPPIKGKFGLVFEMNNSSDGLFTVFTGVQNFSKHLVDRWNGL	240

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Db 181 WGYEDPFLVFLSKYFPGMPFIKGFGLFVGMDSSGVFTVTCGVQNSKIHVLVDKWNGL 240
Qy 241 SKNYWHSEOCNMINGTSCQWAPFMTPOSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SEVNYWHSEOCNMINGTAGQWAPFMTPESSLEFFSPSEACRSKMLTYQESRVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCRESIQNVSTCRFGAPLFLSQPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPKEHSLFDLHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPVYQLRSQEKCFLWSSGSKG 480
Db 421 MMGKTLNTFYTLVLMPOVLQVYVLLGLGGLLLVPVYQLRSQEKCFLWSSGSKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTIVLQEAKL 509
Db 481 SODKEAMQAYSESLSMSPAAGTIVLQEAKL 509

RESULT 7
Q6T8F1 TUPGB
ID Q6T8F1 TUPGB PRELIMINARY; PRT; 509 AA.
AC Q6T8F1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scavenger receptor class B member 1.
GN Name=SCARB1;
OS Tupaia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupiaia.
OX NCBI_TaxID=37347;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Barth H., Cerino R., Arcuri M., Hoffmann M., Schurmann P., Adah M.I.,
RA Giesler B., Zhao X., Ghisetti V., Lavezzi B., Blum H.E.,
RA von Weizsacker F., Vitelli A., Scarselli E., Baumert T.F.;
RT "Scavenger Receptor Class B Type I and Hepatitis C Virus Infection of
RT Primary Tupaia Hepatocytes."
RL J. Virol. 79:5774-5785(2005);
DR EMBL; AY285533; ARL2144.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57369 MW; FOA3PBB1431PFB18 CRC64;

Query Match 84.3%; Score 2260; DB 2; Length 509;
Best Local Similarity 81.3%; Pred. No. 6.9e-168;
Matches 414; Conservative 49; Mismatches 46; Indels 0; Gaps 0;

Qy 1 MGGARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQOVLKVRIDPSSLSFAMWKEIP 60
Db 1 MGGARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQOVLKVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFEVVPNPSEILKGEKVPVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFYLSVYFEVVPNPSEILKGEKVPVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQPRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQRAFMRNRTVGEIL 180
Db 121 FQPAKRGLESDYIIVMPNIVLGAAMNENKPMSLKMTLAFSTLGERAFMRNRTVAEIM 180
Qy 181 WGYEDPFLVFLSKYFPGMPFIKGFGLFVGMDSSGVFTVTCGVQNSKIHVLVDKWNGL 240
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Db 181 WGYEDPFLVFLSKYFPGMPFIKGFGLPAELNNSGLFTVTVGVKDFORIHVLVDKWNGL 240
Qy 241 SKNYWHSEOCNMINGTSCQWAPFMTPOSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNFHSDQCNMINGTSCQWAPFMTPESSLEFFSPSEACRSKMLTYQEPGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LHPNQEHSLFDLHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPVYQLRSQEKCFLWSSGSKG 480
Db 421 AMEGETLRTFYTLVLLPAVLHYAQVYVLLALGCLLLVPVHHIRSQEKCYLFWSSSKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTIVLQEAKL 509
Db 481 PKDKEAIQAYSESLSMTPAPRGIVLQEARL 509

RESULT 8
Q52LZ5 HUMAN
ID Q52LZ5 HUMAN PRELIMINARY; PRT; 509 AA.
AC Q52LZ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Scavenger receptor class B, member 1.
GN Name=SCARB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC093732; AAH93732.1; -; mRNA.
KW Receptor.
SQ SEQUENCE 509 AA; 56973 MW; 0184AE9CEC595374 CRC64;

Query Match 83.7%; Score 2244; DB 2; Length 509;
Best Local Similarity 81.5%; Pred. No. 1.2e-166;
```


Matches 415; Conservative 46; Mismatches 48; Indels 0; Gaps 0;

QY 1 MGGSARARWAVGLGVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGCSAKARWAAGALGVAGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 QY 61 VPFLSVYVPEVWNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 DB 61 IPFLSVYVFPVWNPSEILKGEKQVVRERGYPVYVREFRHKSNITFNNNDTVSFLEYRTFQ 120
 QY 121 FQDRSHGSESDYIILPNILVGLGAVNMESKAGLKLMMTILGLATLQORAFMNRVTGGEIL 180
 DB 121 FQPSKSHGSESDYIILPNILVGLGAVNMENKFWILKLIMTLAFTLGERAFMNRVTGGEIM 180
 QY 181 WGYEDPFFNFINKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNL 240
 DB 181 WGYKDPVLNINKYLPFGMPFKKFGKGLFVEMNNSDGLFTVFTGVQNFISRIHLVDKWNGL 240
 QY 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFSPSEACRSMKLYTHDSGVFEGIPTYR 300
 DB 241 SKVDFWHSDDQCNMINGTSGQWAPFMTPESSLEFSPSEACRSMKLYKESGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 DB 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFYNADPVLAEAVTG 360
 QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIIEPVVPLPLWFFQSG 420
 DB 361 LHPNOEAHSLFLDIHPVTGIPMNCVKLQLSLYMKSVAGIQOTGKIIEPVVPLPLWFAESG 420
 QY 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPVYIQRSEKCFPLFWSGSKKG 480
 DB 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPVYIQRSEKCFPLFWSGSKKG 480
 QY 481 SODKEAIOAYSESLMSPAAGKTVLQEAKL 509
 DB 481 SKDKEAIOAYSESLMTAPKSGVLQEAKL 509

RESULT 9

Q6WIW9 RABIT
 ID Q6WIW9 RABIT PRELIMINARY; PRT; 509 AA.
 AC Q6WIW9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Scavenger receptor class B type I.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
 RA Ritsch A., Tancevski I., Schoger W., Pfeifhofer C., Gander R.,
 RA Eller P., Foegeer B., Stanzl U., Patsch J.R.;
 RT "Molecular characterization of rabbit scavenger receptor class B types
 RT I and II: portal to central vein gradient of expression in the
 RT liver".
 RL J. Lipid Res. 45:214-222(2004).
 DR EMBL; AY283327; AAP40266.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR002159; CD36.
 DR InterPro; IPR005428; CD36_antigen.
 DR Pfam; PF01130; CD36; 1.
 DR PRINTS; PR01610; CD36ANTIGEN.
 DR PRINTS; PR01609; CD36FAMILY.
 KW Receptor.
 SQ SEQUENCE 509 AA; 57052 MW; 00DD47F1AF2DB4E0 CRC64;

Query Match 83.1%; Score 2227; DB 2; Length 509;

Best Local Similarity 80.4%; Pred. No. 2.6e-165;
 Matches 409; Conservative 48; Mismatches 52; Indels 0; Gaps 0;

QY 1 MGGSARARWAVGLGVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGRARARRAAGLGVVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 QY 61 VPFLSVYVPEVWNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLSH 120
 DB 61 APFLSVYVFPVWNPSEILKGEKQVVRERGYPVYVREFRHKANITFNDNDTVSFLEHRSFQ 120
 QY 121 FQDRSHGSESDYIILPNILVGLGAVNMESKAGLKLMMTILGLATLQORAFMNRVTGGEIL 180
 DB 121 FQPDKSGSESDYIILPNILVGLGAVNMENKFWILKLIMTLAFTLQORAFMNRVTGGEIM 180
 QY 181 WGYEDPFFNFINKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNL 240
 DB 181 WGYEDPPLNINKYLPGVFPFKKFGKGLFVEMNNSDGLFTVFTGVQNFISRIHLVDKWNGL 240
 QY 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFSPSEACRSMKLYTHDSGVFEGIPTYR 300
 DB 241 SKVNFHSDQCNMINGTSGQWAPFMTPESSLEFSPSEACRSMKLYKQGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 DB 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLAEAVLG 360
 QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIQOTGKIIEPVVPLPLWFFQSG 420
 DB 361 LHPNEEAHSLFLDIHPVTGIPMNCVKLQLSLYMKAIRGIGQTKIEPVVPLPLWFFQSG 420
 QY 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPVYIQRSEKCFPLFWSGSKKG 480
 DB 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPVYIQRSEKCFPLFWSGSKKG 480
 QY 481 SODKEAIOAYSESLMSPAAGKTVLQEAKL 509
 DB 481 SKDKEAIOAYSESLMTAPKSGVLQEAKL 509

RESULT 10

Q6B417 RAT
 ID Q6B417 RAT PRELIMINARY; PRT; 506 AA.
 AC Q6B417;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Scavenger receptor class B type 2.
 GN Names=Scarb2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley;
 RA Lopez D., Rubin D., McLean M.P.;
 RL "Regulation of the Rat SR-B Isoforms";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY682847; AAT85567.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR002159; CD36.
 DR InterPro; IPR005428; CD36_antigen.
 DR Pfam; PF01130; CD36; 1.
 DR PRINTS; PR01610; CD36ANTIGEN.
 DR PRINTS; PR01609; CD36FAMILY.
 KW Receptor.
 SQ SEQUENCE 506 AA; 56342 MW; 6FDB625301320E2E CRC64;


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Query Match      82.6%; Score 2215.5; DB 2; Length 506;
Best Local Similarity 83.0%; Pred. No. 2.1e-164;
Matches 415; Conservative 35; Mismatches 35; Indels 15; Gaps 2;

Qy 1 MGSARARWAVGLGVVGLLCVAVGVVMIWVPSLKKQVVKVNRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGVSRRARWVGLGVVGLLCVAVGVVMIWVPSLKKQVVKVNRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 VPFLSVYFVEVNPSPILKGEKPVVRERGPVYVREFRHKANITENDNDTVSVEHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VPFLSVYFVEVNPSPILKGEKPVVRERGPVYVREFRHKANITENDNDTVSVEHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 FQDRSHGSESDYIILPNILVGLGAVNMESKSAGLKLMVTLGLATLGQAFMRTVGEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FQDRSHGSESDYIILPNILVGLGAVNMESKSAGLKLMVTLGLATLGQAFMRTVGEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 WGYEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WGYEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFCGAPLFLGHPHYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFCGAPLFLGHPHYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLP 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLP 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 421 AMGGEPLNTFTQVLMPOVLYOYVYVLLGLGGLLLVPVYIQLRSQKCF 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 AMGGEPLNTFTQVLMPOVLYOYVYVLLGLGGLLLVPVYIQLRSQKCF 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 481 SODKEA---IQAYSESIMSP 497
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 469 PEDTTSPPNLIANSQDPPSP 488
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ID SCRB1_PIG STANDARD; PRT; 509 AA.
AC Q8SQCL
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-B1) (High density
DE lipoprotein receptor SR-B1).
GN Name=SCARB1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim J.G., Vallet J.L., Christenson R.K.;
RT "Characterization of porcine high density lipoprotein (HDL) receptor
RT SR-B1."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apoB-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -!- SUBUNIT: The C-terminal region binds to PDZK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
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CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -!- PTM: N-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the CD36 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF467889; AAL75567.1; -; mRNA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36 antigen.
DR PANTHER; PTHR11923; CD36_1.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Glycoprotein; Receptor; Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 22 Potential.
FT TOPO_DOM 33 439 Extracellular (Potential).
FT TRANSMEM 440 460 Potential.
FT TOPO_DOM 461 509 Cytoplasmic (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 509 AA; 57514 MW; F7421796C391C4C1 CRC64;

Query Match      82.6%; Score 2215; DB 1; Length 509;
Best Local Similarity 79.4%; Pred. No. 2.3e-164;
Matches 404; Conservative 54; Mismatches 51; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCVAVGVVMIWVPSLKKQVVKVNRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSRRARQVAAALGFVGLLLAALGAVMIVWPSIIKQVVKVNRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 VPFLSVYFVEVNPSPILKGEKPVVRERGPVYVREFRHKANITENDNDTVSVEHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VPFLSVYFVEVNPSPILKGEKPVVRERGPVYVREFRHKANITENDNDTVSVEHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 FQDRSHGSESDYIILPNILVGLGAVNMESKSAGLKLMVTLGLATLGQAFMRTVGEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 FQPKHSGLESDYIVIPNIIIVLSAVVMEDRPMSLKLIINTFAFSALGERAFVNRVTGEIM 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 WGYEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WGYEDPLIHLINKYFPNPFPGKFGFLFAELNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFCGAPLFLGHPHYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 FVAPNTLFANGSVYPPNEGFCPCMESGQNVSTCRFNAPLFLSHPHFYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLP 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 LHPNTEHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLP 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 421 AMGGEPLNTFTQVLMPOVLYOYVYVLLGLGGLLLVPVYIQLRSQKCF 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 AMGETLQFTQVLMPOVLYOYVYVLLGLGGLLLVPVYIQLRSQKCF 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 481 SODKEAIQAYSESIMSPAAGTGVLOBAKL 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 SODKEAIQAYSESIMSPAAGTGVLOEARL 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 12
ID SCRB1_BOVIN STANDARD; PRT; 509 AA.

AC 018824;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
GN Name=SCARB1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Corpus luteum;
RX MEDLINE=98068685; PubMed=9406850; DOI=10.1016/S0303-7207(97)00173-1;
RA Rajapaksha W.R.A.K.J.S., McBride M., Robertson L., O'Shaughnessy P.J.;
RT "Sequence of the bovine HDL-receptor (SR-BI) cDNA and changes in
RT receptor mRNA expression during granulosa cell luteinization in vivo
RT and in vitro.";
RL Mol. Cell. Endocrinol. 134:59-67(1997).

CC -I- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apolipoprotein
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apolipoprotein lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -I- PTM: N-glycosylated (By similarity).
CC -I- SIMILARITY: Belongs to the CD36 family.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AF019384; AAB70920.1; -; mRNA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36 antigen.
DR PANTHER; PTHR11923; CD36; 1.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; Receptor; Transmembrane.
KW Glycoprotein; Receptor; Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 440 Extracellular (Potential).
FT TRANSMEM 441 461 Potential.
FT TOPO_DOM 462 509 Cytoplasmic (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 509 AA; 57610 MW; B3B7FD368C22C12F CRC64;

Query Match 80.5%; Score 2158; DB 1; Length 509;
Best Local Similarity 76.6%; Pred. No. 6.5e-160;
Matches 390; Conservative 63; Mismatches 56; Indels 0; Gaps 0;

QY 1 MGSARARVAVGLGVVGLLCAVLGVVIMLWPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGNLSRRRVTAALGFTGLLFAVLGIIMVWPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
QY 61 VPYLSVYPEVNVSEILKGEKPVYRERGPYVYRFRHKANITENDNDTVSFVHRSLSH 120
DB 61 VPFYLSVYFPNIVNPGIIGQKRPQVQEHGPFYVYRFRHKNSITFNNDTVSFLEYKSYQ 120
QY 121 FQDRSGHSGESDYIIILPNILVLGAVMMESKSLAGLMMTGLATLQRAFMRNRTVGEIL 180
DB 121 FQDKSRGQESDYIIVNPILVLSASMMENRPGLLKMTLAFSTLQRAFMRNRTVGEIM 180
QY 181 WGYEDPPVNFINKYLPDMFPFKGKGLFVEMNNSDGLFTVFTGVQNFSLHLDVRNGL 240
DB 181 WGYDDPLHLINQYFPNPLPKGKGLFABLNNSDGLFTVFTGVQNFSLHLDVRNGL 240
QY 241 SKNYVHSEOCNMGNTSGOMWAPFMTPOSSLEFFSPPEACRSKMLTYHDSGVGEIGITYR 300
DB 241 SKNYVHSDQCNMGNTSGOMWAPFMTPESSLEFFSPPEACRSKMLTYKQGVGGIPTFR 300
QY 301 FTAPKTLFANGSVYVPPNEGFCPCLESGIQNVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FVAPSTLFGANGSVYVPPNEGFCPCLESGIQNVSTCRFNAPLFLSHPHFYFNADPVLSEAVSG 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPPLMFQSG 420
DB 361 LHPNPKHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPPLMFQSG 420
QY 421 AMGGEPLNFTYOLVMPQVLYVQVYLLGLGLLLVLPVYIYQIRSQEKFLFWSGSKG 480
DB 421 AMEGTLETFTYIQLVMPKVLHYAQVLLALGCVLLIPIIYQIRSQEKFLFWISPKKG 480
QY 481 SODKEAIQAYSELSMSPAAGTGLQBAKL 509
DB 481 SKDKEAVQAYSEFLMTSAPKGTGLQEARL 509

RESULT 13
ID SCRB1_HUMAN STANDARD; PRT; 552 AA.
AC Q8WTV0; Q14016; Q6KFX4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI) (CD36 antigen-like
DE 1) (CD36 and LAMP11 analogous 1) (CLA-1) (Collagen type I receptor,
DE thrombospondin receptor-like 1).
GN Name=SCARB1; Synonyms=CD36L1, CLA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Promyelocyte;
RX MEDLINE=93366811; PubMed=7689561;
RA Calvo D., Vega M.;
RT "Identification, primary structure and distribution of CLA-1, a novel
RT member of the CD36/LAMP11 gene family.";
RN J. Biol. Chem. 268:18929-18935(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA Hirano K.-I., Yamashita S., Matsuzawa Y.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3).
RC TISSUE=Prostate, and Rhabdomyosarcoma;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RN FUNCTION.
 RP MEDLINE=22244044; PubMed=12356718; DOI=10.1093/emboj/cdf529;
 RX Scarselli E., Anselmi H., Cerino R., Roccaecceca R.M., Acali S.,
 RA Filocamo G., Traboni C., Nicosia A., Cortese R., Vitelli A.;
 RT "The human scavenger receptor class B type I is a novel candidate
 RT receptor for the hepatitis C virus";
 RL EMBO J. 21:5017-5025 (2002).
 RN [5]
 RN GLYCOSYLATION.
 RP MEDLINE=22128898; PubMed=12016218; DOI=10.1074/jbc.M202879200;
 RX Kawasaki Y., Nakagawa A., Nagaoa K., Shiratsuchi A., Nakanishi Y.;
 RT "Phosphatidylserine binding of class B scavenger receptor type I, a
 RT phagocytosis receptor of testicular Sertoli cells.";
 RL J. Biol. Chem. 277:27559-27566 (2002).
 RN [6]
 RN INTERACTION WITH HCV E1/E2 ENVELOPE HETERODIMER.
 RP MEDLINE=22928135; PubMed=12913001; DOI=10.1074/jbc.M305289200;
 RX Bartosch B., Vitelli A., Granier C., Goujon C., Dubuisson J.,
 RA Pascale S., Scarselli E., Cortese R., Nicosia A., Cosset F.-L.;
 RT "Cell entry of hepatitis C virus requires a set of co-receptors that
 RT include the CD81 tetraspanin and the SR-B1 scavenger receptor.";
 RL J. Biol. Chem. 278:41624-41630 (2003).
 RN [7]
 RN VARIANT SER-2.
 RP MEDLINE=22407477; PubMed=12519372;
 RX DOI=10.1034/j.1399-0004.2003.630108.x;
 RA Tai E.S., Adiconis X., Ordovas J.M., Carmana-Ramon R., Real J.,
 RA Corella D., Ascasso J., Carmana R.;
 RT "Polymorphisms at the SRB1 locus are associated with lipoprotein
 RT levels in subjects with heterozygous familial hypercholesterolemia";
 RL Clin. Genet. 63:53-58 (2003).
 RN [8]
 RN VARIANTS SER-2; ILE-135 AND SER-167.
 RP PubMed=12966036; DOI=10.1093/hmg/ddg314;
 RX Morabia A., Cayanis E., Costanza M.C., Ross B.M., Flaherty M.S.,
 RA Alvin G.B., Day K., Gilliam T.C.;
 RT "Association of extreme blood lipid profile phenotypic variation with
 RT 11 reverse cholesterol transport genes and 10 non-genetic
 RT cardiovascular disease risk factors";
 RL Hum. Mol. Genet. 12:2733-2743 (2003).
 CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
 CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
 CC cells. Probable receptor for HDL, located in particular region of
 CC the plasma membrane, called caveolae. Facilitates the flux of free
 CC and esterified cholesterol between the cell surface and
 CC extracellular donors and acceptors, such as HDL and to a lesser
 CC extent, apob-containing lipoproteins and modified lipoproteins.
 CC Probably involved in the phagocytosis of apoptotic cells, via its
 CC phosphatidylserine binding activity. Receptor for hepatitis C
 CC virus glycoprotein E2. Binding between SCARB1 and E2 was found to
 CC be independent of the genotype of the viral isolate.
 CC -1- SUBUNIT: Plays a critical role in HCV attachment and/or cell entry
 CC by interacting with HCV E1/E2 glycoproteins heterodimer. The C-
 CC terminal region binds to PDZK1 (By similarity).
 CC -1- INTERACTION:

CC P53345;HRMTILL; NDExp=1; IntAct=EBI-78657, EBI-78458;
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
 CC localized to cholesterol and sphingomyelin-enriched domains within
 CC the plasma membrane, called caveolae.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=3;
 CC IsoId=Q8WTV0-1; Sequences=Displayed;
 CC Notes=May be due to a competing donor splice site. No
 CC experimental confirmation available;
 CC Name=1; Synonyms=SR-B1;
 CC IsoId=Q8WTV0-2; Sequences=VSP_008554;
 CC Name=2; Synonyms=SR-BII;
 CC IsoId=Q8WTV0-3; Sequences=VSP_008554;
 CC Name=4; Synonyms=SR-BIII;
 CC IsoId=Q8WTV0-4; Sequences=VSP_011037, VSP_008554;
 CC TISSUE SPECIFICITY: Widely expressed.
 CC -1- FTM; N-glycosylated.
 CC -1- POLYMORPHISM: The Ser-2 variant is associated with higher plasma
 CC triglyceride concentration in subjects with heterozygous familial
 CC hypercholesterolemia.
 CC -1- SIMILARITY: Belongs to the CD36 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z22555; CA80277.1; -; mRNA.
 CC EMBL; AF515445; AAQ08185.1; -; mRNA.
 CC EMBL; BC022087; -; NOT ANNOTATED CDS; mRNA.
 CC EMBL; BC080647; AAH80647.1; -; mRNA.
 CC FIR; S3656; A48528.
 CC IntAct; Q8WTV0; -;
 CC Ensembl; ENSG00000073060; Homo sapiens.
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 CC MIM; 601040; -;
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0004872; F:receptor activity; TAS.
 CC GO; GO:0005215; F:transporter activity; TAS.
 CC GO; GO:0008203; P:cholesterol metabolism; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC InterPro; IPR002159; CD36.
 CC InterPro; IPR005428; CD36 antigen.
 CC PANTHER; PTHR11923; CD36; 1.
 CC Pfam; PF01130; CD36; 1.
 CC PRINTS; PR01610; CD36ANTIGEN.
 CC PRINTS; PR01609; CD36FAMILY.
 CC KW Alternative splicing; Glycoprotein; Polymorphism; Receptor;
 KW Transmembrane.
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 FT TOPO_DOM 33 443 Extracellular (Potential).
 FT TRANSMEM 444 464 Potential.
 FT TOPO_DOM 465 552 Cytoplasmic (Potential).
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 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 42 MGSKARAAAGALGAGLCAVIGAVMIVMVFSLKQQVL
 FT K -> MALQPSW (in isoform 4).
 FT /FTID=VSP 011037.
 FT Missing (in isoform 2).
 FT /FTID=VSP 008553.
 FT VARSPLIC 43 142 VGAGQARADSHSLACWKGASDRILWPTAANSPPAVL
 FT VARSPLIC 468 552 RLCSGSGHCWGURSKISLACFACRVATFLPIEGIGSLGG
 FT TGS -> EKCYLFWSSSKGSKDKAEIQAYSESLMTSAPKG
 FT

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FT SVLQBAKL (in isoform 1, isoform 2 and
FT isoform 4).
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FT G -> S (in dbSNP:4238001).
FT /FTid=VAR_017098.
FT V -> I.
FT /FTid=VAR_017099.
FT G -> S.
FT /FTid=VAR_017100.
FT S -> G (in dbSNP:10396213).
FT /FTid=VAR_019507.
FT C -> R (in dbSNP:2293440).
FT /FTid=VAR_017101.
FT F -> L (in Ref. 2).
FT F -> S (in Ref. 1).
FT CONFLICT 70 70
FT CONFLICT 97 97
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Query Match 77.1%; Score 2066.5; DB 1; Length 552;
Best Local Similarity 76.5%; Pred. No. 1e-152;
Matches 385; Conservative 49; Mismatches 60; Indels 9; Gaps 2;

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Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVMIVMPSLIIKQVLRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVDMVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNNDNTVSPLEYRTFQ 120
Db 61 IPFYLSVYFVDMVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNNDNTVSPLEYRTFQ 120
Qy 121 FQDRSHGSESDYILNPILVILGAVNMESKAGLKMMTLGLATLQORAFMNRVTGEIL 180
Db 121 FQPSKSHGSESDYIVMPNIIIVLGAAVMENKPMTLKLIIMTLAFTTLGERAFMNRVTGEIM 180
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Db 181 WGYKDPVLNLIKPFQGFPGKFKFGLFAELNNSDGLFTVFTGVQNISRIHLVDKRWGL 240
Qy 241 SKVNYHSEQCNNMINTSGQMWAPFMTPOSSLEFFSPSEACRSMKLTVDHSGVFEGIPTYR 300
Db 241 SKVDFHSDQCNMINTSGQMWPPFMTPESSLEFFSPSEACRSMKLTVDHSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSIYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLAEAVTG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVVKLQISLYIKAVKGIGQTKIBPVVLPILLWFQSG 420
Db 361 LHPNQEASLFLDIHPVTGIPMNCVVKLQISLYIKAVKGIGQTKIBPVVLPILLWFAESG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWGSKKG 480
Db 421 AMEGETLHTFTYTLVLMKPMHYAQVLLALGCVLLVLPVICQIRSQ-----VGAGORAA 475
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DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Scavenger receptor class B member 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Q59FM4_HUMAN PRELIMINARY; PRT; 581 AA.
AC Q59FM4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Scavenger receptor class B member 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
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RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209436; BAD92673.1; -, mRNA.
KW Receptor.
FT NON TER
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Query Match 77.1%; Score 2066.5; DB 2; Length 581;
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Matches 385; Conservative 49; Mismatches 60; Indels 9; Gaps 2;

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Db 29 MGCSAKARWAAGALGVAGLLCAVLGAVMIVMPSLIIKQVLRIDPSSLSFAMWKEIP 88
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Qy 181 WGYEDDPFVNFINKYLPDMFPIKGKFGFLVEMNNSDGLFTVFTGVQNFSKHLVDRWNGL 240
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Qy 241 SKVNYHSEQCNNMINTSGQMWAPFMTPOSSLEFFSPSEACRSMKLTVDHSGVFEGIPTYR 300
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Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
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Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVVKLQISLYIKAVKGIGQTKIBPVVLPILLWFQSG 420
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Qy 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWGSKKG 480
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patsch J.R.;
RT "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RL J. Lipid Res. 45:214-222(2004).

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DR EMBL; AY283278; AAP40267.1; -; mRNA.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
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 DR InterPro; IPR005428; CD36_antigen.
 DR Pfam; PF01130; CD36; 1.
 DR PRINTS; PR01610; CD36ANTIGEN.
 DR PRINTS; PR01609; CD36FAMILY.
 KW Receptor.
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Qy 61 VPFYLSVYFVFNVPNSIILKEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLSH 120
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Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFPSPACRSMKLTYHDSGVFEGIPTYR 300
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Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:45:24 ; Search time 34 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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24	696	26.0	472	2	US-09-270-542-88
25	673	25.1	472	2	US-09-270-542-86
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27	572	21.3	412	2	US-09-949-016-11488

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Sequence 46306, A
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Sequence 61875, A
Sequence 59167, A
Sequence 33112, A
Sequence 48329, A
Sequence 65285, A
Sequence 42865, A
Sequence 60022, A
Sequence 44571, A
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Sequence 21, Appl
Sequence 19, Appl
Sequence 4950, Ap
Sequence 15, Appl
Sequence 6012, Ap

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35 221 8.2 301 2 US-09-270-767-48329
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Langshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."

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/
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; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175,
; OTHER INFORMATION: 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 repre
; OTHER INFORMATION: N-linked glycosylation sites."
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21, 251,
; OTHER INFORMATION: 280, 321, 323, 334, 384 and 470 represent potential disulfide
US-08-559-505-2

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVVRIDPSSLSFAMWKEIP 60
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Db 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVEHRS 120
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Db 121 FQDRSHGSESDYIILPNILVLGGAVNMESKAGLKLMTLGLATLQRAFMNRTVGEIL 180
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Db 181 WGYEDPFVNFINKYLPDMFPKIGKFGFLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
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Db 241 SKVNYHSEOCNMINGTSGQWAPFMT PQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
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Db 421 AMGGEPLNTFTQLVLPQVLYVQVYVLLGGLLLPVVLYQLRSQEKCFLFWSGSKKG 480
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Db 481 SQDKEAIQAYSESLSMSPAAGTGLVLEAKL 509

RESULT 2
US-08-749-907-2
; Sequence 2, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Babst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
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; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Babst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-3
; OTHER INFORMATION: potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; OTHER INFORMATION: 251, 280, 321, 323, 334, 384 and 470 represent potential disul
; OTHER INFORMATION: linkages."
US-08-749-907-2

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVVRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVEHRS 120
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Db 121 FQDRSHGSESDYIILPNILVLGGAVNMESKAGLKLMTLGLATLQRAFMNRTVGEIL 180
Qy 181 WGYEDPFVNFINKYLPDMFPKIGKFGFLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
Db 181 WGYEDPFVNFINKYLPDMFPKIGKFGFLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
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Db 241 SKVNYHSEOCNMGNTSGQWAPFMTQSSLEFFSPACSMKLTTHDSGVFEGIPTYR 300
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Db 301 FTAPKTLFANGSVYPPNNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
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Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSVKQLISLYIKAVKGIGQTKIBPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFTQVLVMPQVLYQVYVLLGGGLLLPVVLYQLRSQEKCFWFWSGSKG 480
Db 421 AMGGEPLNTFTQVLVMPQVLYQVYVLLGGGLLLPVVLYQLRSQEKCFWFWSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 3
US-08-980-980-4
; Sequence 4, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-980-4

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGVGVGLLCVAVLVVMPVILVMPVSLIKQVVKVNRIDPSSLSFAMWKEIP 60
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Db 61 VPFYLSVYFFEVNPNSEILKKEKPVVERGYPVYREFRHKANITFNDNDTVSFVEHSLH 120
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Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 4
US-08-990-979-4
; Sequence 4, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordoval, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-990-979-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 4, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-032-894-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-031-626-4
; Sequence 4, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-031-626-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSARARWAVAGLVGVLGCAVLGVVMIILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGGSARARWAVAGLVGVLGCAVLGVVMIILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSYVFFEVVNPSEILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFYLSYVFFEVVNPSEILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSFVEHRS 120
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Db 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRNGL 240
Qy 241 SKVNYHSEOCNMINGTSGOMWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
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361	Qy	LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIQGTKEIPVPLPLWFEQSG	420
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421	Qy	AMGGPEPLNTFTQLVLPQVLYQYVLLGLGGLLLLPVVIYQLRSQEKCFLPWSGSKKG	480
421	Db	AMGGPEPLNTFTQLVLPQVLYQYVLLGLGGLLLLPVVIYQLRSQEKCFLPWSGSKKG	480
481	Qy	SQDKAIQAYSESLMSPAAGTIVLQEA	509
481	Db	SQDKAIQAYSESLMSPAAGTIVLQEA	509

RESULT 7
 US-09-241-581B-4
 ; Sequence 4, Application US/09241581B
 ; Patent No. 6350859
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 ; GENERAL INFORMATION:
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 ; APPLICANT: Massachusetts Institute of Technology
 ; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabet
 ; STREET: 2800 One Atlantic Center
 ; 1201 West Peachtree Street
 ;
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ;
 ; ZIP: 30309-3450
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/241,581B
 ; FILING DATE: 02-Feb-1999
 ; CLASSIFICATION: <Unknown>

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; 173-175, 212-214, 227-229, 255-257,
; 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
FEATURE:
;
; NAME/KEY: Modified-site
; LOCATION: 21, 470
; OTHER INFORMATION: /note= "The cysteines at positions
; 21, 251, 280, 321, 323, 334, 384 and
; 470 represent potential disulfide
; linkages."
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-241-581B-4

Query Match      100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGSASARWAVAGLVGVVGLLCVAVLGVVMILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
DB      1  MGSASARWAVAGLVGVVGLLCVAVLGVVMILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60

QY      61  VPYLSVYFPEVVPNPSEILGKGPVVRERGPYVYVREPRHKANITFNNDNTVSFVEHRSIH 120
DB      61  VPYLSVYFPEVVPNPSEILGKGPVVRERGPYVYVREPRHKANITFNNDNTVSFVEHRSIH 120

QY      121  FQDRSHGSES DYIIILPNILVLGAVNMESKSAGLKLMTLGLATLQORAPMNRVTGSEIL 180
DB      121  FQDRSHGSES DYIIILPNILVLGAVNMESKSAGLKLMTLGLATLQORAPMNRVTGSEIL 180

QY      181  WGYEDPFVFNFKYLPDMPPIKGKFGFLVEMNNSDSGLFTVFTGVQNFPSKIHLVDWMNGL 240
DB      181  WGYEDPFVFNFKYLPDMPPIKGKFGFLVEMNNSDSGLFTVFTGVQNFPSKIHLVDWMNGL 240

QY      241  SKYNYWHSEOCNMINGTSGQWAPFMTTQSSLEFFSPSEACRSMKLTYHDSGVFEGIPYTR 300
DB      241  SKYNYWHSEOCNMINGTSGQWAPFMTTQSSLEFFSPSEACRSMKLTYHDSGVFEGIPYTR 300

QY      301  FTPAKPTLFANGSVYVPNEGFCPCLESIGQNVSTRCPGAPLFLSHPHFYNADPVLSEAVLG 360
DB      301  FTPAKPTLFANGSVYVPNEGFCPCLESIGQNVSTRCPGAPLFLSHPHFYNADPVLSEAVLG 360

QY      361  LNPDPREHSFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQOTGKIEPVVLPDLWFEOG 420
DB      361  LNPDPREHSFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQOTGKIEPVVLPDLWFEOG 420

QY      421  AMGGEPLNTFYTLVLMPOVLQTVQVYLLGLGGLLLVPIYIQLRSQEKCFLWFSGSKKG 480
DB      421  AMGGEPLNTFYTLVLMPOVLQTVQVYLLGLGGLLLVPIYIQLRSQEKCFLWFSGSKKG 480

QY      481  SQDKEAIQAYSSELSMSPAAGTGVLOEAKL 509
DB      481  SQDKEAIQAYSSELSMSPAAGTGVLOEAKL 509

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RESULT 8
US-08-265-428-4
; Sequence 4, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428

FILING DATE: 530

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: MIT6620

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 815-6508

TELEFAX: (404) 815-6555

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..509

OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger

FEATURE:

LOCATION: 1..509

OTHER INFORMATION: /note= "Putative transmembrane

FEATURE:

LOCATION: 9..32

OTHER INFORMATION: /note= "Putative transmembrane

FEATURE:

LOCATION: 440..464

OTHER INFORMATION: /note= "Putative transmembrane

FEATURE:

LOCATION: 1..385

OTHER INFORMATION: /note= "Modified-site

OTHER INFORMATION: /note= "Positions 102-104, 108-110,

OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312,

OTHER INFORMATION: 330-332 and 383-385 represent potential N-linked glycosylation

FEATURE:

NAME/KEY: Modified-site

LOCATION: 21..470

OTHER INFORMATION: /note= "The cysteines at positions

OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and 470 represent

OTHER INFORMATION: potential disulfide linkages."

US-08-265-428-4

Query Match 100.0%; Score 2681; DB 2; Length 509;

Best Local Similarity 100.0%; Pred. No. 1.6e-285;

Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLICAVLGVVMIIVMSLIKQVVKVIRIDPSSLSFAMWKEIP 60

Db 1 MGSARARWAVGLGVVGLICAVLGVVMIIVMSLIKQVVKVIRIDPSSLSFAMWKEIP 60

Qy 61 VPVYLVYFVFNVPNSILGKRPVVRGPGVYVREPRHKANITFNDNDTVSVFVHRSLSH 120

Db 61 VPVYLVYFVFNVPNSILGKRPVVRGPGVYVREPRHKANITFNDNDTVSVFVHRSLSH 120

Qy 121 FQDRSHGSESDYIILNPNILVGLGAVNMESKAGLKMNTLGLATLQRAFMRNRTVGEIL 180

Db 121 FQDRSHGSESDYIILNPNILVGLGAVNMESKAGLKMNTLGLATLQRAFMRNRTVGEIL 180

Qy 181 WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNL 240

Db 181 WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNL 240

Qy 241 SKVNYWHSEQCQNMINGTSGQWAPFMTPOQSLEFPSPACRSKMLTYHDSGVPEGIPTYR 300

Db 241 SKVNYWHSEQCQNMINGTSGQWAPFMTPOQSLEFPSPACRSKMLTYHDSGVPEGIPTYR 300

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESQIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360

Db 301 FTAPKTLFANGSVYPPNEGFCPCLESQIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360

Db 301 FTAPKTLFANGSVYPPNEGFCPCLESQIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIEPVVLPVLLWFEQSG 420

Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIEPVVLPVLLWFEQSG 420

Qy 421 AMGGEPNTFYTLVLMPOVLQVVOYVLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480

Db 421 AMGGEPNTFYTLVLMPOVLQVVOYVLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480

Qy 481 SQDKEAIQAYSESLMSPAAGTVLQEAKL 509

Db 481 SQDKEAIQAYSESLMSPAAGTVLQEAKL 509

RESULT 9

US-09-385-799-2

Sequence 2, Application US/09385799

Patent No. 6962688

GENERAL INFORMATION:

APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky

TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory

STREET: 2800 One Atlantic Center

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/385,799

FILING DATE: 30-Aug-1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/749,907

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: MIT7538

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..509

OTHER INFORMATION: /function= "Amino acid sequence for the

Hamster Scavenger Receptor Class B-I."

FEATURE:

NAME/KEY: Domain

LOCATION: 9..32

OTHER INFORMATION: /note= "Putative transmembrane domain."

FEATURE:

NAME/KEY: Domain

LOCATION: 440..464

OTHER INFORMATION: /note= "Putative transmembrane domain."

FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-385-799-2

Query Match      100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCVAVLGVVMIIVMPSLIIKQVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGLGVVGLLCVAVLGVVMIIVMPSLIIKQVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Qy 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Qy 181 WGYEDPFPVFNKYLPMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNG 240
Db 181 WGYEDPFPVFNKYLPMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNG 240
Qy 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQVSTCRFCGAPFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQVSTCRFCGAPFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPPDRHSFLDHPVTGTPMNCVSKLQISLYIKAVKGIGQTKIIPVVLPLLWFQSG 420
Db 361 LNPPDRHSFLDHPVTGTPMNCVSKLQISLYIKAVKGIGQTKIIPVVLPLLWFQSG 420
Qy 421 AMGCEPLNTFTQVLAMPQVLYQVYVLLGLGILLVPPVYIQLRSQEKCFLWSGSKG 480
Db 421 AMGCEPLNTFTQVLAMPQVLYQVYVLLGLGILLVPPVYIQLRSQEKCFLWSGSKG 480
Qy 481 SQDKEALQAYSESLSMPAAKGTVLQEA 509
Db 481 SQDKEALQAYSESLSMPAAKGTVLQEA 509

RESULT 10
PCT-US95-07721-4
; Sequence 4, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-1."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257,
; OTHER INFORMATION: 310-312, 330-332 and 383-385 represent
; OTHER INFORMATION: potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions
; OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and
; OTHER INFORMATION: 470 represent potential disulfide
; OTHER INFORMATION: linkages."
; PCT-US95-07721-4

Query Match      100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCVAVLGVVMIIVMPSLIIKQVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVGLGVVGLLCVAVLGVVMIIVMPSLIIKQVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Qy 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Qy 181 WGYEDPFPVFNKYLPMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNG 240
Db 181 WGYEDPFPVFNKYLPMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNG 240
Qy 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
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Db 241 SKVNYHSEOCNMGNTSGOMAPMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 11
US-08-559-505-4
; Sequence 4, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landeshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class BI."

US-08-559-505-4
Query Match 91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVLLCAVLGVNMLVPSLIIKQVILKNVRIDPSSLSFAMWKEIP 60
pb 1 MGSRRARWALGLGALGLLPAALGVNMLVPSLIIKQVILKNVRIDPSSLSFGWKEIP 60

Qy 61 VPEYLSVYFPEVNPSEILKGBKPVVRBGPVYVREFRHKAMITFNDNDTVSFEHRSILH 120
Db 61 VPEYLSVYFPEVNPSEILKGBKPVVRBGPVYVREFRHKAMITFNDNDTVSFEHRSILH 120
Qy 121 PQDRSHGSESDYIILPNLVLGGAVMMESKAGLMMTLGLATLGLQRAFMNRTVGEIL 180
Db 121 PQDRSHGSESDYIILPNLVLGGAVMMESKAGLMMTLGLATLGLQRAFMNRTVGEIL 180
Qy 181 WGYEDPFVNFINKYLPDMPFIKKGFLFVEMNNSDGLFTVFTGVQNFQSKIHLDVBNGL 240
Db 181 WGYDDPFVNFINKYLPDMPFIKKGFLFVEMNNSDGLFTVFTGVQNFQSKIHLDVBNGL 240
Qy 241 SKVNYHSEOCNMGNTSGOMAPMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKIDYHSEOCNMGNTSGOMAPMTPESSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 12
US-08-749-907-4
; Sequence 4, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class BI."
US-08-749-907-4

Query Match      91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSARARVAVGLGVVGLLCAVLGVVMIIVMPSLIKQVILKNVRIDPSSLSFAMWKEIP 60
DB 1 MGSARARVAVGLGVVGLLCAVLGVVMIIVMPSLIKQVILKNVRIDPSSLSFAMWKEIP 60

QY 61 VPYLSYFVEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLSH 120
DB 61 VPYLSYFVEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180

QY 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240

QY 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKIDYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300

QY 301 FTAPKTLFANGSVYPPNEGCPCELSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLFANGSVYPPNEGCPCELSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
DB 361 LNPNKREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420

QY 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
DB 421 AMGGKPLSTYTLVLMPOVLQVQVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480

QY 481 SQKKEAIQAYSESLSMSPAAGTIVLQEAKL 509
DB 481 SQKKEAIQAYSESLSMSPAAGTIVLQEAKL 509

RESULT 13
US-09-241-581B-8
; Sequence 8, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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```
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for
; the murine Scavenger Receptor Class BI."
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-241-581B-8

Query Match      91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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DB 1 MGSARARVAVGLGVVGLLCAVLGVVMIIVMPSLIKQVILKNVRIDPSSLSFAMWKEIP 60

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DB 61 VPYLSYFVEVNVNPSILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQORAFMNRVTGEIL 180

QY 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240

QY 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKIDYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300

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DB 301 FTAPDTLFANGSVYPPNEGCPCELSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
DB 361 LNPNKREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420

QY 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
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QY 481 SQKKEAIQAYSESLSMSPAAGTIVLQEAKL 509
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RESULT 14
US-09-385-799-4
; Sequence 4, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: 1201 West Peachtree Street
```


CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,799
FILING DATE: 30-Aug-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,907
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..509
OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class B1."
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-385-799-4
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSSARARVAVGLGVVGLLCAVLGVVVMILVPSLIIKQVLLKNVRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARVAVGLGVVGLLCAVLGVVVMILVPSLIIKQVLLKNVRIDPSSLSFAMWKEIP 60
QY 61 VPFLSYVPEVVPNPSEILKGEKPVVRERGYPYVYRFRHKANITFNDNDTVSFVHRSLSH 120
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QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKLMTLGLATLQORAFMNRVTGCEIL 180
DB 121 FQDPKSHGSESDYIILPNILVLGSSILMESKPSVLSKLMNTIALVTMGQRAFMRVTGCEIL 180
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DB 181 WGYDDPPVHFLNTYLPDMLPIKGKFGLVFGMNSNSGVFTVFTGVQNFSKIHLVDKRWGL 240
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DB 421 AMGCKPLSTFTQVLVPLQVLYQVYVLLGLGGLLLLPVYIYQLRSQEKCFLFWSGSKKG 480

QY 481 SQDKAEIQAYSESLMSPAARKGTVLQEAKL 509
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RESULT 15
PCT-US95-07721-8
Sequence 8, Application PC/TUS9507721
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class B1 and C1 Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..509
OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class B1."
OTHER INFORMATION: the murine Scavenger Receptor Class B1."
PCT-US95-07721-8

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSSARARVAVGLGVVGLLCAVLGVVVMILVPSLIIKQVLLKNVRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARVAVGLGVVGLLCAVLGVVVMILVPSLIIKQVLLKNVRIDPSSLSFAMWKEIP 60
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DB 61 VPFLSYVPEVVPNPSEILKGEKPVVRERGYPYVYRFRHKANITFNDNDTVSFVHRSLSH 120
QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKLMTLGLATLQORAFMNRVTGCEIL 180
DB 121 FQDPKSHGSESDYIILPNILVLGSSILMESKPSVLSKLMNTIALVTMGQRAFMRVTGCEIL 180
QY 181 WGYEDPPVNFINKYLPDMFFPIKGKFGLVFEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
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QY 241 SKNYWHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKIDYWHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300

Qy	301	FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG	360
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Qy	361	LNPDPREHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIHPVVLPLLWFEQSG	420
Db	361	LNPDPREHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIHPVVLPLLWFEQSG	420
Qy	421	AMGGEPLNTFYTLVLMPOVLQYVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG	480
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Db	481	SODKEAIQAYSESLMSPAAGTIVLOEAKL	509

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:46:19 ; Search time 121 Seconds
(without alignments)
1757.646 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2881
Sequence: 1 MGSARARWAVGLGVGVL.....YSESLMSPAAKGTVLQBAKL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2681	100.0	509	US-09-779-152-4	Sequence 4, Appli
3	2681	100.0	509	US-10-023-610-4	Sequence 4, Appli
4	2681	100.0	509	US-10-178-611-2	Sequence 2, Appli
5	2681	100.0	509	US-10-164-863-2	Sequence 2, Appli
6	2681	100.0	509	US-10-212-848-4	Sequence 4, Appli
7	2681	100.0	509	US-10-706-073-2	Sequence 2, Appli
8	2681	100.0	509	US-10-933-037-2	Sequence 2, Appli
9	2447	91.3	509	US-09-148-012-4	Sequence 4, Appli
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19	2237	83.4	532	US-10-276-774-2382	Sequence 2382, Ap
20	2236	83.4	509	US-10-648-593-219	Sequence 219, App
21	2236	83.4	509	US-10-794-198A-12	Sequence 12, Appl
22	2203	82.2	509	US-10-210-172-116	Sequence 116, App
23	2112.5	78.8	537	US-10-450-763-52676	Sequence 52676, A
24	2066.5	77.1	552	US-10-313-641-12	Sequence 12, Appl
25	2066.5	77.1	552	US-10-428-551-12	Sequence 12, Appl
26	2005	74.8	458	US-10-322-281-568	Sequence 568, App
27	1881	70.2	416	US-10-210-172-118	Sequence 118, App

28	751.5	28.0	478	4	US-10-408-765A-657	Sequence 657, App
29	751.5	28.0	478	4	US-10-794-899-90	Sequence 90, Appl
30	740	27.6	531	4	US-10-403-571-158	Sequence 158, App
31	692	25.8	471	4	US-10-048-917-1	Sequence 1, Appli
32	692	25.8	472	3	US-09-836-544-21	Sequence 21, Appli
33	692	25.8	472	4	US-10-372-683-45	Sequence 45, Appli
34	692	25.8	472	4	US-10-398-593-2	Sequence 2, Appli
35	673	25.1	472	4	US-10-196-703-44	Sequence 44, Appli
36	657.5	24.5	471	6	US-10-408-765A-3022	Sequence 3022, Ap
37	647.5	24.2	520	6	US-11-097-143-4890	Sequence 4890, Ap
38	600	22.4	491	6	US-11-097-143-8385	Sequence 8385, Ap
39	567	20.1	534	6	US-11-097-143-24735	Sequence 24735, A
40	545	20.3	589	6	US-11-097-143-7293	Sequence 7293, Ap
41	528.5	19.7	553	6	US-11-097-143-16122	Sequence 16122, A
42	528.5	19.7	589	4	US-10-108-605-355	Sequence 355, App
43	528.5	19.7	589	6	US-11-013-314-6	Sequence 6, Appli
44	519	19.4	321	5	US-10-773-236-391	Sequence 391, App
45	519	19.4	321	5	US-10-921-235-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-09-148-012-2
; Sequence 2, Application US/09148012
; Patent No. US2002009040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MIT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
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; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
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; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
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; NAME/KEY: CARBOHYD
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LOCATION: (310)..(312)
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US-09-148-012-2

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGSARARWAVAGLVGVLCAVLGVVMIIVMPSLIKQOVLKXVRIDPSSLSFAMWKEIP 60
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DB 61 VPYLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
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DB 481 SODKEAIQAYSESIMSPAAGTVOBAKL 509
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US-09-779-152-4
; Sequence 4, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-4

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSARARWAVAGLVGVLCAVLGVVMIIVMPSLIKQOVLKXVRIDPSSLSFAMWKEIP 60
DB 1 MGSARARWAVAGLVGVLCAVLGVVMIIVMPSLIKQOVLKXVRIDPSSLSFAMWKEIP 60
QY 61 VPYLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
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RESULT 3
US-10-023-610-4
; Sequence 4, Application US/10023610
; Publication No. US20030023059A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/10/023.610
; CURRENT FILING DATE: 2001-12-17
; EARLIER APPLICATION NUMBER: 09/686,106
; EARLIER FILING DATE: 2000-10-10
; EARLIER APPLICATION NUMBER: 09/032,894
; EARLIER FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-10-023-610-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGVGVGLCAVLGVVMIWVPSLIQQOVLKNVRIDPSSLSFAMWKEIP 60
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Qy 61 VPFLSVYFFEVNPNSEILKEKEVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFLSVYFFEVNPNSEILKEKEVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120

Qy 121 FQDRSHGSDYIILPNILVLGAVNMESKAGLKMVTLGLATLQORAFMNRVTGCEIL 180
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Qy 181 WGYEDPPVNFINKYLPDMFPIKGKFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240
Db 181 WGYEDPPVNFINKYLPDMFPIKGKFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240

Qy 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSMKLTVDHSGVPEGIPTYR 300
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Qy 361 LNPDPREHSLFDTHPTVTGIPMNCVKQLISLIYKAVKGIGQTKIPEPVLPLWPFQSG 420
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Qy 421 AMGGEPLNTFTQLVLPQVLYQYVYVLLGLGGLLLVPVIYQLRSQEKCFPLFWSGSKG 480
Db 421 AMGGEPLNTFTQLVLPQVLYQYVYVLLGLGGLLLVPVIYQLRSQEKCFPLFWSGSKG 480

Qy 481 SODKEATQAYSESLMSPAAGTGVLOEAKL 509
Db 481 SODKEATQAYSESLMSPAAGTGVLOEAKL 509

RESULT 4
US-10-178-611-2

; Sequence 2, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-178-611-2

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSYFPEVNVNPSILKGEKPVVRERGPYYVYFRHKANITFNDNDTVSFVHRSLSH 120
Db 61 VPFYLSYFPEVNVNPSILKGEKPVVRERGPYYVYFRHKANITFNDNDTVSFVHRSLSH 120
Qy 121 FQDRSHGSESDYIILNIIIVLGAVNMESKAGLKLMMTLGLATLGORAFMNRITVGEIL 180
Db 121 FQDRSHGSESDYIILNIIIVLGAVNMESKAGLKLMMTLGLATLGORAFMNRITVGEIL 180
Qy 181 WGYEDPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGYEDPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSLSBFFSPACRSKMLTYVHDSGVFEGIPTYR 300
Db 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSLSBFFSPACRSKMLTYVHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYVPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYVPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDHPVTGIPMNCVVKLOISLYIKAVKGIGQTKIEPVVPLPWLPEQSG 420
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Qy 421 AMGGEPLNTFYTLVLMPOVLYVQVYVLLGLGGLLLVPVYIYQLRQSEKCFLEFWSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLYVQVYVLLGLGGLLLVPVYIYQLRQSEKCFLEFWSGSKG 480
Qy 481 SODKEATQAYSESLMSPAANKTVLQEAKL 509
Db 481 SODKEATQAYSESLMSPAANKTVLQEAKL 509

RESULT 5
US-10-164-863-2
; Sequence 2, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
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; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
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; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
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; LOCATION: (255)..(257)
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; FEATURE:
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; LOCATION: (470)..(470)
; OTHER INFORMATION: Potential
; OTHER INFORMATION: Potential
US-10-164-863-2
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Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSYFPEVNVNPSILKGEKPVVRERGPYYVYFRHKANITFNDNDTVSFVHRSLSH 120
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Db 61 VPFFLSVYFFVNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
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Db 121 FOPDRSHGESDYIILPNILVILGAVMMESKAGIKLMMTILGLATLQORAFMNRVTGEIL 180
Qy 181 WGYEDPPFVNFINKYLPDMFPPIKGKFGFLFVEMNNSDSLFTVFTGVQNFSKIHLVDRWNL 240
Db 181 WGYEDPPFVNFINKYLPDMFPPIKGKFGFLFVEMNNSDSLFTVFTGVQNFSKIHLVDRWNL 240
Qy 241 SKVNYHSEQCINMNGTSGQWMAFPMTPOSSLEFFSPACRSMKLTTHDSGVFEGIPTYR 300
Db 241 SKVNYHSEQCINMNGTSGQWMAFPMTPOSSLEFFSPACRSMKLTTHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Qy 421 AMGGEPLNTFTQLVLMPOVLYQVYVLLGGLGGLLLVPVLYQLRSOEKCFLWSSGSKG 480
Db 421 AMGGEPLNTFTQLVLMPOVLYQVYVLLGGLGGLLLVPVLYQLRSOEKCFLWSSGSKG 480
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Db 481 SODKEATQAYSESLMSPAAGTIVLQEA 509

RESULT 6
US-10-212-848-4
; Sequence 4, Application US/10212848
; Publication No. US20040022225A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: WMI-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-848-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLCAVLGVNMLWPSLIIKQVLKNVRIDPSSLSFAMWKEIP 60
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Db 481 SODKEATQAYSESLMSPAAGTIVLQEA 509

RESULT 7
US-10-706-073-2
; Sequence 2, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
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; LOCATION: (108)..(110)
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; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
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NAME/KEY: CARBOHYD
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LOCATION: (470)
OTHER INFORMATION: Potential
US-10-706-073-2

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
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Db 61 VPFLSVYFFEVNPNPSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLH 120
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Db 181 WGYEDPFVNFINKYLPDMFPIKGKFGFLFVEMNNSDSLFTVFTGVQNFSLHLDVRWNL 240
Qy 241 SKVNVHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACKSMKLTTHDSGVFEGIPTYR 300
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Qy 301 FTAPKTLFANGSVYPPNPEGFCPLSEGIQNVSTCRFGAPLFLSHPHYNNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNPEGFCPLSEGIQNVSTCRFGAPLFLSHPHYNNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFDIHPVTGIPMNCVYKLIQISLYIKAVKGIGQTGKIEPVVLPILWFEQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVYKLIQISLYIKAVKGIGQTGKIEPVVLPILWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVQVVLGLGGLLLLVPIYQLRSQEKCFLFWSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVQVVLGLGGLLLLVPIYQLRSQEKCFLFWSGSKG 480
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Db 481 SQDKEAIQAYSESLMSPAKGTVLQEAKL 509

RESULT 8

US-10-933-037-2
; Sequence 2, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-1."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
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; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
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NAME/KEY: Modified-site
LOCATION: 21...470
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251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
linkages."
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-933-037-2

Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSSARARWAVAGLVGVLLCAVLGVVMIWVMSLIIKQVVKVNRIDPSSLSFAMWKEIP	60
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Db	61	VPFVLSVYFVFNVPNSHILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLH	120
Qy	121	FQDRSHGSESDYIILPNILVLGAVVMSKSAKGLKMMTLGLATLQORAFMNRVTGEIL	180
Db	121	FQDRSHGSESDYIILPNILVLGAVVMSKSAKGLKMMTLGLATLQORAFMNRVTGEIL	180
Qy	181	WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQVNFSLHLDVRWNGL	240
Db	181	WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQVNFSLHLDVRWNGL	240
Qy	241	SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR	300
Db	241	SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR	300
Qy	301	FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG	360
Db	301	FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG	360
Qy	361	LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLPLWFQSG	420
Db	361	LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLPLWFQSG	420
Qy	421	AMGGEPLNTFTQVLMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLEWGSKKG	480
Db	421	AMGGEPLNTFTQVLMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLEWGSKKG	480
Qy	481	SQKEALQAYSESLSMPAAKGTVLQEAAL	509
Db	481	SQKEALQAYSESLSMPAAKGTVLQEAAL	509

RESULT 9
US-09-148-012-4
; Sequence 4, Application US/09148012
; Patent No. US2002099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-09-148-012-4

Query Match 91.3%; Score 2447; DB 3; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy	1	MGSSARARWAVAGLVGVLLCAVLGVVMIWVMSLIIKQVVKVNRIDPSSLSFAMWKEIP	60
Db	1	MGSSARARWAVAGLVGVLLCAVLGVVMIWVMSLIIKQVVKVNRIDPSSLSFAMWKEIP	60
Qy	61	VPFVLSVYFVFNVPNSHILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLH	120
Db	61	VPFVLSVYFVFNVPNSHILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLH	120
Qy	121	FQDRSHGSESDYIILPNILVLGAVVMSKSAKGLKMMTLGLATLQORAFMNRVTGEIL	180
Db	121	FQDRSHGSESDYIILPNILVLGAVVMSKSAKGLKMMTLGLATLQORAFMNRVTGEIL	180
Qy	181	WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQVNFSLHLDVRWNGL	240
Db	181	WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQVNFSLHLDVRWNGL	240
Qy	241	SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR	300
Db	241	SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR	300
Qy	301	FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG	360
Db	301	FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG	360
Qy	361	LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLPLWFQSG	420
Db	361	LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLPLWFQSG	420
Qy	421	AMGGEPLNTFTQVLMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLEWGSKKG	480
Db	421	AMGGEPLNTFTQVLMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLEWGSKKG	480
Qy	481	SQKEALQAYSESLSMPAAKGTVLQEAAL	509
Db	481	SQKEALQAYSESLSMPAAKGTVLQEAAL	509

RESULT 10
US-10-178-611-4
; Sequence 4, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 509 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: misc. feature
;   LOCATION: 1..509
;   OTHER INFORMATION: /Function = "Amino acid sequence for the
;   murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-178-611-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSARARVAAGLVGVGLLCAVLGVVMIIVMPSLIKQVVKVRIIDPSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSARARVAAGLVGVGLLCAVLGVVMIIVMPSLIKQVVKVRIIDPSLSFAMWKEIP 60

QY 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRS 120

QY 121 POPDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 POPDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180

QY 181 WGYDDPVPVFNKYLPMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 WGYDDPVPVFNKYLPMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240

QY 241 SKVNYHSEQCNNMNGTSQGMWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 SKIDYHSEQCNNMNGTSQGMWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPT 300

QY 301 FTAPKTLFANGSVYPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 FTAPDTLFANGSVYPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAV 360

QY 361 LNPDPREHSLFDIHPTVTGIPMNCVKQLISLYIKAVKIGQTKIEPVVPLPWLFEQ 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 LNPDPREHSLFDIHPTVTGIPMNCVKQLISLYIKAVKIGQTKIEPVVPLPWLFEQ 420

QY 421 AMGGEPLNTFYTLVMPQVLYVQVYVLLGLGGLLLVPVYQVLRQSEKCFLEWSSKK 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 AMGGEPLNTFYTLVMPQVLYVQVYVLLGLGGLLLVPVYQVLRQSEKCFLEWSSKK 480

QY 481 SQDKEATQAYSESLMSPAAGTVLQEA 509
Db 481 SQDKEATQAYSESLMSPAAGTVLQEA 509

RESULT 11
US-10-164-863-4
; Sequence 4, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 509 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: misc. feature
;   LOCATION: 1..509
;   OTHER INFORMATION: /Function = "Amino acid sequence for the
;   murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-178-611-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSARARVAAGLVGVGLLCAVLGVVMIIVMPSLIKQVVKVRIIDPSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSARARVAAGLVGVGLLCAVLGVVMIIVMPSLIKQVVKVRIIDPSLSFAMWKEIP 60

QY 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRS 120

QY 121 POPDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 POPDRSHGSESDYIILPNILVLGGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180

QY 181 WGYDDPVPVFNKYLPMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 WGYDDPVPVFNKYLPMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240

QY 241 SKVNYHSEQCNNMNGTSQGMWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 SKIDYHSEQCNNMNGTSQGMWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPT 300

QY 301 FTAPKTLFANGSVYPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAV 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 FTAPDTLFANGSVYPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAV 360

QY 361 LNPDPREHSLFDIHPTVTGIPMNCVKQLISLYIKAVKIGQTKIEPVVPLPWLFEQ 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 LNPDPREHSLFDIHPTVTGIPMNCVKQLISLYIKAVKIGQTKIEPVVPLPWLFEQ 420

QY 421 AMGGEPLNTFYTLVMPQVLYVQVYVLLGLGGLLLVPVYQVLRQSEKCFLEWSSKK 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 AMGGEPLNTFYTLVMPQVLYVQVYVLLGLGGLLLVPVYQVLRQSEKCFLEWSSKK 480

QY 481 SQDKEATQAYSESLMSPAAGTVLQEA 509
Db 481 SQDKEATQAYSESLMSPAAGTVLQEA 509

RESULT 12
US-10-706-073-4
; Sequence 4, Application US/10706073
; Publication No. US2004007526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4

; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-10-706-073-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
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QY 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
QY 61 VPFFLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFFLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVILGAVVWESKAGLKMMLTGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVILGAVVWESKAGLKMMLTGLATLQORAFMNRVTGEIL 180
QY 181 WGYEDPFPVNFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
DB 181 WGYEDPFPVNFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVVLPPLWFEQSG 420
DB 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVVLPPLWFEQSG 420
QY 421 AMGGEPLNTFYTLQVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
DB 421 AMGGEPLNTFYTLQVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
QY 481 SQKEAIOAYSSESLMSPAAGTGLQEA 509
DB 481 SQKEAIOAYSSESLMSPAAGTGLQEA 509

RESULT 13

US-10-933-037-4
; Sequence 4, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-933-037-4
Query Match 91.3%; Score 2447; DB 5; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
QY 61 VPFFLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFFLSVYFFVVPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVILGAVVWESKAGLKMMLTGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVILGAVVWESKAGLKMMLTGLATLQORAFMNRVTGEIL 180
QY 181 WGYEDPFPVNFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
DB 181 WGYEDPFPVNFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVVLPPLWFEQSG 420
DB 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVVLPPLWFEQSG 420
QY 421 AMGGEPLNTFYTLQVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
DB 421 AMGGEPLNTFYTLQVLMPOVLYVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKG 480
QY 481 SQKEAIOAYSSESLMSPAAGTGLQEA 509
DB 481 SQKEAIOAYSSESLMSPAAGTGLQEA 509

RESULT 14

US-10-322-281-565
; Sequence 565, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-565

Query Match 88.5%; Score 2374; DB 4; Length 513;
Best Local Similarity 87.6%; Pred. No. 1.8e-227;
Matches 446; Conservative 34; Mismatches 23; Indels 6; Gaps 3;

Qy	1	MGSSARARWAVAGLGVGGLCAVLGVVMILVMPSLIKQOVLKNVRIDPSSLSFAMWKETP	60
Db	11	MGSSSRARW--VGLGALGLLFAALGVVMILVMPSLIKQOVLKNVRIDPSSLSFAMWKETP	68
Qy	61	VOPYLSVVPFVFNVPSEILKEKPVWRERGPVYVREPRHKANITENDNDTVSFVEHRSILH	120
Db	69	VOPYLSVVPFVFNVPSEILKEKPVWRERGPVYVREPRKVNITENDNDTVSFVENRSILH	128
Qy	121	FQPDRESHGESDYIILPNILVLGGAVMMESKSAGLKLMMTLGLATLGQAFAMNRTVGEIL	180
Db	129	FQPDKSHGESDYIIVLPNILVLGSSILMESPVSLKLMMTLALVTVMQRAFAMNRTVGEIL	188
Qy	181	WGYEDPFPVNFINKYLPDMFPPIKGKFGFLFVEWNNSDSGLFTVFTGVQVNFSKIHLVDRWGL	240
Db	189	WGYDDPFPVHFLNTYLPDMFLPIKGKFGFLFVGWNNNSGVFTVFTGVQVNFPSRIHLVDKXWGL	248
Qy	241	SKVNVHSSQCNWINGTSGQWAPMPTPOSSLEFPFSPACRSMKLTVHDSGVPEGIPTVYR	300
Db	249	SKDIYHSSQCNWINGTSGQWAPMPTPESSLEFPFSPACRSMKLTVNESRVEGIP--Y	306
Qy	301	FTAPKTLFANGSVYPPNBSGFCPLSESGIQNVSTCRFGAPLFLSHPHYPYADPVLSEAVLG	360
Db	307	FTAPDTLFANGSVYPPNBSGFCPCRESGIQNVSTCRFGAPLFLSHPHYPYADPVLSEAV--	364
Qy	361	LNPDRSHSLFDIHPVTGIPMNCSSVKLQISLYITKAVKGIQGTCKTEPVPVLLPWEQSG	420
Db	365	LQNPKEHSLFDIHPVTGIPMNCSSVRKQLSLYITKSVKGIQGTCKTEPVPVLLPWEQSG	424
Qy	421	AMGGEPLNTFYTLVLMQVLYQVYVLLGJLGLLLLPVPIYQLRSQEKCFLEWSSKKG	480
Db	425	AMGGEPLNTFYTLVLMQVLYHAQVYVLLGJLGLLLLPVPIICQLRSQEKCFLEWSSKKG	484
Qy	481	SQDKEAIQAYSSESLMSPAKGTVLQEAKL	509
Db	485	SQDKEAIQAYSSESLMSPAKGTVLQEAKL	513

RESULT 15

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US09779-152-2
; Sequence 2, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779.152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-2

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Query Match	83.7%	Score 2244	DB 3	Length 509
Best Local Similarity	81.5%	Pred. No. 1.7e-214		
Matches 415	Conservative 46	Mismatches 48	Indels 0	Gaps 0
Qy	1	MGSGARARWAVGLGVGVGLLCVLTGVMVILWPSLIKQQLVKNVRI	DSSLSFAMWKEIP	60
Db	1	MGCSAKARWAAAGLGVAGLLCAVLGAVNMVWPSLIKQQLVKNVRI	DSSLSFAMWKEIP	60
Qy	61	VPFYLSVYFFEVNPNPSILKGEKVPVRERGPVYRFRHKANI	TFNDNDTSFVFEHSLH	120
Db	61	IPFYLSVYFFDVNPNPSILKGEKQVVRGPGVYRFRHKNI	TFNNNDTSFLEYLTFQ	120

121	Qy	QDPRSHGSSDYIIILNNILVLGA>VMMESKASGILKMMTLGLATLGORAFNMRVTVGELL	180
121	Db	QPSKSHGSSSDYIVMNNILVLGA>VMMENKPMPTLKLTMTLAFTTTLGERAFNMRVTGEM	180
181	Qy	WGYEDDPVNFINKYLPDMFPIKGGKFGILPVMNNSDSGLFTVPTGVQNF ¹ SKTHLVDRWNGL	240
181	Db	WGYKDPVLNLIKYPGMFFPKDKFGILPAELNNSDSGLFTVPTGVQNI ¹ SRHLVDKWNGL	240
241	Qy	SKVNYHSEOCNNINGTSGOWAPDMTPQSSLEFPSP ² EA ² CRSMKLT ² YHDSGVFEGIP ² TYR	300
241	Db	SKYDFHSHDQCNNINGTSGOWPPDMTPP ² ESSLEFP ² SP ² EA ² CRSMKLYKESGVFEGIP ² TYR	300
301	Qy	FTAPKTLFANGSVYPPNEGFCPCLES ³ GIQNVST ³ CRFGAPLFLSHPHFYNADPVLSEAVLG	360
301	Db	FVAPKTLFANGSIYPPNEGFCPCLES ³ GIQNVST ³ CRFGAPLFLSHPHFYNADPVLAEAVTG	360
361	Qy	LNPDPREHSLFLDTHPTVGI ⁴ PMNCVKLO ⁴ SLYTKAVKGI ⁴ GOTGKI ⁴ EPVVLPLLWFEOSG	420
361	Db	LHPNQEAHSLFLDTHPTVGI ⁴ PMNCVSKVLQ ⁴ SLYMKSVAGI ⁴ GOTGKI ⁴ EPVVLPLLWF ⁴ AESG	420
421	Qy	AMGGEPLNTFTQLVLM ⁵ PQVLYQYVYLIGLGGILLV ⁵ PVYI ⁵ Q ⁵ RSQBKCF ⁵ LFWSGSKKG	480
421	Db	AMEGETLHTFTQLVLM ⁵ PKVMHYAQYVLLGALGCVLLV ⁵ PVICIQ ⁵ RESQBKCYL ⁵ F ⁵ WSSSKKG	480
481	Qy	SQKKEATOAYS ⁶ ESLMS ⁶ PAAKGTVL ⁶ OEAKL	509
481	Db	SKQKEATOAYS ⁶ ESLMT ⁶ SA ⁶ PKGSVL ⁶ OEAKL	509

Search completed: February 23, 2006, 12:51:23
Job time : 122 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:47:29 ; Search time 11.5 Seconds
(without alignments)
658.923 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2881
Sequence: 1 MGSSARARWAVGLGVVGLL.....YSESLMSPAAGTGLQEAKL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2236	83.4	509	7	US-11-055-309A-12
2	2236	83.4	509	7	US-11-072-175-219
3	2236	83.4	532	6	US-10-821-234-918
4	97	3.6	1075	7	US-11-098-686-10295
5	91.5	3.4	1081	7	US-11-142-700-23
6	89.5	3.3	441	6	US-10-753-537-20
7	89.5	3.3	458	7	US-11-077-550-114
8	89.5	3.3	548	7	US-11-077-550-24
9	89.5	3.3	610	7	US-11-142-700-16
10	89.5	3.3	858	7	US-11-077-550-22
11	89.5	3.3	860	7	US-11-077-550-175
12	89.5	3.3	862	7	US-11-077-550-94
13	89.5	3.3	862	7	US-11-077-550-171
14	89.5	3.3	864	7	US-11-077-550-102
15	89.5	3.3	865	7	US-11-077-550-100
16	89.5	3.3	866	7	US-11-077-550-88
17	89.5	3.3	866	7	US-11-077-550-104
18	89.5	3.3	867	7	US-11-077-550-80
19	89.5	3.3	867	7	US-11-077-550-96
20	89.5	3.3	867	7	US-11-077-550-98
21	89.5	3.3	870	7	US-11-077-550-92
22	89.5	3.3	871	7	US-11-077-550-84
23	89.5	3.3	871	7	US-11-077-550-86
24	89.5	3.3	871	7	US-11-077-550-90
25	89.5	3.3	876	7	US-11-077-550-82

26	89.5	3.3	876	7	US-11-077-550-106	Sequence 106, App
27	89.5	3.3	876	7	US-11-077-550-108	Sequence 108, App
28	89.5	3.3	888	7	US-11-077-550-112	Sequence 112, App
29	89.5	3.3	1169	7	US-11-077-550-20	Sequence 20, Appl
30	89.5	3.3	1420	7	US-11-077-550-110	Sequence 110, App
31	89	3.3	947	6	US-10-453-372-1010	Sequence 1010, App
32	89	3.3	962	6	US-10-453-372-1042	Sequence 1042, App
33	88	3.3	951	6	US-10-453-372-1012	Sequence 1012, App
34	88	3.3	2515	7	US-11-113-424-53	Sequence 53, Appli
35	86	3.2	1138	7	US-11-049-536-2	Sequence 2, Appli
36	86	3.2	6738	6	US-10-922-2328-56	Sequence 56, Appl
37	85.5	3.2	302	6	US-10-926-709-8	Sequence 8, Appli
38	85.5	3.2	304	7	US-11-142-700-2	Sequence 2, Appli
39	85.5	3.2	2399	7	US-11-052-554A-92	Sequence 92, Appl
40	85	3.2	477	7	US-11-186-584-127	Sequence 127, App
41	85	3.2	477	7	US-11-043-788-243	Sequence 243, App
42	85	3.2	1086	7	US-11-142-700-10	Sequence 10, Appl
43	84.5	3.2	459	6	US-10-453-372-1046	Sequence 1046, Ap
44	84.5	3.2	729	7	US-11-130-821-4	Sequence 4, Appli
45	84	3.1	385	7	US-11-202-731-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-11-055-309A-12
; Publication 12, Application US/11055309A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P02351US
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 12
; LENGTH: 509
; TYPE: PRT
; ORGANISM: HUMAN
US-11-055-309A-12

Query Match	83.4%	Score	2236;	DB 7;	Length	509;			
Best Local Similarity	81.3%;	Pred. No.	3e-205;						
Matches	414;	Conservative	46;	Mismatches	49;	Indels	0;	Gaps	0;
QY	1	MGSSARARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQVLKXVRIDPSSLSFAMWKEIP	60						
Db	1	MGSSAKARWAAGALGVAGLLCAVLGAVMIWVPSLIKQVLKXVRIDPSSLSFAMWKEIP	60						
QY	61	VPVLSVYFPEVNPSEILKGEKPVYRERGPPYVYRERKXANITFNDNDTVSPVHRSLH	120						
Db	61	IPVLSVYFPEVNPSEILKGEKPVYRERGPPYVYRERKXSNITFNNDNDTVSLEYRTFQ	120						
QY	121	FQDRSHGSSDYIILPNILVLGAAVMESKAGLLMTLGLATLGLQAFMNRVTGVEIL	180						
Db	121	FQPSKHGSSDYIVMPNTLVLGAAVMENKPMWTLKIMTLAFTTLGERAFMNRVTGVEIM	180						
QY	181	WGYEDPFVNFINKYLPDMFPFKGKFLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL	240						

Db 181 WGYKDPVLNINKYFPGMPFFKDFGLFAELNNSDGLFTVFTGVQVQNISRIHLVDKWNGL 240
Qy 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYVHDSGVFEGIPTYR 300
Db 241 SKVDFWHSQCNMGTSQGWMPFMTPESSLEFFSPSEACRSKMLMYKESGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLAEAVTG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFEQSG 420
Db 361 LHPNQEAHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFAESG 420
Qy 421 AMGEPLNTFTQVLMPQVQVYVLLGLGGLLLVPIYQVLRSEKCFLEFWSGSKG 480
Db 421 AMEGEHLTHFTYQVLMPKVMHYAQVLLALGCVLLVPVQIRSQEKCYLEFWSGSKG 480
Qy 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509
Db 481 SKDKEAIQAYSESLMTSAPKGSVLQEA 509

RESULT 2
US-11-072-175-219
; Sequence 219, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-219

Query Match 83.4%; Score 2236; DB 7; Length 509;
Best Local Similarity 81.3%; Pred. No. 3e-205;
Matches 414; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MGCSARARWAVGLGVVGLLCVAVGLVVMILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVIMVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRS 120
Db 61 IPFLSVYFDDVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFLEVRTFQ 120
Qy 121 FQDRSHGSESDYILPNILVLGGAVMNESKAGLKMVTLGLATLQORAFMNRVTGVEIL 180
Db 121 FQPSKSHGSESDYIVMNPILVLGAAVMNENKPMTLKIMTLAFTTLGERAFMNRVTGVEIM 180
Qy 181 WGYEDPPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQVQNISRIHLVDKWNGL 240
Db 181 WGYKDPVLNINKYFPGMPFFKDFGLFAELNNSDGLFTVFTGVQVQNISRIHLVDKWNGL 240
Qy 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYVHDSGVFEGIPTYR 300
Db 241 SKVDFWHSQCNMGTSQGWMPFMTPESSLEFFSPSEACRSKMLMYKESGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360

Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLAEAVTG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFEQSG 420
Db 361 LHPNQEAHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFAESG 420
Qy 421 AMGEPLNTFTQVLMPQVQVYVLLGLGGLLLVPIYQVLRSEKCFLEFWSGSKG 480
Db 421 AMEGEHLTHFTYQVLMPKVMHYAQVLLALGCVLLVPVQIRSQEKCYLEFWSGSKG 480
Qy 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509
Db 481 SKDKEAIQAYSESLMTSAPKGSVLQEA 509

RESULT 3
US-10-821-234-918
; Sequence 918, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 918
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-918

Query Match 83.4%; Score 2236; DB 6; Length 532;
Best Local Similarity 81.3%; Pred. No. 3.2e-205;
Matches 414; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MGCSARARWAVGLGVVGLLCVAVGLVVMILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 24 MGCSAKARWAAGALGVAGLLCAVLGAVIMVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 83
Qy 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRS 120
Db 84 IPFLSVYFDDVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFLEVRTFQ 143
Qy 121 FQDRSHGSESDYILPNILVLGGAVMNESKAGLKMVTLGLATLQORAFMNRVTGVEIL 180
Db 144 FQPSKSHGSESDYIVMNPILVLGAAVMNENKPMTLKIMTLAFTTLGERAFMNRVTGVEIM 203
Qy 181 WGYEDPPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQVQNISRIHLVDKWNGL 240
Db 204 WGYKDPVLNINKYFPGMPFFKDFGLFAELNNSDGLFTVFTGVQVQNISRIHLVDKWNGL 263
Qy 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
Db 264 SKVDFWHSQCNMGTSQGWMPFMTPESSLEFFSPSEACRSKMLMYKESGVFEGIPTYR 323
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 324 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLAEAVTG 383
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFEQSG 420
Db 384 LHPNQEAHSLFDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVVPLPLWFAESG 443
Qy 421 AMGEPLNTFTQVLMPQVQVYVLLGLGGLLLVPIYQVLRSEKCFLEFWSGSKG 480
Db 444 AMEGEHLTHFTYQVLMPKVMHYAQVLLALGCVLLVPVQIRSQEKCYLEFWSGSKG 503

; APPLICANT: Stephen M. Allen
 ; APPLICANT: Gary M. Fader
 ; APPLICANT: Saverio Carl Falco
 ; APPLICANT: Anthony J. Kinney
 ; APPLICANT: Jonathan E. Lightner
 ; APPLICANT: Guo-Hua Miao

Query Match

Query Match 3.3%; Score 89.5; DB 6; Length 441;

```

; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-11-077-550-114

Query Match      3.3%; Score 89.5; DB 7; Length 458;
Best Local Similarity 18.7%; Pred. No. 1.3;
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 23;

QY 73 VNPSEILKEKPVVRERGPPVYREPRHKANI-----TF-----NNDTVSFVEHSL-- 119
Db 14 IDNNNIIMPEPPFARGGRY-YKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVC 72
QY 120 HFOPDRSHGSESVDIILPNILVLGGAVMMESKAGLKL--MMTLGLATLQORAF---MN 173
Db 73 YYDPDYLTNDKKNIFLOTWIKLFNRI--KSKPLGEKLEMIINGIPYLGDRRVPLEEFN 130
QY 174 RTVGEILWGYEDPPVNFINKYLPDMEPIKGFGLFVE-----MNSDSGLFTVFTG 224
Db 131 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGVLNENE---TIDIG 176
QY 225 VQNFPSKHLVDRWNGLSKYNVHSEQCWNINGTSGQWAPPMTPOSSLEFFSPEACRSK 284
Db 177 IQN---HFASR-----EGFGGIM-----QMK 194
QY 285 LTYHDSGVFEGIPTRYFTAPKTLFANGSVYPPNEGFCPCLESQIONVSTCRFGAPLFLSH 344
Db 195 -----FCPEYVSFVNNVQENK-GASIFNR 218
QY 345 PHFYADPVLSEAVLGNLPPDRHSFLDIHPVTGIPMNCVKLQISLYIKAVKIGQGTG 404
Db 219 GYF--SDPAL---IL-----MHLEIHLVHLGLYI-----242
QY 405 KIEPVVLPLL-----WFQSGNMGCEPLNTF-----YTQLVLMPOVLQYVQYVL 448
Db 243 KVDD--LPIVNEKKFQMSQTDIAQAEELYTFGGQDPSIITPTSDKSIYDKVLQNRGIV 300
QY 449 LGLGGLLLVP-----VIYQLRSQEKCFLWFSKKGSDKEAIQAYSSELSMPAAKGT 502
Db 301 DRLNKVLVCISDPNININIKYKFKYFVDESEKYSIDVESFDKLYKSLMFGFTETN 360
QY 503 VLOEAKL 509
Db 361 IAENYKI 367

```

RESULT 7

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US-11-077-550-114
; Sequence 114, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 458

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RESULT 8

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US-11-077-550-24
; Sequence 24, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4

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Query Match 3.3%; Score 89.5; DB 7; Length 858;

Best Local Similarity	18.7%;	Pred. No. 3.3;	
Matches	91;	Conservative	67; Mismatches 146; Indels 183; Gaps 213;
Qy	73	VNPSEILKSGKPVVRERGPYYVREFRHKANI-----TF-----NDNDTVSFVEHRSL----	119
Db	14	IDNNNIIMPPPPARGTGRY-YKAFKITDR.IIIPERYTFCKYKEDFNKSGGIFNRDVC	72
Qy	120	HFQDRSHGSESDYIILPNILVLGVAVMSEKSAGLKLU---MNTLGLATLQORAF-----MN	173
Db	73	YYDPDYLTNDKKNIFLQTKWIKLFNRI--KSKPLGKELLEMIIINGIPYLGDRRVPLEEFN	130
Qy	174	RTVGEILLGVEDPPVNFINKYLPDMFPPIKGKFLFVE-----MNNSDSLGFTVPTG	224
Db	131	TNIASVT-----VNKLISNPGEVRKGIIFANLIIIFGPGVLNENE-----TIDIG	176
Qy	225	VQNPSEIKHLVDRWNGLSKVNYVHSEQCNMINGTSGQMWPMTPOSSLEFFSPCAKRSMK	284
Db	177	IQN---HFASR-----EGFGGIM-----QMK	194
Qy	285	LTYHDSGVFEGIPYRFTAPKTLFANGSVYPPNPGFCPCLESGIQNVSTCFGAPLFLSH	344
Db	195	-----FCPEYVSVFNNVOENK-GASIFNRR	218
Qy	345	PHFYNADPVLSEAVGLNPDPREHSLFDIHPVTGIPMNCVQLQISLYIKAVRGIGQTG	404
Db	219	GYP---SDPAL---ILU-----MHLEIHLVHLGYI-----	242
Qy	405	KIEPVVLPLL-----WFEQSGAMGGEPLNTF-----YTQLVLMPOVLQVQVTL	448
Db	243	KVDD--LPIVENEKKPFMQSDTAIQABELYTFGGQDPSIITPSTDKSYIDKVLQNFGRGIV	300
Qy	449	LGLGGLLLVP-----VIYQLRSQEKCFLEWSSKGSQDEKAIQAYSESILMSPAAGT	502
Db	301	DRLNKVLVCISDPNNININYKNKPKDYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETN	360
Qy	503	VLOBAKL	509
Db	361	IAENYKI	367

```

RESULT 11
US-11-077-550-175
; Sequence 175, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 175
; LENGTH: 860

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; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-11-077-550-175

Query Match 3.3%; Score 89.5; DB 7; Length 860;
Best Local Similarity 18.7%; Pred.No.3.3; 146; Indels 183; Gaps 213
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 213

Qy 73 VNPSEILKGKPPVVRERGPPVYREFRHKANI-----TF-----NDNDTVSFVHRSL-- 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 14 IDNNNIIMEPPPARGGTRY-YKAFKITDRIWIIPERYTFGYKPEDENKSSGIFNRDVC 72

Qy 120 HFQDRSHGSESDYILPNLVLGGAVMMESKAGLKL--MMTLGLATLQRAF-----MN 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 YYDPDYLVNTDKNIIFLQTMIKLFNRI--KSKPLGEKLEMIINGIPYLGDRRVPLEEFN 130

Qy 174 RTVGEILGWYEDPVNPFINKYLPDMFPKKGFLFVE-----MNSDSGLFTVPTG 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGPVLNENE-----TIDIG 176

Qy 225 VQNPSEIKHLVDRWNGLSKVNYWHSEQCNMINGTSGQMWAPFMTQSSLEFFSPEACRSMK 284
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 IQN-----HFASR-----EGFGIM-----QMK 194

Qy 285 LTYHDSGVFEGIPTRYETAPKTLFANGSVYPNPGFCPLCESGTONYSTCRFGAPLFLSH 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 195 -----FCPEYVSVFNQQENK-GASIFNRR 218

Qy 345 PHFYNADPVLSEAVGLNPDPREHSLFLDIHPVTGTGIPMNCVKLQISLYIKAVKGIGQTG 404
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 GYF--SDPAL--IL-----MHELTHVLHGLYGI----- 242

Qy 405 KIEPVLPLL-----WFEGSGAMGGBPPLMTF-----YTQLVLMPOVLQVQYVL 448
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 KVDD--LPVYPNEKKFQMSTDAIQABELYTFGGQDPSIITPSTDKSIYDKVLQNFGRIV 300

Qy 449 LGLGGLLLLP-----VIYQLRSQEKCFLFWSGSKGSDQKEAIQAYSESIMSPAAGKT 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 DRLNKVLVCISDPNININIVKNKFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETN 360

Qy 503 VLQEAKL 509
   : : : :
Db 361 IAENYKI 367

RESULT 12
US-11-077-550-94
; Sequence 94, Application US/11077550
; Publication No. US2005024435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foeter, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancome, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4

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US-11-077-550-102
; Sequence 102, Application US/11077550
; Publication No. US2005024435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241.596

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; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-11-077-550-102

Query Match      3.3%; Score 89.5; DB 7; Length 864;
Best Local Similarity 18.7%; Pred. No. 3.3;
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 23;

Qy 73 VNPSEILKGEKPVVRERGYPVYREFRHKANI-----TF-----NNDTVSFVEHRSLS-- 119
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Qy 120 HFQPDRESHSESIIILPNILVLGGAVMMESKAGLKL--MWTGLATLGQRAF-----MN 173
Db 79 YYDPDLNTNDKKNIFLQTMIKLFNRI--KSKPLGKLEMIINGIPYLGDRVRVPLEEFN 136
Qy 174 RTVGEILGWEDPVPVNFINKYLPDMPPIKGFGLFVE-----MNSDSGLFTVFTG 224
Db 137 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGVVLNENE-----TIDIG 182
Qy 225 VQNFSKHLVDRMNGLSKVNYHSEQCNMINGTSGQMWAPFMTTPQSSLEBFFSPEACRSKM 284
Db 183 IQN-----HFASR-----EGFGGIM-----QMK 200
Qy 285 LTYHDSGVFEGIPYRTAPKTLFANGSVYPPNEGFCPCLESIGIQNVSTCRFGAPLFLSH 344
Db 201 -----FCPEYVSVFNNVQENK-GASIFNR 224
Qy 345 PHEYNADPVLSEAVLGNLPPDREHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTG 404
Db 225 GYP--SDPAL--IL-----MHELIHVLHGLYGI-----248
Qy 405 KIEPVVLPLL-----WFEQSGAMGGEPLNTF-----YTQLVLMQVLYQVQYVL 448
Db 249 KVDD--LPVINEKKFFMQSDTAIQABELYTFGQDPSIITPSTDKSIYDKVLQNRGIV 306
Qy 449 LGLGGLLLLP-----VIYQLRSQEKCFLFWSGSKGQDKEAIQAYSESLSMPAAKGT 502
Db 307 DRLMKVLVCISDPNININIKYKFKYFVESEGKYSIDVESFDKLYKSLMFGFTETN 366
Qy 503 VLQEAKL 509
Db 367 IAEYKI 373

RESULT 15
; Sequence 100, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
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; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-11-077-550-100

Query Match      3.3%; Score 89.5; DB 7; Length 865;
Best Local Similarity 18.7%; Pred. No. 3.3;
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 23;

Qy 73 VNPSEILKGEKPVVRERGYPVYREFRHKANI-----TF-----NNDTVSFVEHRSLS-- 119
Db 20 IDNNNIIMPEPPFARGTGRY-YKAFKITDRIWIIPERYTFGKPEDFNKSSGIFNRDVCE 78
Qy 120 HFQPDRESHSESIIILPNILVLGGAVMMESKAGLKL--MWTGLATLGQRAF-----MN 173
Db 79 YYDPDLNTNDKKNIFLQTMIKLFNRI--KSKPLGKLEMIINGIPYLGDRVRVPLEEFN 136
Qy 174 RTVGEILGWEDPVPVNFINKYLPDMPPIKGFGLFVE-----MNSDSGLFTVFTG 224
Db 137 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGVVLNENE-----TIDIG 182
Qy 225 VQNFSKHLVDRMNGLSKVNYHSEQCNMINGTSGQMWAPFMTTPQSSLEBFFSPEACRSKM 284
Db 183 IQN-----HFASR-----EGFGGIM-----QMK 200
Qy 285 LTYHDSGVFEGIPYRTAPKTLFANGSVYPPNEGFCPCLESIGIQNVSTCRFGAPLFLSH 344
Db 201 -----FCPEYVSVFNNVQENK-GASIFNR 224
Qy 345 PHEYNADPVLSEAVLGNLPPDREHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTG 404
Db 225 GYP--SDPAL--IL-----MHELIHVLHGLYGI-----248
Qy 405 KIEPVVLPLL-----WFEQSGAMGGEPLNTF-----YTQLVLMQVLYQVQYVL 448
Db 249 KVDD--LPVINEKKFFMQSDTAIQABELYTFGQDPSIITPSTDKSIYDKVLQNRGIV 306
Qy 449 LGLGGLLLLP-----VIYQLRSQEKCFLFWSGSKGQDKEAIQAYSESLSMPAAKGT 502
Db 307 DRLMKVLVCISDPNININIKYKFKYFVESEGKYSIDVESFDKLYKSLMFGFTETN 366
Qy 503 VLQEAKL 509
Db 367 IAEYKI 373

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Job time : 12.5 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:38:47 ; Search time 8999.94 Seconds
(without alignments)
11274.030 Million cell updates/sec

Title: US-08-765-108-7
Perfect score: 1785
Sequence: 1 CCGTCTCTTCAGTCTCTGA.....TCAGGACGAGGACAGACC 1785

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

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5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

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10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_rtg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1785	100.0	1785	6	AR078245	AR078245 Sequence
2	1785	100.0	1785	6	AR195310	AR195310 Sequence
3	1785	100.0	1785	6	AX305450	AX305450 Sequence
4	1785	100.0	1785	9	MMU37799	U37799 Mus musculus
5	1785	100.0	2496	6	CQ868666	CQ868666 Sequence
6	1785	100.0	2512	9	BC004656	BC004656 Mus muscu
7	1607	90.0	1607	6	AX419948	AX419948 Sequence
8	1530	85.7	1530	9	CT010222	CT010222 Mus muscu
9	1460.6	81.8	2392	9	D89655	D89655 Rattus norv
10	1459.4	81.8	2408	9	BC078504	BC078504 Rattus no
11	1459.4	81.8	2497	9	AB002151	AB002151 Rattus no
12	1452.6	81.4	2401	9	AY451993	AY451993 Rattus no
13	1426	79.9	1674	9	RNU76205	U76205 Rattus norv
14	1396.2	78.2	1825	6	AR091980	AR091980 Sequence
15	1396.2	78.2	1825	6	AR112115	AR112115 Sequence
16	1396.2	78.2	1825	6	AR149157	AR149157 Sequence
17	1369.8	76.7	1788	6	AR078244	AR078244 Sequence
18	1369.8	76.7	1788	6	AR195308	AR195308 Sequence

19	1369.8	76.7	1788	6	AR222273	AR222273 Sequence
20	1369.8	76.7	1788	9	CGU11453	U11453 Cricetulus
21	1342	75.2	1590	9	AF071495	AF071495 Rattus no
22	1215.2	68.1	2272	9	AY682847	AY682847 Rattus no
23	1144.2	64.1	2622	8	BC080647	BC080647 Homo sapi
24	1142.6	64.0	2630	6	AR091979	AR091979 Sequence
25	1142.6	64.0	2630	6	AR112114	AR112114 Sequence
26	1142.6	64.0	2630	6	AR149156	AR149156 Sequence
27	1141	63.9	2566	6	AR261646	AR261646 Sequence
28	1141	63.9	2566	6	AR474634	AR474634 Sequence
29	1141	63.9	2566	6	AR635204	AR635204 Sequence
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31	1127.8	63.2	3144	6	CQ868669	CQ868669 Sequence
32	1117.4	62.6	2670	4	AF467889	AF467889 Sus scrof
33	1115.8	62.5	1681	8	BC093732	BC093732 Homo sapi
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36	1072.4	60.1	1530	4	AY428553	AY428553 Tupaia be
37	1047.6	58.7	1527	6	AX763178	AX763178 Sequence
38	966.6	54.2	1845	8	AF515445	AF515445 Homo sapi
39	959	53.7	4391	8	AB209436	AB209436 Homo sapi
40	947.6	53.1	1659	11	AY892789	AY892789 Synthetic
41	947.6	53.1	1659	11	BT008093	BT008093 Synthetic
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45	765.4	42.9	1440	6	CQ722206	CQ722206 Sequence

ALIGNMENTS

RESULT 1	AR078245	Sequence 3 from patent US 5962322.	1785 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR078245	Sequence 3 from patent US 5962322.	1785 bp	DNA	linear	PAT 31-AUG-2000
DEFINITION	AR078245	Sequence 3 from patent US 5962322.	1785 bp	DNA	linear	PAT 31-AUG-2000
ACCESSION	AR078245	Sequence 3 from patent US 5962322.	1785 bp	DNA	linear	PAT 31-AUG-2000
VERSION	AR078245.1	GI:10004991	1785 bp	DNA	linear	PAT 31-AUG-2000
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1785)					
AUTHORS	Kozarsky, K., Rigotti, A. and Krieger, M.					
TITLE	Methods for modulation of cholesterol transport					
JOURNAL	Patent: US 5962322-A 3 05-OCT-1999;					
FEATURES	Location/Qualifiers					
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Db	1	CCGTCTCTTCAGTCTCTGAGCCCGAGAGCCCTTCGCGCGCAGCGGACATGGCGGCA	60		
Qy	61	GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCTGCTGTTGCTGCGC	120		
Db	61	GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCTGCTGTTGCTGCGC	120		
Qy	121	TCGGCGTTGTCATGCTCTCATGTCGCCCTCCCTCATCAAGCAGCGAGTCTCAAGAATG	180		
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Qy	181	TCGGCAGACCCGAGCAGCGCTCTCTCGGATGTGGAGGAGTCCCGTCCCTTCT	240		
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Qy	241	ACTTGTCTGTACTTCTTCAAGTGTCTCAACCAACGAGGTCTCTCAACGCGCAGAAGC	300		

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QY 361 CTTTCAATGACAAACGACACCGTGTCTTCTGTGGAGAACCGCAGCCTCCATTTCCAGCCTG 420
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QY 421 ACAAGTCCGATGGCTCAGAGAGTGACTACATTTGTACTGCCCTAACATCTTGGTCTCTGGGG 480
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QY 481 GCTCGATATTGATGGAGACGACGCTGTGAGCCTGGAAGCTGATGATGACCTTTGGCGCTGG 540
Db 481 GCTCGATATTGATGGAGACGACGCTGTGAGCCTGGAAGCTGATGATGACCTTTGGCGCTGG 540
QY 541 TCACCATGGGCCAGCGTGTCTTTATGAACCGCACAGTTGGTGATGATCCTGTGGGGCTATG 600
Db 541 TCACCATGGGCCAGCGTGTCTTTATGAACCGCACAGTTGGTGATGATCCTGTGGGGCTATG 600
QY 601 ACGATCCCTTCTGTGCATTTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
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QY 961 CCGATACCTCTGTTTCCAAACGGGTCCGTCTACCCACCCAAACGAAGGCTTCTGCCCATGCC 1020
Db 961 CCGATACCTCTGTTTCCAAACGGGTCCGTCTACCCACCCAAACGAAGGCTTCTGCCCATGCC 1020
QY 1021 GAGAGTCTGGCAATTCAGAAATGTACAGACCTGACAGTGTGGTGGCCCTCTGTTCTCTCC 1080
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Db 1141 ACCCAAGGAGCATCTTGTCTTCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
QY 1201 GTTCTGTGAAGATCGAGTGAACCTCTACATCAAAATCTGTCAAGGGCATCGGGCAAAACAG 1260
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QY 1261 GGAAGATCGACCAAGTGTCTGCGGTGTGTCGATGTCGAGTGTGAGAGGATCCCGCTCTTCT 1320
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QY 1321 GCAAGCCCTGAGCACTGTTCTACACGAGTGTGGTCTGATGCCCCAGGTCTTCACTACG 1380

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Db 1441 TGGCAGCCAGGAGAAATGCTTTTCTTTTGGAGTGTAGTAAAGAGGGCTCCAGGATA 1500
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QY 1621 GGTACAGCAGCCAGCCAGTCCCTACACCCGGCTTCTGAGGACTCTCTCAGCGGACAGC 1680
Db 1621 GGTACAGCAGCCAGCCAGTCCCTACACCCGGCTTCTGAGGACTCTCTCAGCGGACAGC 1680
QY 1681 CCACCATGTCATGGCTTGAGCCCCCAGATGTACACCTGTCCGACGACGACATGG 1740
Db 1681 CCACCATGTCATGGCTTGAGCCCCCAGATGTACACCTGTCCGACGACGACATGG 1740
QY 1741 ATGCCACCGATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1785
Db 1741 ATGCCACCGATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1785

RESULT 2
AR195310 LOCUS 1785 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7 from patent US 6350859.
ACCESSION AR195310
VERSION AR195310.1 GI:20244747
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Krieger M., Acton, S.L. and Rigotti, A.
TITLE Class BI and CI scavenger receptors
JOURNAL Patent: US 6350859-A 7-26-FEB-2002;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1785; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCTCTCTCAGGTCTCTGAGCCCCCAGAGCCCTTCCGCGCACGCGGACATGGGCGGCA 60
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Db 61 GCTTCCAGGGCGCGCTGGGTGGCTTGGGGTGGGGCGCCCTGGGGCTGCTGTTTGTCTGCGC 120
QY 121 TCGGCGTGTGTATGATCTCATATGTCCTTCCCTCATCAAGCAGCAGGTGCTCAAGATG 180
Db 121 TCGGCGTGTGTATGATCTCATATGTCCTTCCCTCATCAAGCAGCAGGTGCTCAAGATG 180
QY 181 TCCGATAGACCCGACGACGCTCTCTCGGGATGTGGAGGAGATCCCGCTCCCTTCT 240
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QY 241 ACTTGTCTGTCTACTTCTTGAAGTGTGTCAACCCAAACGAGGTCTTCAACGCGGACAGAC 300

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Qy 361 CTTCAATGACAAACGACACCGTGTCTTCTGTTGGAGAACCGGAGCCTCGATTCCAGCGTG 420
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DEFINITION Sequence 201 from Patent WO0188188.
ACCESSION AX305450
VERSION AX305450.1 GI:17644972
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Ishikawa, K., Asai, S., Takahashi, Y., Nagata, T. and Ishii, Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 201 22-NOV-2001;
School Juridical Person Nihon University (JP)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 4

MMU37799

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

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MMU37799 1785 bp mRNA linear ROD 26-JAN-1996
Mus musculus scavenger receptor class B type I (msr-BI) mRNA,
complete cds.

U37799.1 GI:1167551

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

Acton, S., Rigotti, A., Landschulz, K.T., Xu, S., Hobbs, H.H. and
Krieger, M.

Identification of scavenger receptor SR-BI as a high density
lipoprotein receptor

Science 271 (5248), 518-520 (1996)

8560269

2 (bases 1 to 1785)

Acton, S. and Krieger, M.

Direct Submission

Submitted (06-OCT-1995) Susan L. Acton, Biology, MIT, 77
Massachusetts Ave., Cambridge, MA 02139, USA

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Morris,D.W. and Malandro,M.S.
TITLE Novel therapeutic gpcr targets in cancer
JOURNAL Patent: WO 2004074321-A 78 02-SBP-2004;
Sagres Discovery, Inc. (US)

FEATURES
Location/Qualifiers

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RESULT 6
BC004656
LOCUS
DEFINITION
MGC:5988 IMAGE:3498018), complete cds.
ACCESSION

BC004656 2512 bp mRNA linear ROD 09-JUL-2005
Mus musculus scavenger receptor class B, member 1, mRNA (cDNA clone
MGC:5988 IMAGE:3498018), complete cds.
BC004656

VERSION	BC004656.1	GI:13435557	
KEYWORDS	MGC.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1. (bases 1 to 2512) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavani, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Shailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	1247932		
REFERENCE	2. (bases 1 to 2512) NIH MGC Project Direct Submission Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
REMARK	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 9 Row: 1 Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14389422.		
COMMENT	Location/Qualifiers		
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SOURCE	1..2512 /gene="Scarb1" /note="synonyms: MSR-BI, CD36, SR-BI, Clal, Cla-1, CD3611, SRBI, SR-B1"		
gene			
ORIGIN			
Query Match	100.0%; Score 1785; DB 9; Length 2512;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1785; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Qy	61	GCTCCAGGCGCGCTGGGTGGCTTGGGTGGCGCCCTGGGGCTCTGTTTCTGCTGCGC	120
Db	203	GCTCCAGGCGCGCTGGGTGGCTTGGGTGGCGCCCTGGGGCTCTGTTTCTGCTGCGC	262
Qy	121	TCGGGTGTCATGTCCTCATGTGTCCTTCCTCATCAAGCAGCAGTCTCAAGATG	180
Db	263	TCGGGTGTCATGTCCTCATGTGTCCTTCCTCATCAAGCAGCAGTCTCAAGATG	322
Qy	181	TCGGCATAGACCCGAGCAGCTGTCTTCCTTCGGGATGTGGAAGGAGATCCCGTCTCTTCT	240
Db	323	TCGGCATAGACCCGAGCAGCTGTCTTCCTTCGGGATGTGGAAGGAGATCCCGTCTCTTCT	382
Qy	241	ACTTGTCTGTCTACTTCTTCAAGTGTCTCAACCCAAACGAGGTCTCAACCGCGCAGAAC	300
Db	383	ACTTGTCTGTCTACTTCTTCAAGTGTCTCAACCCAAACGAGGTCTCAACCGCGCAGAAC	442
Qy	301	CAGTAGTCCGGGAGCGTGGACCTTATGTCTACAGGGAGTTTCAGACAAAGGTCAACATCA	360
Db	443	CAGTAGTCCGGGAGCGTGGACCTTATGTCTACAGGGAGTTTCAGACAAAGGTCAACATCA	502
Qy	361	CCTTCAATGACACACGACACCGTGTCTTCCTTCGGAGAACCGCAGCTCCATTTCCAGCTG	420
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Qy	421	ACAAGTCGCATGGCTCAGAGAGTGACTTACATTGTGTACTGCCTTAACATCTTGCTGGGG	480
Db	563	ACAAGTCGCATGGCTCAGAGAGTGACTTACATTGTGTACTGCCTTAACATCTTGCTGGGG	622
Qy	481	GCTCGATATTGATGGAGAGCAGCTGTGAGCTGTAAGCTGATGATGACCTTGGCGCTG	540
Db	623	GCTCGATATTGATGGAGAGCAGCTGTGAGCTGTAAGCTGATGATGACCTTGGCGCTG	682
Qy	541	TCACCATGGCGGAGCGTGGCTTTTATGAACCGCAGCAGTGTGTGAGATCCTGTGGGGCTATG	600
Db	683	TCACCATGGCGGAGCGTGGCTTTTATGAACCGCAGCAGTGTGTGAGATCCTGTGGGGCTATG	742
Qy	601	ACGATCCCTTCGTGCAATTTCTCAACACGACCTCCAGACATGCTTCCCATAAAGGGCA	660
Db	743	ACGATCCCTTCGTGCAATTTCTCAACACGACCTCCAGACATGCTTCCCATAAAGGGCA	802
Qy	661	AATTGGCCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAAGG	720
Db	803	AATTGGCCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAAGG	862

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QY 721 GCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 780
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QY 863 GCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 922
DB |||||
QY 781 ATTATTTGGCAATTCAGACAGTGAATGATGATCAATGGGACTTCGGGCGAGATGTGGGCAC 840
DB |||||
QY 923 ATTATTTGGCAATTCAGACAGTGAATGATGATCAATGGGACTTCGGGCGAGATGTGGGCAC 982
DB |||||
QY 841 CTTTCATGACACCGGAATCTCGTGGAAATTTTCAGCCCGGAGGCGATGAGGTCCATGA 900
DB |||||
QY 983 CTTTCATGACACCGGAATCTCGTGGAAATTTTCAGCCCGGAGGCGATGAGGTCCATGA 1042
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QY 901 AGCTGACCTTCAACGAATCAAGGCTGTTTGAAGGCAATTCACGATTCGCTTCACGGCC 960
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QY 961 CCGATACTCTGTTTGCACCGGCTCGCTTACCCACCAACGAAGGCTTCGCGCCATGCC 1020
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QY 1103 CCGATACTCTGTTTGCACCGGCTCGCTTACCCACCAACGAAGGCTTCGCGCCATGCC 1162
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QY 1021 GAGAGTCTGGCAATTCAGATGTCAGACCTGCGAGGTTTGGTGGCCCTCTGTTCTCTCC 1080
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QY 1081 ACCCCCACTTTTACACCGCGACCTCTGTTTGTTCAGAAAGCTGTTTGTGCTGAACCCCTA 1140
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QY 1141 ACCCAAGGAGCAATCTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1200
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QY 1283 ACCCAAGGAGCAATCTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1342
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DB |||||
QY 1343 GTTCTGTGAAGATGACGCTGAGCTCTACATCAATCTGTCAAGGGATCGGGCAACAG 1402
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QY 1403 GGAAGATCGAGCAGTAGTGTGCGCTGCTGTGTTTGAACAGAGCGGAGCAATGGGTG 1462
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DB |||||
QY 1463 GCAAGCCCTTGAGCAGCTTCTACACGAGCTGTGTGCTGATGCCCGAGGTTCTTCACTACG 1522
DB |||||
QY 1381 GCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTGTGCCCATCATCTGCCAAC 1440
DB |||||
QY 1523 GCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTGTGCCCATCATCTGCCAAC 1582
DB |||||
QY 1441 TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTGTAAAGGGGCTCCAGGATA 1500
DB |||||
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DB |||||
QY 1643 AGGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTCAACAGCTGCGCAAGGGCAGCGTGC 1702
DB |||||
QY 1561 TGCAGAGCCAGCTATAGGCTTCTGAAGCACTATAAGCCGCCCAAACTGATAGCTT 1620
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DB |||||
QY 1621 GGTTCAGACCCAGCCAGTCCCTTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
DB |||||
QY 1763 GGTTCAGACCCAGCCAGTCCCTTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1822
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QY 1681 CCACAGTGCATGGCTGAGCCGCCAGATGTCAACCTGTGCGCAGCGCAGCAGCATGG 1740
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DB |||||
QY 1741 ATGCCACCGCATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1785
DB |||||
QY 1883 ATGCCACCGCATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1927
DB |||||

RESULT 7
AX419948
LOCUS AX419948 1607 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 285 from Patent WO0198537.
ACCESSION AX419948
VERSION AX419948.1 GI:21524315
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Lyamichev, V., Allawi, H., Dong, F., Neri, B.P. and Vener, I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 285 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..1607
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/db_xref="taxon:10090"
ORIGIN
Query Match 90.0%; Score 1607; DB 6; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 GCTCAAGAATGTCCGATAGACCCGAGCAGCCCTGCTTCGGGATGTGGAAGAGAGATCCC 229
DB 1 GCTCAAGAATGTCCGATAGACCCGAGCAGCCCTGCTTCGGGATGTGGAAGAGAGATCCC 60
QY 230 GGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCTCAA 289
DB 61 GGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCTCAA 120
QY 290 CGGCCAAGAACCCAGTAGTCCGGAGCGTGGACCCCTATGCTACAGGAGTTCAGACAAA 349
DB 121 CGGCCAAGAACCCAGTAGTCCGGAGCGTGGACCCCTATGCTACAGGAGTTCAGACAAA 180
QY 350 GGTCAACATCACCTTCAATGACAAACGACACCGTGTCTTCGTGGAGAACCGCAGCTCCA 409
DB 181 GGTCAACATCACCTTCAATGACAAACGACACCGTGTCTTCGTGGAGAACCGCAGCTCCA 240
QY 410 TTTCCAGCTGACAAAGTCGATGGCTCAGAGAGTGACTACATTTGTACTGCTTAACATCTT 469
DB 241 TTTCCAGCTGACAAAGTCGATGGCTCAGAGAGTGACTACATTTGTACTGCTTAACATCTT 300
QY 470 GGTCTCTGGGGGGCTCCATATTGATGGAGAGCAAGCCCTGTGAGCTGAAGCTGATGAC 529
DB 301 GGTCTCTGGGGGGCTCCATATTGATGGAGAGCAAGCCCTGTGAGCTGAAGCTGATGAC 360
QY 530 CTTGGCGCTGGTCAACATGGCGCAGCGTGTCTTTATGAACCGCACAGTTGGTGAGATCCT 589
DB 361 CTTGGCGCTGGTCAACATGGCGCAGCGTGTCTTTATGAACCGCACAGTTGGTGAGATCCT 420
QY 590 GTGGGCTATGACGATCCCTTCTGTGCAATTTCTCAACAGTACTCTCCGACAGATGCTTCC 649
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QY 650 CATAAAGGGCAAAATTTGGGCTGTTTGTGGATGAAACAACTCGAAATCTGGGGTCTTCAC 709
DB 481 CATAAAGGGCAAAATTTGGGCTGTTTGTGGATGAAACAACTCGAAATCTGGGGTCTTCAC 540
QY 710 TGTCTTCAGGGCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGAACAAATGGAACGAGCT 769
DB 541 TGTCTTCAGGGCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGAACAAATGGAACGAGCT 600
QY 770 CAGCAAGATCGATTATTGGCAATTTTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGCA 829
DB 601 CAGCAAGATCGATTATTGGCAATTTTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGCA 660

ORIGIN

Query Match 85.7%; Score 1530; DB 9; Length 1530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGCGGAGCTTCAGGGGCGCTGGGTGGCCCTTGGGGTGGCGCCCTGGGGCTGCTG 60

QY 111 TTGTCTGGCTGGCGTGTGATGATCTCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTG 170
DB 61 TTGTCTGGCTGGCGTGTGATGATCTCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTG 120

QY 171 CTCAGGAATGTCGATAGACCCGAGCAGCTGTCTTCGGGATGTGGAGGAGATCCCC 230
DB 121 CTCAGGAATGTCGATAGACCCGAGCAGCTGTCTTCGGGATGTGGAGGAGATCCCC 180

QY 231 GTCCCTTTCTACTTGTCTACTTCTTCGAAAGTGGTCAACCAACGAGGTCTCTCAAC 290
DB 181 GTCCCTTTCTACTTGTCTACTTCTTCGAAAGTGGTCAACCAACGAGGTCTCTCAAC 240

QY 291 GGCAGAGCCAGTAGTCCGGGAGCGTGAACCTATGTCTACAGGGAGTTTCAGACAAAG 350
DB 241 GGCAGAGCCAGTAGTCCGGGAGCGTGAACCTATGTCTACAGGGAGTTTCAGACAAAG 300

QY 351 GTCAACATACCTTCAATGACACGACACCGTGTCTTCGGGAGAACCCGACCTCCAT 410
DB 301 GTCAACATACCTTCAATGACACGACACCGTGTCTTCGGGAGAACCCGACCTCCAT 360

QY 411 TTCAGAGCTGACAGTCCGCTGCTCAGAGAGTGACTACATTTGCTTGCCTTAACATCTTG 470
DB 361 TTCAGAGCTGACAGTCCGCTGCTCAGAGAGTGACTACATTTGCTTGCCTTAACATCTTG 420

QY 471 GTCTGGGGGGCTCGATATTGATGGAGCAAGCCTGTGAGCCTGGAAGCTGATGATGACC 530
DB 421 GTCTGGGGGGCTCGATATTGATGGAGCAAGCCTGTGAGCCTGGAAGCTGATGATGACC 480

QY 531 TTGGCGCTGGTCCACATGGGCGACGCTTTTATGAACCGCACAGTTGTGAGATCCTG 590
DB 481 TTGGCGCTGGTCCACATGGGCGACGCTTTTATGAACCGCACAGTTGTGAGATCCTG 540

QY 591 TGGGGCTATGACGATCCCTTCTGTCATTTCTCAACACGATCTCCAGACATGCTTCCC 650
DB 541 TGGGGCTATGACGATCCCTTCTGTCATTTCTCAACACGATCTCCAGACATGCTTCCC 600

QY 651 ATAAAGGGCAATTTGGCGCTTTTGGGATGAACTCACTCGAATTTCTGGGGTCTTCAC 710
DB 601 ATAAAGGGCAATTTGGCGCTTTTGGGATGAACTCACTCGAATTTCTGGGGTCTTCAC 660

QY 711 GTCTTACGGGGCTCCAGAAATTTACAGAGATCCATCTGTGGACAAATGGAACGGACTC 770
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QY 831 ATGTGGGCACTTTCATGACACCCGAATCTCTGGTGGAAATTTTCACCGCGGAGGATGC 890
DB 781 ATGTGGGCACTTTCATGACACCCGAATCTCTGGTGGAAATTTTCACCGCGGAGGATGC 840

QY 891 AGGTCCATGAGCTGACCTACAGATCAAGGTGTTCAGGCAATTCACGATATCCG 950
DB 841 AGGTCCATGAGCTGACCTACAGATCAAGGTGTTCAGGCAATTCACGATATCCG 900

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QY 1311 GCATGGGTGGCAAGCCCTGAGCACGTTCTACACGACGCTGTGTGTGATGCCCCAGGTT 1370
DB 1261 GCATGGGTGGCAAGCCCTGAGCACGTTCTACACGACGCTGTGTGTGATGCCCCAGGTT 1320

QY 1371 CTTCACTAGCGCAGTATGTGTCTGGGCTTGGAGGCTCTGTGTGTGTTGCCATC 1430
DB 1321 CTTCACTAGCGCAGTATGTGTCTGGGCTTGGAGGCTCTGTGTGTGTTGCCATC 1380

QY 1431 ATCTGCAACTGCGCAGCAGGAGAAATGCTTTTCTTTGGAGTGTGTAGTAAAAAGGGC 1490
DB 1381 ATCTGCAACTGCGCAGCAGGAGAAATGCTTTTCTTTGGAGTGTGTAGTAAAAAGGGC 1440

QY 1491 TCCAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAG 1550
DB 1441 TCCAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAG 1500

QY 1551 GGCAAGCTGTGCAAGAGCCCAAGCTATAG 1580
DB 1501 GGCAAGCTGTGCAAGAGCCCAAGCTATAG 1530

RESULT 9
D89655
LOCUS Rattus norvegicus mRNA for scavenger receptor class B, complete cds.
DEFINITION D89655
ACCESSION D89655
VERSION D89655.1 GI:1752796
KEYWORDS scavenger receptor Class B.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS Miyamoto, K., Mizutani, T. and Numata, Y.
TITLE cDNA cloning of rat scavenger receptor class B
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2392)
AUTHORS Miyamoto, K.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1996) Kaoru Miyamoto, Institute for molecular and cellular regulation, gunma univ., Biosignal research center; Showa-machi, 3-39-15, Maebashi, Gunma, 371, Japan
[E-mail: kmiyamot@fmsr.sak.fukui-med.ac.jp, Tel: 81-272-20-8878, Fax: 81-272-20-8878]
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/strain="Wistar"
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/sex="female"
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121..1650
CDS

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Best Local Similarity 90.2%; Pred. No. 7e-309;
Matches 1562; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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DB	71	CGGTCCCTTCCAGTCTCTGAGCCCGGAGAGCTCTCGGCGCGCAGCGGACATGGGGCGCA	130
QY	61	GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGGCGCCCTTGGGGCTGCTGTTTGTGCGC	120
DB	131	GCTCCAGGGCACTGGGTGGCTTGGGGCTGGGGCTGCTGTTTGTGCGC	190
QY	121	TCCGGGTGTCATGCTCTCATGGTGGCTTCCCTCATAGCAGCAGGTGCTCAAGATG	180
DB	191	TCCGGGTATCATGATCTCATGGTGGCTTCCCTCATAGCAGCAGGTGCTCAAGATG	250
QY	181	TCCGCATAGACCCGAGCAGCTGTCTTCCGGGATGTGGAAGGAGATCCCGCTCCCTTTCT	240
DB	251	TCCGCATAGACCCGAGCAGCTGTCTTCCGGGATGTGGAAGGAGATCCCTGTTCCCTTCT	310
QY	241	ACTTGTCTGTACTTCTTCCAGAGTGTCTAAACCCAAACGAGGTCTTCAACGGCGCAGAGC	300
DB	311	ACTTGTCTGTACTTCTTCCAGAGTGTCTAAACCCCAAGAGGTCTTCAACGGCGCAGAGC	370
QY	301	CAGTGTCCGGGAGCGTGGACCTTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA	360
DB	371	CAGTGTCCGGGAGCGGACCTTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA	430
QY	361	CTTTCATAGCAACGACGACGCTGTCTTCCGTGAGAACCCGACGCTTCCATTTCCAGCCTG	420
DB	431	CTTTCATAGCAATGACACGCTGTCTTCCGTGAGAACCCGACGCTTCCATTTCCAGCCTG	490
QY	421	ACAAGTCGATGGCTCAGAGAGTGAATCAATGTAATGTAATGTAATGTAATGTAATGTAATG	480
DB	491	ACAGGTCCCAGGGCTCAGAGAGTGAATCAATGTAATGTAATGTAATGTAATGTAATGTAATG	550
QY	481	GCTCGATATGATGGAGAGCAGCTGTGAGCCTGAGCTGATGATGATGATGATGATGATGATG	540
DB	551	GGGCGATGATGATGGAGAGCAGCTGTGAGCCTGAGCTGATGATGATGATGATGATGATGATG	610
QY	541	TCACCATGGGCGCAGCGTCTTTTATGAACCGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	600
DB	611	TCACCATGGGCGCAGCGGCTTTTATGAACCGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	670
QY	601	ACGATCCCTTGTGCAATTTTCTCAACAGTACCTTCCAGACATGCTTCCATTAAGGGCA	660
DB	671	AAGATCCCTTGTGCAATTTTCTCAACAGTACCTTCCAGACATGCTTCCATTAAGGGCA	730
QY	661	AATTTGGCTTGTGTTGGAGTGAACAACTGCAATCTTGGGGTCTTCACTGTCTTCAAGG	720
DB	731	AATTTGGCTTGTGTTGGAGTGAACAACTGCAATCTTGGGGTCTTCACTGTCTTCAAGG	790
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DB	791	GTGTCCAGAAATTTTCCAGCAGTACCTTGTGAGTGAATGTAAGTGAACGAGTCTCAGCAGTCA	850
QY	781	ATTATTGGCATTCAGAGCAGTGTAAATCATATCAATATGAGTCTTCCGGGCGAGATGTGGGCGAC	840

RESULT 10
BC076504
LOCUS
DEFINITION
Rattus norvegicus scavenger receptor class B, member 1, mRNA (cdna
clone MGC:91637 INRAB:7099863), complete cds.
ACCESSION
BC076504
VERSION
BC076504.1
KEYWORDS
MG.
SOURCE
Rattus norvegicus (Norway rat)

BC076504 2408 bp mRNA linear ROD 07-JUL-2004
Rattus norvegicus scavenger receptor class B, member 1, mRNA (cdna
clone MGC:91637 INRAB:7099863), complete cds.

Db	851	ACTATTGGCATTCGGAAACAGTGCACCATGATCAATGGTACTGCGGGCGAGATGTGGGCAC	910
QY	841	CTTTTCATGACACCCGGAATCTCTGCTGGAATTTCTTACAGCCGGAGGATGACAGGTCCATGA	900
Db	911	CATTTCATGACACCCGGAATCTCTGCTGGAATTTCTTACAGCCGGAAGCTGACGATCATGA	970
QY	901	AGTGACCTTACAAACGAATCAAGGGTGTGTAAGGCAATCCACGATATCGCTTTCACGGCCC	960
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QY	961	CCGATATCTGTTTTCGCAAGGGTCTGCTTACCCACCCCAAGAGGCTTCTGCGCATGCC	1020
Db	1031	CCGATATCTGTTTTCGCAAGGGTCTGCTTACCCACCCCAAGAGGCTTCTGCGCATGCC	1090
QY	1021	GACAGTCTGSCATTCAGAATGTGACACCTGACAGCTTGGTGGCTCTCTTCTTCTCTCCC	1080
Db	1091	GCGAGTCCGCGCATTCAGAATGTGACACCTGACAGCTTGGTGGCTCTCTTCTTCTCCC	1150
QY	1081	ACCCCACTTTTACAAACGCGGACCTCTGTGTGTGTCAGAAGCTGTTCTTGGTCTGAACCCCTA	1140
Db	1151	AGCCCACTTTTACAAATGCTGACCCGCTGTGTGTCAGAAGCTGTTCTTGGTCTGAACCCCTG	1210
QY	1141	ACCCCAAGGAGCATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCATGAACCT	1200
Db	1211	ACCCCAAGGAGCATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCATGAACCT	1270
QY	1201	GTTCCTGTGAAGTGCAGCTGAGCTCTACATCAATCTGTCAAGGGCATCGGCGCAACAG	1260
Db	1271	GTTCCTGTGAAGTGCAGCTGAGCTCTGTACATCAATCTGTCAAGGGCATCGGCGCAACAG	1330
QY	1261	GGAAGATCGAGCCAGTAGTCTTCCGCTGTGTGTGTTGCAACAGAGCGGAGCAATGGGTG	1320
Db	1331	GGAAGATCGAGCCAGTAGTCTTCCGCTGTGTGTGTTGCAACAGAGCGGAGCAATGGGTG	1390
QY	1321	GCAAGCCCTGAGCAGCTTCTACACGAGTGTGTGCTGATGCCCCAGGTTCTTTCACATGAC	1380
Db	1391	GCAAGCCCTGAGCAGCTTCTACACGAGTGTGTGCTGATGCCCCAGGTTCTTTCACATGAC	1450
QY	1381	CGCAGTATGTGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAAC	1440
Db	1451	CGCAGTATGTGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAAC	1510
QY	1441	TGCGCAGCCAGGAGAAATGCTTTTCTTTTGGAGTGTGTAGTAAAGGGCTCCGAGGATA	1500
Db	1511	TGCGCAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCCGAGGATA	1570
QY	1501	AGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTCAACAGTGCACAGGGCAACGGTGC	1560
Db	1571	AGAGGCCATTCAGGCTTACTCTGAGTCTCTGAGTCTGATGTCAACAGTGCACAGGGCAACGGTGC	1630
QY	1561	TGCAAGAAGCCAGCTATAGGGTCTTGAAGACATATAGCCCCCCCCCAAACTCATAGCTT	1620
Db	1631	TGCAAGAAGCCAGCTATAGGGTCTTGAAGACATATAGCCCCCCCCCAAACTCATAGCTT	1690
QY	1621	GCTCAGACAGCCAGCCAGTCCCTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1680
Db	1691	GCTCAGACAGCCAGCCAGTCCCTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1750
QY	1681	CCACAGTGCCTTGGCTTGGCCCCCAGATGTCAACCTGTGCGCACGAC	1731
Db	1751	CCGCGAGTGCACGCTCTGAGCCCCCAGATGTCACTGTGCCCAACGGCAC	1801

Qy	241	ACTTGTCTGTCTACTTCTTTGGAAGTGGTCAACCCAAAACGAGGTCCTCAACGGGCCAGAAGC	300
Db	393	ACTTGTCCGTCTACTTCTTCGAGGTGGTCAACCCACGAGGTCCTAAATGGCCAGAAGC	452
Qy	301	CAGTAGTCCGGAGCGGTGGACCCCTATGTCTACAGGGAGTTTCAGACAAAAGGTCAACATCA	360
Db	453	CAGTAGTCCGGAGCGCGGACCCCTATGTCTACAGGGAGTTTCAGACAAAAGGTTCACATCA	512
Qy	361	CTTTCATGTACAACGACACACCGCTGCTTCGTGGAGAACCGCAGCGCTCCATTTCCAGCGTG	420
Db	513	CTTTCATGTACNATGACACCGTGTCTTACATAGAGAACCGAGGCTTCGTTTCAGCCAG	572
Qy	421	ACAAAGTCGCATGGCTTCAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCCCTGGGG	480
Db	573	ACAGTCCACGGGCTCAGAGAGTGACTACATTTGTACTGCCCTAACATCTTGGTCCCTGGAG	632
Qy	481	GCTCGATATTGATGGAGAGCAAGCGCTGTGAGCCTGGAAGCTGATGATGACCTTGGCGCTGG	540
Db	633	GGGCAGTGATGATGGAGACAAAGCCCAACAGCCTGAAGCTGCTAATGACCTTGGGGTTGG	692
Qy	541	TCACCATGGGCGACGCTGCTTTTATGAACCGCACAGTTGGTGGAGATCCTGTGGGGCTATG	600
Db	693	TCACCATGGGCGACGGGCTTTTATGAACCGCACCGTGTGGTGGAGATCCTGTGGGGCTACG	752
Qy	601	ACGATCCCTTCGTGCATTTTCTCAACACGTACTCTCCACAGACATGCTTCCCATAAAGGGCA	660
Db	753	AAGATCCCTTTGTGAAATTTCTCAGCAATATTTTCCACAGACATGTTCCCCCATCAAGGCA	812
Qy	661	AAATTGGCCTCTTTTGTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGTCTTTCACGG	720
Db	813	AAATTGGCCTCTTCTGTTGGGATGAACGACTCGAGTTCTGGCGTCTTTCACCGTCTTTCACAG	872
Qy	721	CGGTCCAGAAATTTCAGCAGGATCCATCTGTGGGACAAATGGACGGACTCAGCAGATCG	780
Db	873	GTGTCCAGAAATTTCAGCAAGATCCATCTGTGGGATGAAGTGGAAACGGGCTCAGCGAGGTCA	932
Qy	781	ATTATTGGCATTTACAGCAGTGTAAACATGATCAATGGAGCTTCGCGGCAGATGTGGGCAC	840
Db	933	ACTATTGGCATTCGGNACNATGCAACATGATCAATGTGTACTGCGCGGAGATGTGGGCAC	992
Qy	841	CTTTCATGACACCCGAATCTCTCGTGGAAATTTCTTCAGCCGGAGGCGATGAGTTCATGA	900
Db	993	CATTTCATGACACCCGAATCTCTCTGGAATTTCTTCAGCCAGAGCCTGCAGATCTATGA	1052
Qy	901	AGCTGACCTACAAACGAATCAAGGTGTTTGAAGCATTTCCACGATTCGTTTCAGCGGCC	960
Db	1053	AGCTCACCTACACGAATTCAGAGGGTGTTCGAAGGCATCCCCACCTTATCGCTTTCACGGCCC	1112
Qy	961	CCGATACTCTGTTTGCACAAAGGTCGGTCTACCCACCAACGAAGGCTTCTGCCCATGCC	1020
Db	1113	CCGATACTCTGTTTGCACAAAGGTCGGTCTACCCACCACTATGAAGGCTTCTGCCCGTGCC	1172
Qy	1021	GAGAGTCTGGCATTCAGAAATGTACGACCTGCAGGTTTGGTGCGCCTCTGTTCCTCTCCC	1080
Db	1173	GGAGTCCGGCATTCAGAAATGTACGACCTGCAGGTTTGGTGCGCCTCTGTTCCTCTCCC	1232
Qy	1081	ACCCCACTTTTACAAACCGGACCCCTGTGTGTGAGAAGCTGTTCTTGGTCTGAACCCCTA	1140
Db	1233	AGCCCACTTTTACAAATCTGACCCCGTGTGTGAGAAGCTGTTCTTGGTCTGAACCCCTG	1292
Qy	1141	ACCCAAAGGACNTTCTGTTTCTTAGACATCCATCCGGTCACCTGGGATCCCCATGAAT	1200
Db	1293	ACCCAAAGGAGCATTTCTTGTTCCTTAGACATCCACCCGGTCACCTGGGATCCCCATGAAT	1352
Qy	1201	GTTCGTGAAGATGAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCGGGCAAAACAG	1260
Db	1353	GTTCCGTGAAGATGAGCTGAGTCTGTACATCAAAATCCGTCAAGGGCGTTCGGGCAAAACAG	1412
Qy	1261	GGAAGATCGAGCCAGTAGTTCTGCGGTTTGTGTGTGTTTCGAAACAGACGGGAGCAATGGGTG	1320
Db	1413	GGAAGATCGAGCCAGTAGTCTCTGCCATTGCTGTGGTTTCGAAACAGACGGGAGTAGTGGGTG	1472

QY	1321	GCAAGCCCTGAGGACGTTTCTACACGACAGCTGGTGTGATGCCCCAGGTTCTTCACTACG	1381
DB	1473	GCAAGACCCCTGAACACACGCTTCTACACGACAGCTGGTGTGATGCCCCAGGTTCTTCACTACG	1532
QY	1381	CGCAGTATGTGCTGCTCGGGGCTTGGAGGCTCTCTGTTGCTGGTGCCCATCATCTGCCAAC	1440
DB	1533	CGCAGTATGTGCTGCTCGGGGCTTGGAGGCTCTCTGCTTCTGGTGCCCATCATTTACCAAC	1592
QY	1441	TGCGCAGCCAGGAGAAATGCTTTTGTTTTGGAGTGGTAGTAAAGGGCTCCCAAGATA	1500
DB	1593	TGCGCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATA	1652
QY	1501	AGGAGGCCATTCAAGGCTTACTCTGAGTCCCTGATGTGTACACAGCTGCCAAGGGCACGCTGC	1560
DB	1653	AGGAGGCCATGCAGGCTTACTCTGAGTCTCTGATGTCCACAGCTGCCAAGGGCACGCTAC	1712
QY	1561	TGCAAGAGCCACAGCTATAGGCTCTCGAAGCACTATAAGCCCCCCCCAACTGTAGCTTT	1620
DB	1713	TGCAAGAGCCACAGCTGTAGGGCCAGAGACACCCAGGCCCCCCCCAACTGTAGCTTT	1772
QY	1621	GCTCAGACCCAGCCACCCAGTCCCTTACACCCCGCTTCTTGGAGGACTCTCTCAGCGGACAGC	1680
DB	1773	GCTCAGACCCAGCCCGCCAGTCCCTTACACCCCACTCTCTCGAGGACTCTCTCAGCGGACAC	1832
QY	1681	CCAACAGTGCCATGGCTGAGGCCCCCAAGATGTACAC	1717
DB	1833	CCGCCAGTGCCACGCTCTCTGAGCCCCCAGATGTACAC	1869

RESULT 12	
AY451993	2401 bp mRNA linear ROD 22-NOV-2003
LOCUS	Rattus norvegicus scavenger receptor class B type 1 (Scarbi) mRNA, complete cds.
DEFINITION	
ACCESSION	AY451993
VERSION	AY451993.1 GI:38350548
KEYWORDS	
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 2401)
AUTHORS	McLean, M.P. and Sandhoff, T.W.
TITLE	Expression and hormonal regulation of the high-density lipoprotein (HDL) receptor scavenger receptor class B type I messenger ribonucleic acid in the rat ovary
JOURNAL	Endocrine 9 (3), 243-252 (1998)
PUBMED	10221589
REFERENCE	2 (bases 1 to 2401)
AUTHORS	Lopez, D. and McLean, M.P.
TITLE	Sterol regulatory element-binding protein-1a binds to cis elements in the promoter of the rat high density lipoprotein receptor SR-BI gene
JOURNAL	Endocrinology 140 (12), 5669-5681 (1999)
PUBMED	10579331
REFERENCE	3 (bases 1 to 2401)
AUTHORS	McLean, M.P., Sandhoff, T.W. and Lopez, D.
TITLE	Direct Submission
JOURNAL	Submitted (28-OCT-2003) OB/GYN, University of South Florida, 4 Columbia Drive, Room 529, Tampa, FL 33610, USA
FEATURES	Location/Qualifiers
source	1. .2401
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gene	1. .2401
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CDS	108..1637

gene	
CDS	

/gene="Scarb1"
/function="HDL receptor responsible for facilitating the
flux of free and esterified cholesterol between
lipoproteins and the cell surface"
/note="lipoprotein receptor; SR-B1, clal, CD36; integral
membrane protein localized in caveolae-containing regions
of the plasma membrane"
/codon_start=1
/product="scavenger receptor class B type 1"
/protein_id="AA18387.1"
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PFTVTVQNFSLKHLVDKWLSEVNWHSQNMINGTAGQMWAPFMTPESSLEPFS
PEARSKMLTYQBSRVEGPIPTYPATDPLFANGSVVPNEGFCPCRESGIONVFC
RFGAPLFLSOPHFYNADPVLSEAVLGLNPDPKHSLFLDLPVGTGIWNSVKWQLSL
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L"

ORIGIN

Query Match 81.4%; Score 1452.6; DB 9; Length 2401;
Best Local Similarity 89.9%; Pred. No. 3.9e-307;
Matches 1557; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

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Qy	61	GCTCCAGGCGCGTGGGTGGCTTGGGGTGGCGCCCTGGGGCTGCTGTTCGCGC	120
Db	118	GCTCCAGGCGCGTGGGTGGCTTGGGGTGGCGCTTAGGGCTGCTGTTCGCGC	177
Qy	121	TCGCGGTGTGATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180
Db	178	TCGCGGTGTGATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	237
Qy	181	TCCGCATAGACCCGAGCAGCTGCTCTTGGGGATGTGGAAGGAGATCCCGTCTCTTCT	240
Db	238	TCCGCATAGACCCGAGCAGCTGCTCTTGGGGATGTGGAAGGAGATCCCGTCTCTTCT	297
Qy	241	ACTTGTCTGTCTACTTCTTCAAGTGGTCAACCCAAAGAGGTCTCAACGCGCAGAAGC	300
Db	298	ACTTGTCTGTCTACTTCTTCAAGTGGTCAACCCCAAGAGGTCTCAACGCGCAGAAGC	357
Qy	301	CAGTAGTCCGGAGCGTGGACCTATGTCTACAGGAGTTTCAACAAAGGTCAACATCA	360
Db	358	CAGTAGTCCGGAGCGGACCTATGTCTACAGGAGTTTCAACAAAGGTCAACATCA	417
Qy	361	CTTTCAATGACACGACACCGTGTCTTCTGGGAGTGTGGAAGGAGATCCCATTTCCAGCCTG	420
Db	418	CTTTCAATGACACGACACCGTGTCTTCTGGGAGTGTGGAAGGAGATCCCATTTCCAGCCTG	477
Qy	421	ACAAAGTCCGATGGCTCAGAGAGTGAATACATGTACTGCTTAAACATCTTGGTCTCGGGG	480
Db	478	ACAGTCCGAGGCTCAGAGAGTGAATACATGTACTGCTTAAACATCTTGGTCTCGGGG	537
Qy	481	GCTCGATATTGATGGAGGCAAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG	540
Db	538	GGGCAGTGATGATGGAGGCAAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG	597
Qy	541	TCACATGGGCGAGCGTCTTTATGACCCGACAGTGTGTGATCTCTGTGGGGCTATG	600
Db	598	TCACATGGGCGAGCGGCTTTATGAAACCCGACAGTGTGTGATCTCTGTGGGGCTATG	657
Qy	601	ACGATCCCTCTCGTCAATTTCTCAACAGTACCTCCGACAGATGCTTCCCATAAAGGCA	660
Db	658	AAGATCCCTCTGCAATTTCTCAGCAATATTTCCAGGAGATGTTCCCATCAAGGCA	717
Qy	661	AATTGGCTGTGTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAAGG	720

RESULT 13
RNU76205

LOCUS DEFINITION	1674 bp mRNA linear	ROD 21-JUL-2000
ACCESSION	U76205	
VERSION	U76205.1	GI:1679691
KEYWORDS		
SOURCE ORGANISM	Rattus norvegicus (Norway rat)	
REFERENCE		
AUTHORS	Johnson,M.S., Svensson,P.A., Heiou,K., Billig,H., Levan,G., Carlsson,L.M. and Carlsson,B.	
TITLE	Characterization and chromosomal localization of rat scavenger receptor class B type I, a high density lipoprotein receptor with a putative leucine zipper domain and peroxisomal targeting sequence	
JOURNAL	Endocrinology 139 (1), 72-80 (1998)	
PUBMED	9421400	
REFERENCE	2 (bases 1 to 1674)	
AUTHORS	Johnson,S.C.M., Svensson,P.A. and Carlsson,B.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-OCT-1996) Research Center for Endocrinology & Metabolism (RCM), Endocrinology division, Inst. of Internal Medicine, Sahlgrenska University Hospital, Bruna Straaket 16, Goteborg 413 45, Sweden	
FEATURES	Location/Qualifiers	
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	/tissue_type="liver"	
	49..1578	
	/function="high density lipoprotein dock-and-delivery receptor"	
	/function="putatively delivers cholesterol to steroid-producing organs"	
	/note="SR-BI"	
	/codon_start=1	
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CDS		
ORIGIN		
Query Match	79.9%;	Score 1426; DB 9; Length 1674;
Best Local Similarity	90.7%;	pred. No. 2.6e-301;
Matches 1519; Conservative	0; Mismatches 155; Indels 0; Gaps 0;	
Qy	3	GTCTCTTCAGTGCTCTGAGCCCCGAGAGCCCTTCGCGGCACGCGGACATGGCGGAGC 62
Db	1	GTCTCTTCAGTTCCTGAGCCACGCACTCTCGCGCGCGCACGCGGACATGGCGTCAGC 60
Qy	63	TCCAGGCGCGCTGGGTGGCCCTTGGGGTGGCGCCCTGGGGCTGTGTTTGTCTGCGCTC 122
Db	61	TCCAGGCGCACGCTGGGTGGCCCTTGGGGCTGGCGCTTCTAGGGCTGTGTGTCTGCGCTC 120
Qy	123	GGCGTTGTGATGATCTTCATGGTGCCCTCCCTCATCAAGCAGCAGGAGGCTCAAGAATGTC 182
Db	121	GGCGTTATCATGATTCCTCATGGTGCCCTCGCTCATCAAGCAGCAGGAGGCTCAAGAATGTC 180

Db 1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAAGGA 1609
Qy 1505 GGCCATTGAGGCTTACTCTGAGTCCCTGATGTACACAGCTGCGCAAGGGCAGGGTCTGCA 1564
Db 1610 GGCCATTGAGGCTTACTCTGAGTCTCTGATGTACACAGCTGCCAAGGGCAGGGTCTGCA 1669
Qy 1565 AGAAGCCAAAGCTATAGGGTCTGGAAGACACTATAGCCCCCCCCAACCTGATAGCTTGGTC 1624
Db 1670 AGAAGCCAAAGCTATAGGGTCTGGAAGACACTATAGCCCCCCCCAACCTGATAGCTTGGTC 1729
Qy 1625 AGACCAGCCACCCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGCCAC 1684
Db 1730 AGACCAGCCATCCAGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCGC 1789
Qy 1685 CAGTGCCATGGCCTGAGCCCCCAGATGTCACACCTGT 1721
Db 1790 CAGTGCCATGGCCTGAG-CCCCAGATGTCACACCTGT 1825

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Job time : 9000.94 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:34:57 ; Search time 1077.59 Seconds
(without alignments)
11039.845 Million cell updates/sec

Title: US-08-765-108-7
Perfect score: 1785
Sequence: 1 CGGTCTCTTCAGTCTCTGA.....TCAGGGACGAGGACACACC 1785

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	1785	2	AAX23404
2	1785	100.0	1785	2	AAX23404 Mouse sca
3	1785	100.0	1785	6	AAB30616 Mouse sca
4	1785	100.0	1785	6	AB199330 Mouse isc
5	1785	100.0	1785	6	AD333917 Murine sc
6	1785	100.0	2496	13	ADJ53336 Murine SR
7	1785	100.0	2496	13	ABD33431
8	1785	100.0	2496	13	ADR67032
9	1761	98.7	1785	14	ADZ13454
10	1607	90.0	1607	6	ABL46318
11	1582	88.6	1761	14	ABE03939
12	1517	85.0	2382	14	ADZ13452
13	1459.4	81.8	2497	10	ADB58616
14	1459.4	81.8	2497	10	ADB53264
15	1459.4	81.8	2497	10	ABT42207
16	1459.4	81.8	2497	13	ADV41414
17	1366.2	78.2	1825	9	ACD44926
18	1366.2	78.2	1825	12	ADJ46120
19	1369.8	76.7	1788	2	AAT10116

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21	1369.8	76.7	1788	2	AAX230615
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23	1369.8	76.7	1788	6	AAD333915
24	1369.8	76.7	1788	12	ADJ53334
25	1316.8	73.8	1788	14	ABE03941
26	1306.8	73.2	1546	14	AEA33429
27	1291	72.3	1531	13	ADS73684
28	1144.2	64.1	2637	14	ADZ13457
29	1144.2	64.1	3116	14	ADZ13463
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31	1142.6	64.0	2630	9	ACD44925
32	1142.6	64.0	2630	12	ADJ46118
33	1141	63.9	2565	2	AAX232194
34	1141	63.9	2566	3	AAA40750
35	1141	63.9	2566	9	AAI62623
36	1141	63.9	2566	12	ADJ61166
37	1133	63.5	2628	10	AD540209
38	1133	63.5	2630	2	AAX24497
39	1133	63.5	2630	2	AAX24589
40	1127.8	63.2	3143	14	ADZ13465
41	1127.8	63.2	3144	13	ABD33433
42	1127.8	63.2	3144	13	ADR67035
43	1119	62.7	2604	10	ADR09617
44	1056.8	59.2	3185	14	ADZ13461
45	1048.4	58.7	1530	13	ADS73689

ALIGNMENTS

RESULT 1
AAX23404

ID AAX23404 standard; DNA; 1785 BP.

AC AAX23404;

XX

DT 17-JUN-1999 (first entry)

XX

DE Mouse scavenger receptor class B-I DNA.

XX

KW Scavenger receptor class B type I; mouse; steroid production; HDL; cholesterol; cholesteryl ester transport; high-density lipoprotein; lipoprotein; liver; steroidogenic tissue; SR-BI; contraception; treatment; disorder; overproduction; underproduction; menopause; breast cancer; prostate cancer; endometriosis; fibroid tumour; ss.

XX

OS Mus sp.

XX

PN WO9911288-A1.

XX

PD 11-MAR-1999.

XX

PF 04-SEP-1998; 98WO-US018463.

XX

PR 05-SEP-1997; 97US-0057943P.

XX

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX

PI Krieger M;

XX

DR WPI; 1999-204984/17.

DR P-PSDB; AAW93575.

XX

PT Modification of steroid production in mammals - by administering modulator of SR-BI expression or activity.

PS Disclosure; Page 80-81; 86pp; English.

XX

CC This invention describes a method for modifying steroid production in a mammal which comprises administering a compound that alters cholesterol or cholesteryl ester transport from high-density lipoprotein (HDL) or other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger

Qy 1561 TGCAAGAGCCAGCTATAGGGTCTTGAAGACATATAAGCCCCCAAACTGTAGCTT 1620
Db |||||
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Db |||||
1621 GGTGAGACCAAGCCAGTCCCTTACACCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
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Db |||||
1681 CCACCACTGCGATGGCTGAGCCGCCAGATGTACACCTGTCCGACGACGCGACATGG 1740
Qy 1741 ATGCCCACTGTCGCAAAACAACTCAGGACACGAGGACAGACC 1785
Db |||||
1741 ATGCCCACTGTCGCAAAACAACTCAGGACACGAGGACAGACC 1785

RESULT 3

ABI99330
ID ABI99330 standard; cDNA; 1785 BP.
XX
AC ABI99330;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:201.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.

XX
XX WO200188198-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-JP004192.
XX
XX 18-MAY-2000; 2000JP-00145977.
XX

XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX

XX WPI; 2002-034733/04.
XX P-FSDb; ABB57092.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.

XX Claim 2; Page 573-576; 2690pp; English.

XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention

XX Sequence 1785 BP; 386 A; 524 C; 475 G; 400 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 1785; DB 6; Length 1785;

Pred. No. 0;

Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGTCTCTTCAAGTCTCTGAGCCCCGAGAGCCCTTTCGGCGCACGCGGACATGGGGCGCA 60
Db 1 CGGTCTCTTCAAGTCTCTGAGCCCCGAGAGCCCTTTCGGCGCACGCGGACATGGGGCGCA 60
Qy 61 GCTCCAGAGCGCGCTGGGTGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGTGCTGCTGCGC 120
Db 61 GCTCCAGAGCGCGCTGGGTGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGTGCTGCTGCGC 120
Qy 121 TCGGCGTGTGTATGATATCTCATGTCCTTCCCTCATCAAGCAGCAGGTGCTCAAGAATG 180
Db 121 TCGGCGTGTGTATGATATCTCATGTCCTTCCCTCATCAAGCAGCAGGTGCTCAAGAATG 180
Qy 181 TCGGCGATAGACCGGAGCAGCTGTCTTGGGATGTGGAGGAGATCCCGTCCCTTTCT 240
Db 181 TCGGCGATAGACCGGAGCAGCTGTCTTGGGATGTGGAGGAGATCCCGTCCCTTTCT 240
Qy 241 ACTTGTCTGTCTACTTCTCGAAGTGGTCAACCCAAACGAGGTCTTCAACGGCCAGAACG 300
Db 241 ACTTGTCTGTCTACTTCTCGAAGTGGTCAACCCAAACGAGGTCTTCAACGGCCAGAACG 300
Qy 301 CAGTAGTCCGGGAGCGTGACCCCTATGTCTACAGGAGTTTACAGCAAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGGAGCGTGACCCCTATGTCTACAGGAGTTTACAGCAAAAGGTCAACATCA 360
Qy 361 CTTTCAATGACACGACACCGTGTCTTGGTGGAGAACCGCAGCTCCATTTCCAGCCTG 420
Db 361 CTTTCAATGACACGACACCGTGTCTTGGTGGAGAACCGCAGCTCCATTTCCAGCCTG 420
Qy 421 ACAAGTCGATGGCTCAGAGAGTGACTACATTTGCTTACTTGCCTAAACATCTTGGTCTCTGGGG 480
Db 421 ACAAGTCGATGGCTCAGAGAGTGACTACATTTGCTTACTTGCCTAAACATCTTGGTCTCTGGGG 480
Qy 481 GCTCGATATTGATGGAGAGCAAGCTGTGAGCTGAAAGCTGATGATGATGATGATGATG 540
Db 481 GCTCGATATTGATGGAGAGCAAGCTGTGAGCTGAAAGCTGATGATGATGATGATGATG 540
Qy 541 TCACCATGGGCGCAGCGTCTTTTATGAACGGACAGTTGGTGAGATCTGTGGGGCTATG 600
Db 541 TCACCATGGGCGCAGCGTCTTTTATGAACGGACAGTTGGTGAGATCTGTGGGGCTATG 600
Qy 601 ACGATCCCTTCGTGTCATTTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
Db 601 ACGATCCCTTCGTGTCATTTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
Qy 661 AATTGGCGCTGTTTGTGGGATGAAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAACGG 720
Db 661 AATTGGCGCTGTTTGTGGGATGAAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAACGG 720
Qy 721 GCGTCCAGAAATTTACAGCAGGATCCATCTGGTGACAAATGGAACGGACTCAGCAAGATCG 780
Db 721 GCGTCCAGAAATTTACAGCAGGATCCATCTGGTGACAAATGGAACGGACTCAGCAAGATCG 780
Qy 781 ATTATTGGCATTCAGACGAGTGTAACATGATCAATGGGACTTCCGGGAGATGTGGGCAC 840
Db 781 ATTATTGGCATTCAGACGAGTGTAACATGATCAATGGGACTTCCGGGAGATGTGGGCAC 840
Qy 841 CTTTCATGACACCCGAATCTCGCTGGAATTTTCAGCCCGGAGGATGAGGTTCATGA 900
Db 841 CTTTCATGACACCCGAATCTCGCTGGAATTTTCAGCCCGGAGGATGAGGTTCATGA 900
Qy 901 AGCTGACCTACACGAAATCAAGGTTGTTGAAGGCAATTCACGATTCGCTTCAACGGCCC 960
Db 901 AGCTGACCTACACGAAATCAAGGTTGTTGAAGGCAATTCACGATTCGCTTCAACGGCCC 960
Qy 961 CCGATATCTGTGTTGCCAACCGGTCCGTCTACCCACCCAAACGAGGCTTCTGCGCCATGCC 1020
Db 961 CCGATATCTGTGTTGCCAACCGGTCCGTCTACCCACCCAAACGAGGCTTCTGCGCCATGCC 1020
Qy 1021 GAGAGTCTGCAATTCAGAAATGTTCAGACCTGAGGTTTGGTGGCCCTCTGTTTCTCTCCC 1080
Db 1021 GAGAGTCTGCAATTCAGAAATGTTCAGACCTGAGGTTTGGTGGCCCTCTGTTTCTCTCCC 1080

DR P-PSDB; ABO84950.
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
PS Disclosure; SEQ ID NO 564; 182pp; English.
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents murine CA cDNA of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2496 BP; 517 A; 741 C; 660 G; 578 T; 0 U; 0 Other;

Query Match 100.0%; Score 1785; DB 13; Length 2496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTCTCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGCACGCGGACATGGGGGCA 60
DB 143 CCGTCTCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGCACGCGGACATGGGGGCA 202

QY 61 GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGCGCCCTCGGGCTGCTGTTTCTGCGC 120
DB 203 GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGCGCCCTCGGGCTGCTGTTTCTGCGC 262

QY 121 TCGGCGTTGTATGATCTCTATGTCGTCCTCCCTCATCAGCAGCAGCTCTCAAGATG 180
DB 263 TCGGCGTTGTATGATCTCTATGTCGTCCTCCCTCATCAGCAGCAGCTCTCAAGATG 322

QY 181 TCGGCGATAGACCCGAGCAGCTGCTCTTCGCGGATGTGGAAGAGATCCCGCTCCCTTTCT 240
DB 323 TCGGCGATAGACCCGAGCAGCTGCTCTTCGCGGATGTGGAAGAGATCCCGCTCCCTTTCT 382

QY 241 ACTTGTCTGTACTTCTTTCGAGTGTGTCACCCAAACGAGGTCTCAACGGCCGAGAAC 300
DB 383 ACTTGTCTGTACTTCTTTCGAGTGTGTCACCCAAACGAGGTCTCAACGGCCGAGAAC 442

QY 301 CAGTAGTCCGGGAGCGTGGACCTATGCTCTACAGGAGTTTCAGACAAAGGTCAACATCA 360
DB 443 CAGTAGTCCGGGAGCGTGGACCTATGCTCTACAGGAGTTTCAGACAAAGGTCAACATCA 502

QY 361 CTTTCAATGACAAACGACCGCTGCTCTTCGCGGAGAACCGCAGCTCCATTTCCAGCCTG 420
DB 503 CTTTCAATGACAAACGACCGCTGCTCTTCGCGGAGAACCGCAGCTCCATTTCCAGCCTG 562

QY 421 ACAAGTCGATGGCTCAGAGAGTGAATCAATTTGATGCTTAAATCTTGGTCTCTGGGG 480
DB 563 ACAAGTCGATGGCTCAGAGAGTGAATCAATTTGATGCTTAAATCTTGGTCTCTGGGG 622

QY 481 GCTCGATTTGATGGAGACGACCGCTGAGCTGAGCTGATGATGACCTTGGCGCTGG 540
DB 623 GCTCGATTTGATGGAGACGACCGCTGAGCTGAGCTGATGATGACCTTGGCGCTGG 682

QY 541 TCACCATGGGCGAGCGTCTTTTATGAACCGCACAGTTTGGTGGATCCTCTGGGGCTATG 600
DB 583 TCACCATGGGCGAGCGTCTTTTATGAACCGCACAGTTTGGTGGATCCTCTGGGGCTATG 742

QY 601 ACGATCCCTTCGTGCATTTTCTCAACACGTA CTTCCAGACATGCTTCCCATAAAGGCA 660
DB 743 ACGATCCCTTCGTGCATTTTCTCAACACGTA CTTCCAGACATGCTTCCCATAAAGGCA 802

QY 661 AATTTGGCCCTGTTTGGTGGATGAACAACACTCGAAATTTCTGGGGTCTTCACTGCTTCAACGG 720
DB 803 AATTTGGCCCTGTTTGGTGGATGAACAACACTCGAAATTTCTGGGGTCTTCACTGCTTCAACGG 862

QY 721 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAAACGGAATCAGCAAGATCG 780
DB 863 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAAACGGAATCAGCAAGATCG 922

QY 781 ATATTGGCAATTCAGAGCAGTGTAAATGGAATTCCTGGGACTTCCGGGCGAGATGGGGCAC 840
DB 923 ATATTGGCAATTCAGAGCAGTGTAAATGGAATTCCTGGGACTTCCGGGCGAGATGGGGCAC 982

QY 841 CTTTCAATGACACCCGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATCGAGGTCCATGA 900
DB 983 CTTTCAATGACACCCGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATCGAGGTCCATGA 1042

QY 901 AGCTGACCTTACAAACGAATCAAGGGTGTGTTGAAGGCATTTCCACGTATCGCTTTCACGGCCC 960
DB 1043 AGCTGACCTTACAAACGAATCAAGGGTGTGTTGAAGGCATTTCCACGTATCGCTTTCACGGCCC 1102

QY 961 CCGATACTCTGTTTGGCAACGGGTCCGTCTACCCACCCCAACGAAGGCTTTCGCCCATGCC 1020
DB 1103 CCGATACTCTGTTTGGCAACGGGTCCGTCTACCCACCCCAACGAAGGCTTTCGCCCATGCC 1162

QY 1021 GAGAGTCTGGCATTGAGAATGTGAGCACTGCAAGTGTGCTGCGCTCTGTTTCTCTCCC 1080
DB 1163 GAGAGTCTGGCATTGAGAATGTGAGCACTGCAAGTGTGCTGCGCTCTGTTTCTCTCCC 1222

QY 1081 ACCCCACATTTTACAAACGGCCCTGTTGTGAGAAGCTGTTTGTGTTGTAACCCCTA 1140
DB 1223 ACCCCACATTTTACAAACGGCCCTGTTGTGAGAAGCTGTTTGTGTTGTAACCCCTA 1282

QY 1141 ACCAAAGAGCATTCCTTGTTCCTAGACATCATCCGGTCACTGGGATCCCCATGAAT 1200
DB 1283 ACCAAAGAGCATTCCTTGTTCCTAGACATCATCCGGTCACTGGGATCCCCATGAAT 1342

QY 1201 GTTCTGTGAAGATGCACTGAGCTCTACATCAATCTCTCAAGGGCATCGGCAACAG 1260
DB 1343 GTTCTGTGAAGATGCACTGAGCTCTACATCAATCTCTCAAGGGCATCGGCAACAG 1402

QY 1261 GGAAGTCGAGCAGTGTGTTGCGCTGCTGTGTTGTAACAGAGCGGAGCAATCGGTG 1320
DB 1403 GGAAGTCGAGCAGTGTGTTGCGCTGCTGTGTTGTAACAGAGCGGAGCAATCGGTG 1462

QY 1321 GCAAGCCCTGAGCAGTGTCTACACGAGCTGGTGTGCTGATGCCAGGTTCTTCACTAG 1380
DB 1463 GCAAGCCCTGAGCAGTGTCTACACGAGCTGGTGTGCTGATGCCAGGTTCTTCACTAG 1522

QY 1381 CGCAGTATGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAAC 1440
DB 1523 CGCAGTATGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAAC 1582

QY 1441 TGGCAGCCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAAAGGGCTCCAGGATA 1500
DB 1583 TGGCAGCCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAAAGGGCTCCAGGATA 1642

QY 1501 AGGAGCCATTCAGGCTCTACTCTGAGTCCCTGATGTCAACAGTGTCCAGGGGACCGGTGC 1560
DB 1643 AGGAGCCATTCAGGCTCTACTCTGAGTCCCTGATGTCAACAGTGTCCAGGGGACCGGTGC 1702

QY 1561 TGCAAGAAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
DB 1703 TGCAAGAAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1762

QY 1621 GGTTCAGACGAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
DB 1763 GGTTCAGACGAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1822

QY 1681 CCACAGTGGCATGGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGCGCATGG 1740
DB 1823 CCACAGTGGCATGGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGCGCATGG 1882

Db 520 CCTCAATGACACGACACCGTCTCTTCTGGGAGAACCGCAGCTCAATTTCCAGCGTG 579
Qy 421 ACAAGTCGCATGCTCAGAGAGTCACTACATTTGTAATGCTTAAACATCTTGTCTCTGGGG 480
Db 580 ACAAGTCGCATGCTCAGAGAGTCACTACATTTGTAATGCTTAAACATCTTGTCTCTGGGG 639
Qy 481 GCTCGATATTGATGAGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 540
Db 640 GCTCGATATTGATGAGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 699
Qy 541 TCACATGGGCGACGCTGCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGCTATG 600
Db 700 TCACATGGGCGACGCTGCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGCTATG 759
Qy 601 ACGATCCCTTGTGTCATTTTCTCAACAGTACCTCCAGACATGCTTCCATAAAGGGCA 660
Db 760 ACGATCCCTTGTGTCATTTTCTCAACAGTACCTCCAGACATGCTTCCATAAAGGGCA 819
Qy 661 AATTGGGCTGTTGTTGGGATGAACACTCGAATTTCTGGGCTTCACTGTCTTACGG 720
Db 820 AATTGGGCTGTTGTTGGGATGAACACTCGAATTTCTGGGCTTCACTGTCTTACGG 879
Qy 721 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 780
Db 880 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 939
Qy 781 ATTATGGCAATTCAGACAGTGTAAATGATGATCAATGGGACTTCCGGGCGAGATGTGGGCAC 840
Db 940 ATTATGGCAATTCAGACAGTGTAAATGATGATCAATGGGACTTCCGGGCGAGATGTGGGCAC 999
Qy 841 CTTTCATGACACCGGAATCTCGCTGGAAATCTTTCAGCCCGAGGAGATGAGAGTCCATGA 900
Db 1000 CTTTCATGACACCGGAATCTCGCTGGAAATCTTTCAGCCCGAGGAGATGAGAGTCCATGA 1059
Qy 901 AGCTGACCTCAACGAATCAAGGCTGTTGAAGCAATCCACGATGCTTTCACGGCC 960
Db 1060 AGCTGACCTCAACGAATCAAGGCTGTTGAAGCAATCCACGATGCTTTCACGGCC 1119
Qy 961 CCGATACCTGTTGGCCAAACGGGTCCTGTACCCACCAACGAAGCTTCTGCCCATGCC 1020
Db 1120 CCGATACCTGTTGGCCAAACGGGTCCTGTACCCACCAACGAAGCTTCTGCCCATGCC 1179
Qy 1021 GAGAGTCTGGCAATTCAGAAATGACACCTGACAGTTTGGTGGCCCTCTGTCTTCTCCC 1080
Db 1180 GAGAGTCTGGCAATTCAGAAATGACACCTGACAGTTTGGTGGCCCTCTGTCTTCTCCC 1239
Qy 1081 ACCCCCACTTTTACACGCGGACCTGTGTTGTGAGAGCTGTTCTTGGTCTGAACCTTA 1140
Db 1240 ACCCCCACTTTTACACGCGGACCTGTGTTGTGAGAGCTGTTCTTGGTCTGAACCTTA 1299
Qy 1141 ACCCAAGGAGCATTCTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
Db 1300 ACCCAAGGAGCATTCTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1359
Qy 1201 GTTCTGTGAAGATCAGCTGAGCTCTTACATCAATCTGTAAGGCGATCGGCAACAG 1260
Db 1360 GTTCTGTGAAGATCAGCTGAGCTCTTACATCAATCTGTAAGGCGATCGGCAACAG 1419
Qy 1261 GGAAGATCGAGCAGTAGTCTGCGCTGCTGTGTTGTAAGAGCTGTTCTTGGTCTGAACCTTA 1320
Db 1420 GGAAGATCGAGCAGTAGTCTGCGCTGCTGTGTTGTAAGAGCTGTTCTTGGTCTGAACCTTA 1479
Qy 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGATGCCCGAGCTTCTTCACTACG 1380
Db 1480 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGATGCCCGAGCTTCTTCACTACG 1539
Qy 1381 CGCAGTATGTCTCTGGGCTTGGAGCCTCTCTGTGCTGTGCTCCCATCATCTGCCAAC 1440
Db 1540 CGCAGTATGTCTCTGGGCTTGGAGCCTCTCTGTGCTGTGCTCCCATCATCTGCCAAC 1599
Qy 1441 TGGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGGGCTCCAGATA 1500
Db 1600 TGGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGGGCTCCAGATA 1659

Qy 1501 AGGAGGCCATTAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCAACGCTGC 1560
Db 1660 AGGAGGCCATTAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCAACGCTGC 1719
Qy 1561 TGCAGAGCCAGCTACTAGGCTCCTGAGACACACTATAAGCCGCCCAAACTGATAGCTT 1620
Db 1720 TGCAGAGCCAGCTACTAGGCTCCTGAGACACACTATAAGCCGCCCAAACTGATAGCTT 1779
Qy 1621 GGTCAAGACAGCCAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
Db 1780 GGTCAAGACAGCCAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1839
Qy 1681 CCACAGTCCATGCGCTGAGCCCGGAGTGTCAACCTTCTCCGACGCGACATGG 1740
Db 1840 CCACAGTCCATGCGCTGAGCCCGGAGTGTCAACCTTCTCCGACGCGACATGG 1899
Qy 1741 ATGCCACGATGTGCANAACTCAGGACGCGGACAGACC 1785
Db 1900 ATGCCACGATGTGCANAACTCAGGACGCGGACAGACC 1944

RESULT 9

AEBO3942
ID AEBO3942 standard; cDNA; 1785 BP.

XX AEBO3942;

XX AC AC

XX 25-AUG-2005 (first entry)

XX Murine Scavenger Receptor Class B-1 coding sequence, SEQ ID 3 #2.

XX Antilipemic; transgenic animal; Scavenger Receptor Class B-1;

XX high density lipoprotein receptor; cholesterol; lipid; gene; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 51..1580

XX FT /tag= a

XX FT /product= "SR-BI"

XX PN US2005136005-A1.

XX XX 23-JUN-2005.

XX PF 02-SEP-2004; 2004US-00933037.

XX PR 23-JUN-1994; 94US-00265428.

XX PR 19-JUN-1995; 95WO-US007721.

XX PR 15-NOV-1996; 96US-00749907.

XX PR 27-MAR-1997; 97US-00765108.

XX PR 30-AUG-1999; 99US-00385799.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Kozarsky K, Rigotti A, Krieger M;

XX WPI; 2005-457475/46.

XX P-PSDB; AEB03940.

XX New genetically engineered mouse or derivative cells with inactivated SR-

XX BI gene expression or activity, useful as a model for designing drugs

XX that can modulate cholesterol transport.

XX Disclosure; SEQ ID NO 3; 21pp; English.

XX The present invention relates to a novel genetically engineered mouse, or

XX calls derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene

XX expression or SR-BI activity has been inactivated. SR-BI is a high

XX density lipoprotein (HDL) receptor. It was found that estrogen

XX downregulates SR-BI under conditions of upregulation of the low density

lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
adrenal membranes and other non-placental steroidogenic tissues from
animals treated with estrogen, but not in other non-placental non-
steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
tissue causes a decrease in blood cholesterol levels. The animal is
useful as a model for designing drugs that can modulate cholesterol
transport or that can stimulate or inhibit the binding to and lipid
movements mediated by SR-BI and redirect uptake and metabolism of lipids
and cholesterol by cells. The present sequence is a coding sequence for
SR-BI, which was used to illustrate the invention. Note: The SEQ ID 3
given in the sequence listing (the sequence shown in AEO30393) is stated
to be 1785 nucleotides in length. However, there appears to be a 1 to 3
nucleotide deletion at the end of each line of the sequence shown in the
sequence listing, resulting in a sequence that is 1761 nucleotides in
length. Therefore a corrected version of the sequence has been produced
with Ns added to replace the missing nucleotides (the sequence shown in
AEO303942). SEQ ID 3 is stated to encode SEQ ID 4 (given in AEO303940).

Query Match	98.7%	Score 1761;	DB 14;	Length 1785;
Best Local Similarity	98.7%;	Pred. No. 0;		
Matches 1761;	Conservative 0;	Mismatches 24;	Indels 0;	Gaps 0;
Qy	1	CCGTCCTCTTCAGGTCTGAGCCCGAGAGCCCTTCGCGCAGCGCGACATGCGCGCA	60	
Db	1			
Qy	61	GCTCCAGGCGCGCTGGGTGGCTTGGGTGGCGCCCTGGGGCTGCTGTTTCTCTCGC	120	
Db	61			
Qy	121	TCGGCGTTGATCATGATCCTCATGTGTGCCCTCCTCATCAGCAGCAGGTGCTCAAGAA	180	
Db	121	TCGGCGTTGTCATGATCCTCATGTGTGCCCTCCTCATCAAGCAGCAGGTGCTCAAGA	180	
Qy	181	TCCGCATAGACCCGAGCAGCTGTCTTTCGGGATGTGGAAGAGATCCCCTGCTCTTCT	240	
Db	181	TCCGCATAGACCCGAGCAGCTGTCTTTCGGGATGTGGAAGAGATCCCCTGCTCTTCT	240	
Qy	241	ACTTGTCTGTCTACTTCTTTCGAAGTGTCTCAACCCAAACGAGGTCTCAAACGCGCAGA	300	
Db	241	ACTTGTCTGTCTACTTCTTTCGAAGTGTCTCAACCCAAACGAGGTCTCAAACGCGCAGA	300	
Qy	301	CAGTAGTCCGGAGCGTGGACCCCTATGTCTACAGGGATTCAGACAAAGSTCAACATCA	360	
Db	301	CAGTAGTCCGGAGCGTGGACCCCTATGTCTACAGGGATTCAGACAAAGSTCAACATCA	360	
Qy	361	CTTTCATGACAAACGACACCGCTGTCTTCGTGGAGAACCGCAGCGCTCCATTTCCAG	420	
Db	361	CTTTCATGACAAACGACACCGCTGTCTTCGTGGAGAACCGCAGCGCTCCATTTCCAG	420	
Qy	421	ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGATCTGCCTTAACATCTTGTCTCTG	480	
Db	421	ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGATCTGCCTTAACATCTTGTCTCTG	480	
Qy	481	GCTCGATATTGATGGAGCAGCAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTG	540	
Db	481	GCTCGATATTGATGGAGCAGCAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTG	540	
Qy	541	TCACATGGGCGCAGCGTCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGGCTATG	600	
Db	541	TCACATGGGCGCAGCGTCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGGCTATG	600	
Qy	601	ACGATCCCTTCGTGCAATTTTCTCAACACGTACCTCCACAGACATGCTTTCCATAAAGG	660	
Db	601	ACGATCCCTTCGTGCAATTTTCTCAACACGTACCTCCACAGACATGCTTTCCATAAAGG	660	
Qy	661	AAATTGGCGCTTTTGTGGGATGAACAACCTCGAATTTCTGGGGCTTCTCACTGTCTTCA	720	
Db	661	AAATTGGCGCTTTTGTGGGATGAACAACCTCGAATTTCTGGGGCTTCTCACTGTCTTCA	720	
Qy	721	CGCTCCAGAAATTTTCAGCAGGATCCATCTGTGTGGACAAATGAAACGGACTCAGCAG	780	

RESULT 10

841 CCTCATGACACCGAATCTCGTGGATTTCTTACGCCCGGAGGCATGAGGTCCATGA 900
901 AGCTGACCTACACGAATCAAGGGTGTGTTGAAGGCATTTCCACGATATCGCTTTCACGGGCC 960
901 AGCTGACCTACACGAATCAAGGGTGTGTTGAAGGCATTTCCACGATATCGCTTTCACGGGCC 960
961 CCGATATCTCTGTTTGGCCAAACGGGTCCGCTACACCAACGAAGGCTTCTGCCCATGCC 1020
961 CCGATATCTCTGTTTGGCCAAACGGGTCCGCTACACCAACGAAGGCTTCTGCCCATGCC 1019
1021 GAGAGTCTGGCATTCAGAAATGTCAGCACTTCAGGCTTGGTGGCCCTCTGTTCTCTCC 1080
1020 GAGAGTCTGGCATTCAGAAATGTCAGCACTTCAGGCTTGGTGGCCCTCTGTTCTCTCC 1078
1081 ACCCCCACTTTTACACCGCCGACCTCTGTTGTTCAGAAAGTGTCTTGGTCTGAACCTTA 1140
1079 ACCCCCACTTTTACACCGCCGACCTCTGTTTTCAGAAAGTGTCTTGGTCTGAACCTTA 1137
1141 ACCCAAGGAGCATCTCTGTTTCTAGACATCCATCCGCTCACTGGGATCCCATGAAC 1200
1138 ACCCAAGGAGCATCTCTT-TTCCTAGACATCCATCCGCTCACTGGGATCCCATGAAC 1196
1201 GTTCTGTGAAGATGACGCTGAGCTCTACATCAATCTGTCAAGGCGATCGGCGAAGACAG 1260
1197 GTTCTGT-AGATGACGCTGAGCTCTACATCAATCTGTCAAGGCGATCGGCG-AGACG 1254
1261 GGAAGATCGAGCCAGTAGTCTGCGGTTGCTGTGTTTTCGAACAGCGGAGCAATGGGTG 1320
1255 GGAAGATCGAGCCAGTAGTCTGCGGTTGCTGTGTTTTCGAACAGCGGAGCAATGGGTG 1313
1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGTGTGCTGATGCCCGAGGTTCTTCACTACG 1380
1314 GCAAGCCCTGAGCAGCTTCTACACGAGCT-GTGCTGATGCCCGAGGTTCTTCACTACG 1372
1381 CGCAGTATGTCTGCTGGGCTTGGAGCCCTCTGTTGCTGTGCTCCATCATCTGCCAAC 1440
1373 CGCAGTATGTCTGCT-GGGCTTGGAGCCCTCTGTTGCTGTGCTCCATCATCTGCCAAC 1431
1441 TGGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTGTAAAGGGCTCCAGGATA 1500
1432 TGGCAG-CAGGAGAAATGCTTTTGTGTTTGGAGTGTGTAAAGGGCTCCCA-GATA 1489
1501 AGGAGGCATTCAGGCTTCTGAGTCCCTGATGTCCAGAGTGTCCAAAGGCGACGCTGC 1560
1490 AGGAGGCATTCAGGCTTCTGAGTCCCTGATGTCCAGAGC-GCCAAAGGCGACGCTGC 1548
1561 TGCAGAGCCAGCTATAGGCTTCTGAAGACATATAAGCCCCCCTGATGATCTT 1620
1549 TGCAGAGCCAGCTATAGGCTTCTGAAGACAC-AGCCCCCCTGATGATCTT 1605
1621 GGTTCAGACCCAGCCAGTCCCTTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGC 1680
1606 GGTTCAGACCCAGCCAGTCCCTTACACCCCG-CTTGGAGTCTCTCAGCGGACAGC 1662
1681 CCACAGTGCATGGCTGAGCCCTCCAGATGTCTACACTGTTCGACACGCGACATATGG 1740
1663 CCACAGTGCATGGCTGAGCCCTCCAGATGTCTA-CTGTGCGACGCGACATATGG 1719
1741 ATGCCACGCTATGCGAAGAACACTCAGGAGC 1774
1720 ATGCCACGCTATGCGAAGAACAACTCAGGAGC 1753

RESULT 12

ID ADZ13452 standard; cDNA; 2382 BP.

AC ADZ13452;

XX 16-JUN-2005 (first entry)

DE Murine cancer-associated cDNA #108.

XX

KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX cytostatic; gene; ss.
OS Mus sp.
XX WO2005031001-A2.
XX 07-APR-2005.
XX 23-SEP-2004; 2004WO-US031617.
XX 23-SEP-2003; 2003US-00669920.
XX (CHIR) CHIRON CORP.
XX Morris DW, Malandro MS;
XX WPI; 2005-273395/28.
XX P-PSDB; ADZ13453.

PT Nucleic acid array useful for detecting cancer associated nucleic acid,
XX comprises two or more nucleic acid probes.
PS Disclosure; SEQ ID NO 972; 198pp; English.

CC The invention relates to a nucleic acid array for detecting a cancer
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX that binds to a polypeptide, an isolated antibody or its fragment which
XX binds to a polypeptide, which is prepared by immunizing a host animal
XX with a composition comprising the polypeptide or its antigen binding
XX fragment and collecting cells from the host expressing antibodies against
XX the antigen or its antigen binding fragment, a composition comprising the
XX antibody and a carrier, a method of screening for anticancer activity, a
XX method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX method of treating cancer and a method of inhibiting expression of a CA
XX nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX absence of cancer cells in an individual which involves contacting cells
XX from the individual with the antibody and detecting a complex of a CA
XX protein from the cancer cells and the antibody, where the detection of
XX the complex correlates with the presence of cancer cells in the
XX individual. The composition is useful for inhibiting growth of cancer
XX cells in an individual or for delivering a therapeutic agent to cancer
XX cells in an individual. The invention is also useful for diagnosing
XX cancer, for treating cancer and for inhibiting expression of a CA gene in
XX a cell. This sequence represents murine cancer-associated cDNA of the
XX invention.

SQ Sequence 2382 BP; 486 A; 720 C; 626 G; 550 T; 0 U; 0 Other;

Query Match 85.0%; Score 1517; DB 14; Length 2382;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 0; Indels 129; Gaps 1;

QY 1 CCCTCTCTCTTCCAGTCTGTGAGCCCGCAGAGCCCTTCCGCGCACGGGACATGGGGCGCA 60
DB 160 CCCTCTCTCTTCCAGTCTGTGAGCCCGCAGAGCCCTTCCGCGCACGGGACATGGGGCGCA 219
QY 61 GCTCCAGGGCGCGCTGGGTGGCTTGGGGTTGGGGCGCCCTTGGGGGCTGCTGTTTCTGTCGC 120
DB 220 GCTCCAGGGCGCGCTGGGTGGCTTGGGGTTGGGGCGCCCTTGGGGGCTGCTGTTTCTGTCGC 279
QY 121 TCGGCGTGTGTATGATCTCTCATGTGTCCTTCCCTCATAGCAGCAGGTGCTCAAGATG 180
DB 280 TCGGCGTGTGTATGATCTCTCATGTGTCCTTCCCTCATAGCAGCAGGTGCTCAAGATG 339
QY 181 TCCGCATAGACCCGAGCAGCTCTCTCGGGATGTGGAGGAGATCCCGTCCCTTCTTCT 240
DB 340 TCCGCATAGACCCGAGCAGCTCTCTCGGGATGTGGAGGAGATCCCGTCCCTTCTTCT 399
QY 241 ACTTGTCTGTCTACTTCTTTCGAAGTGTGTCAACCAACGAGGTCTCTCAACGCGCAGAAGC 300

Db 400 ACTTGTCTGTCTACTTCTTGGAGTGTCTCAACCAACGAGGTCTCTCAACGGCCAGAGC 459
Qy 301 CAGTAGTCCGGAGCGTGGACCTTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Db 460 CAGTAGTCCGGAGCGTGGACCTTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 519
Qy 361 CTTTCAATGACAACGACACCGTGTCTTCTGTGGAGAACCGCAGCTCCATTTCCAGCCTG 420
Db 520 CTTTCAATGACAACGACACCGTGTCTTCTGTGGAGAACCGCAGCTCCATTTCCAGCCTG 579
Qy 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCTCTGGGG 480
Db 580 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCTCTGGGG 639
Qy 481 GCTCGATATTGATGGAGAGACGCTGTGAGCCTGAAGCTGTATGATGACCTTGGCGCTGG 540
Db 640 GCTCGATATTGATGGAGAGACGCTGTGAGCCTGAAGCTGTATGATGACCTTGGCGCTGG 699
Qy 541 TCACCATGGGCCAGCGTGTCTTTATGAACCGCACAGTTGTGTGAGATCCTGTGGGGCTATG 600
Db 700 TCACCATGGGCCAGCGTGTCTTTATGAACCGCACAGTTGTGTGAGATCCTGTGGGGCTATG 759
Qy 601 ACGATCCCTTCTGTGCAATTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
Db 760 ACGATCCCTTCTGTGCAATTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 819
Qy 661 AATTGGCCTGTTTGTGGAGTGAACAACTCGAAATTCCTGGGGTCTTCACTGTCTTCAAGG 720
Db 820 AATTGGCCTGTTTGTGGAGTGAACAACTCGAAATTCCTGGGGTCTTCACTGTCTTCAAGG 879
Qy 721 GCGTCCAGAAATTTCCAGCAGATCCATCTGTGTGACAAATGGAACGGAATCAGCAAGATCG 780
Db 880 GCGTCCAGAAATTTCCAGCAGATCCATCTGTGTGACAAATGGAACGGAATCAGCAAGATCG 939
Qy 781 ATTATTGGCAATTCAGAGCAGTGAACATGATCAATGGGACTTCGGGGCAGATGTGGGCAC 840
Db 940 ATTATTGGCAATTCAGAGCAGTGAACATGATCAATGGGACTTCGGGGCAGATGTGGGCAC 999
Qy 841 CTTTCATGACACCGAATCTCGTGTGAATTTCTCAGCCCGGAGGATGAGGCTTCATGA 900
Db 1000 CTTTCATGACACCGAATCTCGTGTGAATTTCTCAGCCCGGAGGATGAGGCTTCATGA 1059
Qy 901 AGCTGACTCAACGAATCAAGGTGTGTGAAGSCATTCACAGTATCGCTTCAAGCSCCC 960
Db 1060 AGCTGACTCAACGAATCAAGGTGTGTGAAGSCATTCACAGTATCGCTTCAAGCSCCC 1119
Qy 961 CCGATACTCTGTGTTGCCAACGGGTCCGTCTACCCACCCCAACGAAGGCTTCTGCCCATGCC 1020
Db 1120 CCGATACTCTGTGTTGCCAACGGGTCCGTCTACCCACCCCAACGAAGGCTTCTGCCCATGCC 1179
Qy 1021 GAGAGTCTGGCATTCAGAAATGTACGACCTGTGAGGTTTGGTGGCCCTCTGTCTCTCCC 1080
Db 1180 GAGAGTCTGGCATTCAGAAATGTACGACCTGTGAGGTTTGGTGGCCCTCTGTCTCTCCC 1239
Qy 1081 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTCTTGTGTGTCGACCCCTA 1140
Db 1240 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTCTTGTGTGTCGACCCCTA 1299
Qy 1141 ACCCAAGGAGCATTTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT 1200
Db 1300 ACCCAAGGAGCATTTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT 1359
Qy 1201 GTTCTGTGAGATGAGTGAAGCTCTTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Db 1360 GTTCTGTGAGATGAGTGAAGCTCTTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1419
Qy 1261 GGAAGATCGAGCAGTAGTGTCTGCGGTGTGTGTCGAGCTGTGTGTCGAGCGGAGCATGGGTG 1320
Db 1420 GGAAGATCGAGCAGTAGTGTCTGCGGTGTGTGTCGAGCTGTGTGTCGAGCGGAGCATGGGTG 1479
Qy 1321 GCAAGCCCTTGAGCAGCTGTCTTACACGAGCTGGTGTGTCGATGCCCGCAGGTCTTCTCACTACG 1380

Db 1480 GCAAGCCCTTGAGCAGCTTCTTACACGACGTGTGTGCTGATGCCCCAGGTTCTTCACTACG 1539
Qy 1381 CCGAGTATCTGTCTGTGGGGCTTGGAGGCTCTCTGTGTGCTGGTCCCATCATCTGCCAAC 1440
Db 1540 CCGAGTATCTGTCTGTGGGGCTTGGAGGCTCTCTGTGTGCTGGTCCCATCATCTGCCAAC 1599
Qy 1441 TGGCAGCAGCAGGAGAAATGCTTTTGTGAGTGGTAGTAAAGGGCTCCCAAGGATA 1500
Db 1600 TGGCAGACC----- 1608
Qy 1501 AGGAGCCATTTCAGGCTTACTCTGAGTCCCTGATGTCAACAGTGCACAGGGCACGGTGC 1560
Db 1609 ----- 1608
Qy 1561 TGCAGAGCCAAAGCTATAGGCTCCTGAAGACACTATAAGCCCCCAAACTGATAGCTT 1620
Db 1609 -----AGGGTCTCTGAAGACACTATAAGCCCCCAAACTGATAGCTT 1650
Qy 1621 GGTTCAGACGACGACCCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
Db 1651 GGTTCAGACGACGACCCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1710
Qy 1681 CCACCACTGCTGAGTGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGACGACATGG 1740
Db 1711 CCACCACTGCTGAGTGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGACGACATGG 1770
Qy 1741 ATGCCCCAGCTGTGCAGAAACAACTCAGGGACCGGACAGACC 1785
Db 1771 ATGCCCCAGCTGTGCAGAAACAACTCAGGGACCGGACAGACC 1815

RESULT 13

ADB58616

ID ADB58616 standard; DNA; 2497 BP.

XX

AC ADB58616;

XX

DT 04-DEC-2003 (first entry)

XX

DE Toxicity-related gene, SEQ ID 3642.

XX

XX Toxic; toxin; gene expression profile; hepatotoxicity; liver;

KW drug screening; toxicity assay; ds.

XX

OS Unidentified.

XX

PN WO2003064624-A2.

XX

PD 07-AUG-2003.

XX

XX 31-JAN-2003; 2003WO-US003194.

XX

XX 31-JAN-2002; 2002US-00060087.

PR

PR 15-MAR-2002; 2002US-0364045P.

PR

PR 15-MAR-2002; 2002US-0364055P.

PR

PR 30-DEC-2002; 2002US-0436643P.

XX

XX (GENE-) GENE LOGIC INC.

XX

XX Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Elashoff M;

XX

XX WPI; 2003-689530/65..

XX

XX Predicting a toxic effect of a compound, useful in identifying toxicity

XX

XX markers in liver tissues or cells for drug screening and toxicity assays,

XX

XX comprises preparing gene expression profile of tissue or cells exposed to

XX

XX the compound.

XX

XX Claim 1; SEQ ID NO 3642; 1156pp; English.

XX

XX The present invention relates to a method for predicting a toxic effect

XX

XX of a compound. The method comprises preparing a gene expression profile

XX

XX of a tissue or cell sample exposed to the compound, and comparing the

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3806.
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX

OS Rattus norvegicus.

PN WO2003065993-A2.

XX 14-AUG-2003.

XX 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

XX 13-MAR-2002; 2002US-0363534P.

XX 08-APR-2002; 2002US-0370248P.

XX 10-APR-2002; 2002US-0371134P.

XX 10-APR-2002; 2002US-0371135P.

XX 10-APR-2002; 2002US-0371150P.

XX 11-APR-2002; 2002US-0371413P.

XX 19-APR-2002; 2002US-0373601P.

XX 19-APR-2002; 2002US-0373602P.

XX 22-APR-2002; 2002US-0374139P.

XX 08-MAY-2002; 2002US-0378370P.

XX 09-MAY-2002; 2002US-0378652P.

XX 09-MAY-2002; 2002US-0378653P.

XX 09-MAY-2002; 2002US-0378655P.

XX 09-JUL-2002; 2002US-0394230P.

XX 09-JUL-2002; 2002US-0394253P.

XX 04-SEP-2002; 2002US-0407688P.

XX 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

XX Elashoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX

XX Claim 44; SEQ ID NO 3806; 874pp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
XX Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

Query Match 81.8%; Score 1459.4; DB 10; Length 2497;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1556; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
Qy 1 CCGTCTCTTCAGTCTGAGCCCGAGAGCCCTTCGCGCGCAGCGGACATGGCGGCA 60
Db 153 CCGTCTCTTCAGTCTGAGCCCGAGAGCTCTCGCGCGCAGCGGACATGGCGGCA 212
Qy 61 GCTCCAGGCGCGTGGGTGGCTTGGGGTGGCGCCCTGCTGTTGCTGCGC 120

Db 213 GCTCCAGGCGCAGCTGGGTGGCTTGGGCGTGGTGTGCTGCTGCTGCGC 272
Qy 121 TGGGCGTTCATGATCCCTATGTTGCTTCCCTCATCAAGCAGCAGGCTCAAGAATG 180
Db 273 TGGGCGTTCATGATTCCTATGTTGCTTCCCTCATCAAGCAGCAGGCTCAAGAATG 332
Qy 181 TCCGATAGACCCGAGCAGCTGCTTCCGATGTGGAGAGAGATCCCGTCCCTTTCT 240
Db 333 TCCGATAGACCCGAGCAGCTGCTTCCGATGTGGAGAGAGATCCCTTTCTTCT 392
Qy 241 ACTTGTCTCTACTTCTTCAAGTGGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 300
Db 393 ACTTGTCCGTCTACTTCTTCAAGTGGTCAACCCAGCGAGGTCTTAAATGGCAGAAC 452
Qy 301 CAGTAGTCGGGAGCGTGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Db 453 CAGTAGTCGGGAGCGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCA 512
Qy 361 CTTTCAATGACCAACGACACCGGTGCTTCTGAGAGAACGCGAGCCTCCATTTCCAGCCTG 420
Db 513 CTTTCAATGACCAATGACACCGGTGCTTCTAFAGAGAACCGAGCCTTCGTTCCAGCCAG 572
Qy 421 ACAAGTCGATGGCTCAGAGAGTACTACATTGTACTGCTTAACATCTTGGTCTTGGGG 480
Db 573 ACAGGTCCCGAGGCTCAGAGAGTACTACATTGTACTGCTTAACATCTTGGTCTTGGGAG 632
Qy 481 GCTCGATATGATGGAGAGCAGCCTGTGAGCTGAAGCTGATGATGACCTTGGCGCTGG 540
Db 633 GGGCAGTGTATGATGGAGGCAAGCCCAAGGCTTGAAGCTTGAATGACCTTGGGGTTGG 692
Qy 541 TCACCATGGCGCAGCGTCTTTTATGAACCGACAGTGTGTGAGATCCTGTGGGGCTATG 600
Db 693 TCACCATGGCGCAGCGGCTTTATGAACCGACAGTGTGTGAGATCCTGTGGGGCTACG 752
Qy 601 AGGATCCCTTCGTGCAATTTTCAACACAGTACCTCCAGACATGCTTCCCATAAAGGGCA 660
Db 753 AAGATCCCTTCGTGAATTTCTCCAGCAATATTTCCAGACATGTTCCCATCAAGGCA 812
Qy 661 AATTGGCTGTTTGTGGATGAACACTCGAATTTCTGGGTCTTCACTGTCTTCAAG 720
Db 813 AATTGGCTGTTTGTGGATGAACACTCGAATTTCTGGGTCTTCACTGTCTTCAAG 872
Qy 721 GCGTCCAGAAATTTACAGCAGTCCATCTGTGAGCAAAATGGAACGAGCTCAGCAAGATCG 780
Db 873 GTGTCCAGAAATTTACAGCAAGTCCATCTGTGAGTAAAGTGAACGCGCTCAGCGAGTCA 932
Qy 781 ATTTATGGCATTACAGCAGTGTAAACATGATCAATGGGACTTCCGGGAGATGTGGCAC 840
Db 933 ACTATTGGCATTCCGGAACAGTGCACATGATCAATGGTACTGCGCGGAGATGTGGCAC 992
Qy 841 CTTTATGACACCGGAATCTTCTGCTGGAATTTCTCAGCCGAGGAGCATGCGGTCATGA 900
Db 993 CATTTATGACACCGGAATCTTCTGCTGGAATTTCTCAGCCAGAGGCTCGAGATCATGA 1052
Qy 901 AGCTGACCTACAGCAAGTCAAGGCTGTTGAAGGCAATTCACGATCGCTTCAAGGCCC 960
Db 1053 AGCTGACCTACAGCAAGTCAAGGCTGTTGAAGGCAATTCACGATTCGCTTCAAGGCCC 1112
Qy 961 CCGATATCTGTTTGGCAAGCGGTCCGCTTACCCACCAACGAGGCTTCTGCGCATGCC 1020
Db 1113 CCGATATCTGTTTGGCAAGCGGTCCGCTTACCCACCACTAATGAAGGCTTCTGCGCGTGC 1172
Qy 1021 GAGAGTCTGCATTGAGATGTGAGACCTGAGGTTTGGTGGCGCTCTGTTTCTCTCCC 1080
Db 1173 GCGAGTCCGCGATTGAGAAATGTGAGACCTGAGGTTTGGTGGCGCGCTGTTTCTCTCCC 1232
Qy 1081 ACCCCCACTTTTACAAACGCGACCTGTTGTGTCAGAAAGTGTCTTGGTCTGAACCTTA 1140
Db 1233 AGCCCCACTTCTACAAATGTGACCCCGTCTGTGTCAGAGCTGTCTTGGTCTGAACCTG 1292
Qy 1141 ACCCAAGGAGCAATCTTGTGTTCTTACAGATCCATCCGCTCACTGGGATCCCATGAAT 1200

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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:45:57 ; Search time 7281.38 Seconds
(without alignments)
11469.657 Million cell updates/sec

Title: US-08-765-108-7

Perfect score: 1785

Sequence: 1 CCGTCTCTTCAGGTCTTGA.....TCAGGGACCGGACAGACC 1785

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_ges1:*

10: gb_ges2:*

11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	2441	4	AK033114 Mus muscu
2	1785	100.0	2497	4	AK028191 Mus muscu
3	1513.8	84.8	2310	4	AK010622 Mus muscu
4	1364	76.4	1364	10	AY412682 Mus muscu
5	959	53.7	2751	4	BC022087 Homo sapi
6	957.4	53.6	2515	4	CR607701 full-leng
7	941.6	52.8	1364	10	AY412680 Homo sapi
8	852.4	47.8	902	5	BUS17714 AGENCOURT
9	821.4	46.0	879	3	BI651436 603298176
10	802.2	44.9	979	5	BQ917716 AGENCOURT
11	802.2	44.9	1364	10	AY412681 full-leng
12	790.8	44.3	907	2	BI218548 602938062
13	763.2	42.8	838	2	BG970988 602792027
14	758.2	42.5	987	3	BI410841 602963757
15	734.4	41.1	883	3	BI854754 603381709
16	732.8	41.1	814	2	BI249128 602992465
17	728.4	40.8	766	3	BI330909 602983203
18	719.8	40.3	802	2	BI159464 602919988
19	716.6	40.1	765	7	CK031774 AGENCOURT
20	708	39.7	792	7	CK128415 AGENCOURT
21	700.2	39.2	837	3	BI872207 603396535
22	693.6	38.9	824	2	BG921302 602824148

23	689.2	38.6	794	3	BI327672	BI327672 602979182
24	683.2	38.3	704	7	CO432282	CO432282 UI-M-HXO-
25	681	38.2	918	5	BQ947347	BQ947347 AGENCOURT
26	670.8	37.6	1088	3	BM553238	BM553238 AGENCOURT
27	656	36.8	842	3	BI663520	BI663520 603287994
28	652.4	36.5	835	2	BF235778	BF235778 602026938
29	651.4	36.5	740	2	BI079037	BI079037 602873305
30	644.8	36.1	830	2	BG519503	BG519503 602577778
31	640.4	35.9	643	1	AI323064	AI323064 mj57c02.y
32	638	35.7	771	1	AI037085	AI037085 ue19b11.y
33	635.6	35.6	909	2	BF533326	BF533326 602073786
34	634.2	35.5	753	2	BI145538	BI145538 602910547
35	630.4	35.3	655	8	CK220978	CK220978 MNS36731
36	627.8	35.2	819	7	CK023231	CK023231 AGENCOURT
37	625.8	35.1	723	2	BG965924	BG965924 602829714
38	623.2	34.9	968	5	BQ877329	BQ877329 AGENCOURT
39	620.4	34.8	728	7	CO425633	CO425633 UI-M-HUO-
40	616.4	34.5	618	7	CF900992	CF900992 A0322E06-
41	616.4	34.5	618	7	CF901018	CF901018 A0322H01-
42	612.4	34.3	636	3	BI328695	BI328695 602984633
43	608.8	34.0	719	3	BI332830	BI332830 602985640
44	604.8	33.9	913	5	BO670423	BO670423 AGENCOURT
45	601.2	33.7	661	2	BF151308	BF151308 uz14f08.y

ALIGNMENTS

RESULT 1	AK033114	AK033114	2441 bp	mus mRNA	linear	HTC 03-APR-2004
LOCUS	AK033114	Mus musculus	15 days embryo	male testis	cDNA, RIKEN full-length	
DEFINITION	AK033114	Mus musculus	15 days embryo	male testis	cDNA, RIKEN full-length	
ACCESSION	AK033114	GI:26328836				
VERSION	AK033114.1	GI:26328836				
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1	Carninci, P. and Hayashizaki, Y.				
AUTHORS	1	Carninci, P. and Hayashizaki, Y.				
TITLE	1	High-efficiency full-length cDNA cloning				
JOURNAL	1	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	1	10349636				
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	2	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	2	11042159				
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Tashiro, H., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Tashiro, H., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	3	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	3	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	3	11076861				
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
AUTHORS	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	4	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	4	Nature 409, 685-690 (2001)				
PUBMED	4	11076861				
REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research				
AUTHORS	5	The FANTOM Consortium and the RIKEN Genome Exploration Research				

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (Bases 1 to 2441)
JOURNAL
REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayate, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-research@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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QY 121 TCGGGCTGTTCATGATCCCTCATGTCCTCCCTCATCAAGCAGCAGGAGTCTCAAGAATG 180
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1261	Qy	GGAAGATCGAGCCAGTAGTTCTGCGCTTGTGTGTGTTGGAACAGAGCGGAGCAATGGGTG	1320
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LOCUS		2497 bp mRNA linear	HTC 03-APR-2004
DEFINITION		Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610205J15 product:scavenger receptor class BI, full insert sequence.	
ACCESSION		AK028191	
VERSION		AK028191.1	GI:26389859
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE		1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
AUTHORS		2	Carninci, P. and Hayashizaki, Y.
TITLE			High-efficiency full-length cDNA cloning
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)
PUBLISHED			10349636
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBLISHED			

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Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

AK010622

LOCUS

DEFINITION

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clone:2410030L01 product:scavenger receptor class B1, full insert
sequence.

ACCESSION

AK010622

VERSION

AK010622.1 GI:12846195

AK010622 2310 bp mRNA linear HTC 03-APR-2004

Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410030L01 product:scavenger receptor class B1, full insert
sequence.

AK010622 2310 bp mRNA linear HTC 03-APR-2004

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clone:2410030L01 product:scavenger receptor class B1, full insert
sequence.

AK010622 2310 bp mRNA linear HTC 03-APR-2004

Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410030L01 product:scavenger receptor class B1, full insert
sequence.


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RESULT 4
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DEFINITION genomic survey sequence.
ACCESSION AY412682
VERSION AY412682.1 GI:39768647
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1364)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1364)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 ATGTGGAAGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTCTGCTGCTACTTCTT 272
Db 1 ATGTGGAAGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTCTGCTGCTACTTCTT 60
Qy 273 CCAAAAGAGTCTCAACGGCCAGAACCCAGTAGTCGGGAGCGTGACCTATGCTAC 332
Db 61 CCAAAAGAGTCTCAACGGCCAGAACCCAGTAGTCGGGAGCGTGACCTATGCTAC 120
Qy 333 AGGAGTTTCAGACAAAGGTCAACATCCTTCAATGACAAACGACCCGTCTCTCGTG 392
Db 121 AGGAGTTTCAGACAAAGGTCAACATCCTTCAATGACAAACGACCCGTCTCTCGTG 180
Qy 393 GAGAACCGCAGCCTCCATTTTCCAGCCTGACAGTCGATGGCTCAGAGAGTACTACATT 452
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181	Db		GAGAACCGCAGCCTCCCATTTCCAGCCTGACAAGTGCAGATGGCTCAGAGAGTGAATCACTT	241
453	Qy		GTACTGCTCTAAACATCTTGGTCTCTGGGGGGCTCGATATTGATGGAGAGCAAGCCTGTGAGC	512
241	Db		GTACTGCTCTAAACATCTTGGTCTCTGGGGGGCTCGATATTGATGGAGAGCAAGCCTGTGAGC	300
513	Qy		CTGAAGCTGATGATGAACCTTGGCGCTGGTCAACCAATGGGCCAGCGTCTTTTATGAACCGC	572
301	Db		CTGAAGCTGATGATGAACCTTGGCGCTGGTCAACCAATGGGCCAGCGTCTTTTATGAACCGC	360
573	Qy		ACAGTTGGTGAGATCCCTGTGGGGCTATGACGATCCCTTCGTGCATTTCTCAACACGTAC	632
361	Db		ACAGTTGGTGAGATCCCTGTGGGGCTATGACGATCCCTTCGTGCATTTCTCAACACGTAC	420
633	Qy		CTCCAGACATGCTTCCCATAAAGGGCAAAATTGGCCCTGTTTGTGGAGTGAACAACTCG	692
421	Db		CTCCAGACATGCTTCCCATAAAGGGCAAAATTGGCCCTGTTTGTGGAGTGAACAACTCG	480
693	Qy		AATTCTGGGCTCTTCACTGCTTTCACGGGCGTCCAGAAATTTACAGAGATCCATCTGGTG	752
481	Db		AATTCTGGGCTCTTCACTGCTTTCACGGGCGTCCAGAAATTTACAGAGATCCATCTGGTG	540
753	Qy		GACAAATGGAACCGACTCAGCAAGATCGATTATTGGCATTTACAGACGAGTGTAAATGATC	812
541	Db		GACAAATGGAACCGACTCAGCAAGATCGATTATTGGCATTTACAGACGAGTGTAAATGATC	600
813	Qy		AATGGGACTTCCGGGCAGATGTGGCACCCCTTCATGACACCCGAATCTCTGCTCGAATTC	872
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873	Qy		TTCAGCCCGGAGGCAATCAGGTCCATGAAGCTGACCTACAAACGAATCAAGGCTGTTGAA	932
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933	Qy		GGCATTCACAGTATCGTTTACGGCCCCCGATACCTCTGTTGGCCACGGGTCCGTCTAC	992
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993	Qy		CCACCCAAAGAGGCTTCTGCCCATGCCAGAGTCTGSCATTCAGAAATGTCAGCACCTGC	1052
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1053	Qy		AGGTTTGGTGCGCTCTGTGTTTCTCTCCACCCCCACTTTTACACGGCCGACCTGTGTG	1112
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1173	Qy		CATCCGCTCACTGGATCCCATGAACTGTTCTGTGAAGATGACGCTGAGCCTCTACATC	1232
961	Db		CATCCGCTCACTGGATCCCATGAACTGTTCTGTGAAGATGACGCTGAGCCTCTACATC	1020
1233	Qy		AAATCTGTCAAGGCGATCGGGCAAAACAGGGAAGATCGAGCCAGTAGTTCCTGCCGTGCTG	1292
1021	Db		AAATCTGTCAAGGCGATCGGGCAAAACAGGGAAGATCGAGCCAGTAGTTCCTGCCGTGCTG	1080
1293	Qy		TGTTTCGAAACAGACGGAGCAATGGGTGGCAAGCCCTGAGCACGTTCTTACACGAGCTG	1352
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1353	Qy		GTGCTGATGCCCAAGGTTCTTCACTACGCGCAGTATGCTGCTGGGGCTTGGAGGCTC	1412
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1413	Qy		CTGTTGCTGTGCTGCCCATCATCTGCCAACTCGCGCAGCAGGAGAATGCTTTTGTGTTGG	1472
1201	Db		CTGTTGCTGTGCTGCCCATCATCTGCCAACTCGCGCAGCAGGAGAATGCTTTTGTGTTGG	1260
1473	Qy		AGTGGTAGTAAAAAGGCTCCACGATAAGGAGGCCATTCAGGCGCTACTCTGAGTCCCTG	1532

Db	1261	ATGTTGTAAGTAAAGGGCTCCAGGATAGAGGCGCAATTCAGGCTTACTTGTAGTCCCTG	1322
Qy	1533	ATGTCACCAAGCTGCCAAGGCGACGGTGTGCAAGAGCCAAAGCT	1576
Db	1321	ATGTCACCAAGCTGCCAAGGCGACGGTGTGCAAGAGCCAAAGCT	1364
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BC022087			
LOCUS			
DEFINITION		2751 bp mRNA linear	HTC 01-APR-2004
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBLISHED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
FEATURES			
source			

ORIGIN	Query Match	Best Local Similarity	Score	957.4	DB 4	Length	2515
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						Gaps	0
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Db	161	GCCCTTGTGAGCCCGGGGTGGGCCCCGAGCGCGCAGACATGGGCTGTCTCCGCAAGGCGCG	220				
Qy	74	CTGGGTGGCCCTTGGGGTGTGGCGCCCTGGGGCTGTCTGTTCGTCTGCGCTGCGCGTGTTCAT	133				
Db	221	CTGGGCTGCGGGCGCTTGGCGGTGTGGGGCTTACTGTGCGCTGTGTGGGCGGTGTTCAT	280				
Qy	134	GATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATGTCCGCATAGACCC	193				
Db	281	GATCGTGATGTGCGGTGCGTCTCATCAAGCAGCAGGTCTTAAAGAACGTGCGCATCGACCC	340				
Qy	194	GAGCAGCTGTCTTTCGGATGTGGAGAGATCCCGTCCCTTCTTACTTGTCTGTCTA	253				
Db	341	CAGTAGCCTGTCTTCAACATGTGGAGGAGATCCCTATCCCTTCTATCTCTCCGCTCA	400				
Qy	254	CTTCTTGGAGTGTGTCAACCAACAGAGGTCTCAAGCGGCAGAGCCAGTAGTCCGGGA	313				
Db	401	CTTCTTGGAGTGTGTCAACCAACAGAGGTCTCAAGCGGCAGAGCCAGTAGTCCGGGA	460				
Qy	314	CGGTGGAGCCCTTATGCTTACAGGAGTTCAGACAAAGGTCAACATCACCTTCAATGACAA	373				
Db	461	GCGGGGCCCTACGTGTACAGGAGTTCAGGCACAAAGCAACATCACCTTCAACACAA	520				
Qy	374	CGACACCGTGTCTTTCGTGGAGAACCGCAGCTCCATTTCCAGCTGACAGTCCGATGG	433				
Db	521	CGACACCGTGTCTTTCGTGGAGAACCGCAGCTCCATTTCCAGCTGACAGTCCGATGG	580				
Qy	434	CTCAGAGAGTGACTTACATTGTACTTGCCTTAACATCTTGGTCTGGGGGGCTCGATTGAT	493				
Db	581	CTCGAGAGCGACTTACATCGTTCATGCCCCAACATCCTGGTCTGGGTGGCGGGTGAATG	640				
Qy	494	GGAGAGCAAGCCTGTGAGCCCTGAAAGCTGATGATGACCTTGGCGCTGTGCACCATGGGCA	553				
Db	641	GGAGAAATAGCCCATGACCTTGAAGCTCATGACCTTGGCATTCACCACTCCGCGGA	700				
Qy	554	CGGTGCTTTTATGAACCGCAGTGTGTGAGATCCTGTGGGGCTATGACGATCCCTTGT	613				
Db	701	ACGTGCTTTCATGAACCGCAGTGTGGGTGAGATCATGTGGGGCTTACAGGACCCCTTGT	760				
Qy	614	GCATTTTCTCAACAGCTTACCTCCAGACATGCTTCCCATTAAGGGCAATTTGGCCTGTT	673				
Db	761	GAATCTCATCAACAAGTACTTTCAGGCGATGTTCCCTTTCAGGACAAAGTTCGGATTAAT	820				
Qy	674	TGTTGGGATGAACAACTCTGAGTCTTGGGCTCTTCACTGTCTTTCAGGGCGTCCAGAAATTT	733				
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Qy	734	CAGCAGGATCCATCTGTGTGGAACAAATGSAACGGAATCAGCAAGATCGATTATTGGCATTC	793				
Db	881	CAGCAGGATCCATCTGTGTGGAACAAATGSAACGGAATCAGCAAGATCGATTATTGGCATTC	940				
Qy	794	AGACAGTGTAAATGATCAATGGGACTTTCGGGCGAGATGTGGGCAATCTTTCATGACAC	853				
Db	941	CGATCAGTGAACATGATCAATGGAATCTTTCGGGCAAAATGTGGCGGCTTTCATGACTCC	1000				
Qy	854	CGAATCCTCGCTGGAATCTTTCAGCCGGGAGCATGCAAGTCCATGAGCTGACCTCAAA	913				
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Qy	974	TGCCAAACGGGTTCGTCTACCCCAAGAAAGGCTTCTGGCCCATGCGGAGAGTCTGGCAT	1033				

Query Match 52.8%; Score 941.6; DB 10; Length 1364;
Best Local Similarity 80.6%; Pred. No. 2.2e-238;
Matches 1100; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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QY 213 ATGTGGAAGGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTCCGAAGTGGTCAAC. 272
DB 1 ATGTGGAAGGAGATCCCTATCCCTTCTATCTCTCTCTACTTCTTCTTGTGAGCTCATGAAC 60

QY 273 CCAAAACGAGGTCCTCAACGGGCCAAGCCAGTAGTCCGGGAGCGTGACACCTATGTCTAC 332
DB 61 CCCAGCGAGATCTTGAAAGGGGGAAGCCGAGTGGGGAGCGCGGCCCTAGGTGTAC 120

QY 333 AGGAGGTTTCAACAAGAGGTCAACATCACCTTTCAATGACACACGACACCGGTGCTTCGTG 392
DB 121 AGGAGTTTCAGGCACAAAGCAACATCACCTTCAACAAACAAAGACACCGTGTCTTCTC 180

QY 393 GAGAACCGCAGCCTTCATTTCCAGCCTGACAAAGTCGATGCTCAGAGAGTGAATCAATT 452
DB 181 GAGTACCGCACCTTCCAGTTCCAGCCTTCCAGTCCCAAGTCCCAAGCCTCGAGAGCGACTAC 240

QY 453 GTACTGTCTAACATCTTGGTCTCTGGGGGCTCGATATTGATGGAGACGACCTGTGAGC 512
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QY 513 CTGAAGCTGATGATGACCTTGGCGCTGGTCAACATGGGCCAGCGTGTCTTTATGAACCGC 572
DB 301 CTGAAGCTCATCATGACCTTGGCATTCACCACTCCCTCGCGGAAGCTGCTTTCATGAACCGC 360

QY 573 ACAGTTGTGAGATCTGTGGGGCTATGACGATCCCTTGTGTGCAATTTCTCAACACGATAC 632
DB 361 ACTGTGGTGTGAGATCATGTGGGGGCTACAAAGGACCCCTTGTGTAATCTCATCAACAAGTAC 420

QY 633 CTCCACAGATGCTTCCCATAAAGGGCAAAATTTGGCCTGTTTGTGGATGAACAACTCG 692
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QY 753 GACAAATGGAACGGAATCAGCAAGATGATTTATTTGGCATTCAGAGCAGTGTAAATGATC 812
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DB 601 AATGGAATCTTGGGCAAAATGTGGCGGCTTCAAGTCTCTGAGTCTCTCGCTGGAGTTC 660

QY 873 TTACGCCGGAGGATGATGAGTCCATGAAGCTGACCTACACGAATCAAGGAGTCAAGGAGTTC 932
DB 661 TACAGCCGGAGGCTGCGGATCCATGAGCTATATGTACAAGGAGTCAAGGAGTCTTTGAA 720

QY 933 GGCATTTCCAGATATGCTTCAACGGCCCCGATATCTCTGTTTGGCAACGGGTCCGTCTAC 992
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QY 1053 AGGTTTGTGGCGCTCTGTTTCTCTCCACCCCACTTTTCAACGGCGACCTGTGTG 1112
DB 841 AGGTTTGTGGCGCTTGTCTCTCCATCTCTCTCCATCTCTCAACGGCGACCTGTGTG 900

QY 1113 TCAGAGCTGTTTGTGTTGATGAAACCTTCAACCAAGGAGGATTCCTTGTTCCTTACATC 1172
DB 901 GCAGAAGCGGTGACTGGGCTTCACCTTCAACCAAGGAGGACACTCTCTTGTTCCTGAGATC 960

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QY 1353 GTCTGATGCGCCAGAGTTCTTCACTACGCGCAGTATGTGTCTGGGGCTTGGAGGCGCTC 1412
DB 1141 GTGTTGATGCCAAGGTGATGCACTATGCCAGTACGTCTCTTGGGCTGGGCTGGGCTC 1200
QY 1413 CTGTTCTGTGTCGCCATCATCTGCCAACTGCGCAGCAGCAGGAGAAATGCTTTTGTGTTGG 1472
DB 1201 CTGCTGTGCTGCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1360
QY 1473 AGTGTAGTAAAGAGGCTCCAGAGTAAGGAGGCTTTCAGGCGCTACTCTGAGTCCCTG 1532
DB 1261 AGTAGTAGTAAAGAGGCTCAAGAGTAAAGAGGCTTTCAGGCGCTTTCAGGCGCTTTCAGT 1320
QY 1533 ATGTCAACGCTGCCAAGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576
DB 1321 ATGACATCAGCTCCCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1364
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RESULT 8
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BUS17714 902 bp mRNA linear EST 12-SEP-2002
AGENCOURT 10165932 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6515330 5', mRNA sequence.

BUS17714
BUS17714.1 GI:22825240
EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 902)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14092 Row: b column: 03

High quality sequence stop: 700.

Location/Qualifiers

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/tissue_type="tumor, biopsy sample"
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/clone_lib="NCI CGAP Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 47.8%; Score 852.4; DB 5; Length 902;
Best Local Similarity 99.7%; Pred. No. 9.5e-215;
Matches 864; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy 600 GAACATCCCTTCGTGCAATTTCTCAACAGTACCTCCAGACATGCTCCCAATAGGGC 659
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Qy 1200 TGTTCGTGAGATGCACTGAGCTCTACATCAATCTGTCAAGGGATC- GGGCAAC 1258
Db 781 TGTTCGTGAGATGCACTGAGCTCTACATCAATCTGTCAAGGGATC- GGGGCAAC 840
Qy 1259 AGGGAAGATCGAGCCAGTGTCTGCCC 1285
Db 841 AGGGAAGATCGAGCCAGTGTCTGCCC 867
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ACCESSION Bi651436
VERSION Bi651436.1 GI:15565672
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 879)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 819.

FEATURES

source

1..879
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

ORIGIN

Query Match 46.0%; Score 821.4; DB 3; Length 879;
Best Local Similarity 98.8%; Pred. No. 1.6e-206;

Matches 870; Conservative 0; Mismatches 6; Indels 5; Gaps 4;

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Qy 952 TCAGGGCCCGGATACCTCTGTTGCCAAGCGGTCCGTCTACCCACCCCAAGGCTTCT 1011
Db 181 TCAGGGCCCGGATACCTCTGTTGCCAAGCGGTCCGTCTACCCACCCCAAGGCTTCT 240
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Qy 1072 TTCTCTCCCAACCCCACTTTTACAAAGCCCAAGCCCTGTGTTGTTCAGAAAGCTGTTCCTGGTC 1131
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Qy 1132 TGRACCCCTACCCAAAGGAGCATTCCTGTTCTTAGACATCCATCCCGTCACTGGGATCC 1191
Db 361 TGRACCCCTACCCAAAGGAGCATTCCTGTTCTTAGACATCCATCCCGTCACTGGGATCC 420
Qy 1192 CCATGAAGTGTCTGTGAAGATGAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCG 1251
Db 421 CCATGAAGTGTCTGTGAAGATGAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCG 480
Qy 1252 GGCAAAACAGGGAAGATCGAGCCAGTAGTCTCGCGTGTGCTGTGTTGTTGTAACAGAGCGAG 1311
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Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1243 row: 1 column: 15
High quality sequence stop: 798.

FEATURES
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/db_xref="taxon:10090"
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/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 44.3%; Score 790.8; DB 2; Length 907;
Best Local Similarity 94.8%; Pred. No. 2.2e-198;
Matches 861; Conservative 0; Mismatches 42; Indels 5; Gaps 4;

Qy 699 GGGGTCTTCACTGTTTACCGGGCGTCCAGAAATTCAGCAGATCCATCTGGTGACAAA 758
Db 1 GGGGTCTTCACTGTTTACCGGGCGTCCAGAAATTCAGCAGATCCATCTGGTGACAAA 60
Qy 759 TGGACCGGACTCAGCAGATCGATATTGGCAATTCAGACGAGTGAATCAATCAATGGG 818
Db 61 TGGACCGGACTCAGCAGATCGATATTGGCAATTCAGACGAGTGAATCAATCAATGGG 120
Qy 819 ACTTCCGGGAGATGTGGGACCTTCATGACACCGCAATCTCTCGTGGAAATCTTCAGC 878
Db 121 ACTTCCGGGAGATGTGGGACCTTCATGACACCGCAATCTCTCGTGGAAATCTTCAGC 180
Qy 879 CCGAGGCGATCAGGTCCATGAAGTCACTCAACGAATCAAGGGTGTGTTGAAGGCATT 938
Db 181 CCGAGGCGATCAGGTCCATGAAGTCACTCAACGAATCAAGGGTGTGTTGAAGGCATT 240
Qy 939 CCCAGTATCGTTACGGCCCCCGATCTCTGTTGGCAACGGGTGCGTACCCACCC 998
Db 241 CCCAGTATCGTTACGGCCCCCGATCTCTGTTGGCAACGGGTGCGTACCCACCC 300
Qy 999 AACGAAGGCTTCTGCCATCGCGAGAGTCTGGCAATTCAGATGTCAGCACCCTGAGGTTT 1058
Db 301 AACGAAGGCTTCTGCCATCGCGAGAGTCTGGCAATTCAGATGTCAGCACCCTGAGGTTT 360
Qy 1059 GGTGGCCTCTGTTTCTCTCCACCCCACTTTTACACGCGGACCCCTGTGTTTCAGAA 1118
Db 361 GGTGGCCTCTGTTTCTCTCCACCCCACTTTTACACGCGGACCCCTGTGTTTCAGAA 420
Qy 1119 GCTGTTCTGTGTGAACCCCTAACCCAAAGGAGCATTCCTTGTTCCTAGACATCCATCCG 1178
Db 421 GCTGTTCTGTGTGAACCCCTAACCCAAAGGAGCATTCCTTGTTCCTAGACATCCATCCG 480
Qy 1179 GTCACTGGATCCCATGAATCTGTTGTGAAGATGCGAGCTGAGCCTCTACATCAAAATCT 1238
Db 481 GTCACTGGATCCCATGAATCTGTTGTGAAGATGCGAGCTGAGCCTCTACATCAAAATCT 540
Qy 1239 GTCAAGGCGATCGGGCAACAGGGAAGATCGAGCCAGTAGTTCCTGCCGTGCTGTGGTTC 1298
Db 541 GTCAAGGCGATCGGGCAACAGGGAAGATCGAGCCAGTAGTTCCTGCCGTGCTGTGGTTC 600
Qy 1299 GAAACAGCGGAGCATGGGTGGGAGCCCTTGAGCAGGTTCTACACGCGAGCTGGTGTG 1358
Db 601 GAAACAGCGGAGCATGGGTGGGAGCCCTTGAGCAGGTTCTACACGCGAGCTGGTGTG 660

Qy 1359 ATG-CCCCAGGTTCTTCACTACCGCAGTATGTGCTGGGGCTTGGAGCCTCCTGTT 1417
Db 661 ATGCCCCAGGTTCTTCACTACCGCAGTATGTGCTGGGGCTTGGAGCCTCCTGTT 720
Qy 1418 GCTGGTGCCCATCATCTGCCAACTGCGCAGCAGGAGAAATGCTTTTGTGGAGTGG 1477
Db 721 TGCTGGTGCCCATCATCTG-CAACTGGCGCAGCAGGAGAAATGCTTTTGTGGAGTGG 779
Qy 1478 TA--GTAAAGAGGCTCCAGAGTAAGAGGCGCATTCAGGCTACTCTGAGTCCCTGATG 1535
Db 780 TACGTGAAAAGAGGCTCCAGAGTAAGAGGCGCATTCAGGCTACTCTGAGTCCCTGTTG 839
Qy 1536 TCACCACTGCTCCCAAGGCGCAGGCTGCTGCAAGAGCAAGCTATAGGCTCTCGAAGACACT 1595
Db 840 TCCAGTTGCAAGGGCGCGGTGGTCCCAAGAGCAGGTATAGGG-CTTGAAGACACT 898
Qy 1596 ATAAAGCCC 1603
Db 899 TTAGCCCC 906

RESULT 13
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LOCUS
DEFINITION
602792027F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923247 5', mRNA sequence.
ACCESSION
BG870988
VERSION
BG870988.1 GI:14221528
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 838)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10844 row: e column: 08
High quality sequence stop: 829.

FEATURES
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1. 838
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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/lab_host="DH10B (TI phage-resistant)"
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/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 42.8%; Score 763.2; DB 2; Length 838;
Best Local Similarity 97.2%; Pred. No. 4.6e-191;
Matches 819; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

Qy 614 GCATTTTCTCAACACGTTACCTCCAGACATGCTTCCCATTAAGGCAAAATTTGSCCTGTT 673
Db 1 GCATTTTCTCAACACGTTACCTCCAGACATGCTTCCCATTAAGGCAAAATTT--GGCTGT 58
Qy 674 TGTGGGATGAACAACACTCGAATTTCTGGGGTCTTCACTGTCTTCAAGGGCGTCCAGAAATTT 733


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Db 481 GTCACTGGGATCCCATGAACCTGTTCTGTGAAGATGCAGCTGAGCCTCTACATCAAAATC 540
Qy TGTCAAGGGCATCGGCAAAACAGAGGATGATCAGCCAGTAGTGTCTGCGGTGCTGTGCTT 1297
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Qy CGAACAGAGCGGAGCAATGGGTGGCAAGCCCTGAGCACGTTCTACACGAGCTGTGTGCT 1357
Db CGAACAGAGCGGAGCAATGGGTGGCAAGCCCTGAGCACGTTCTACACGAGCTGTGTGCT 660
Qy GATG-CGCCAGTGTCTTCACTACGCGGAGTATGTCTGTGCGGCTTGGAGCCCTCTCTGT 1416
Db GATGCCCCAGTGTCTTCACTACGCGGAGTATGTCTGTGCGGCTTGGAGCCCTCTCTGT 720
Qy TGCTGTGTCCTCATCTGCGC-RACTGCGAGCCAGGAGAAATGCTTTTGTGTTGGAGT 1475
Db TGCTGTGTCCTCATCTGCGC-RACTGCGAGCCAGGAGAAATGCTTTTGTGTTGGAGT 780
Qy GGTAGTAAAGAGGCTCCAGGATAAGAGGCCATTTCAGGCGCTA---CTCTGAGTCCCTG 1532
Db GGTAGTAAAGAGGCTCCAGGATAAGAGGCCATTTCAGGCGCTA---CTCTGAGTCCCTG 838
Qy ATGTCACAGCTGTCAGAGGCGACCGGTGCTGCAAGAACCAAGTATAGGCTCTTGAAGAC 1592
Db ATGTCACAGCTGTCAGAGGCGACCGGTGCTGCAAGAACCAAGTATAGGCTCTTGAAGAC 898
Qy ACTATAGCCCCCAAACTGATAGCTTGTGTCAGACGACCCAGTCCCTACACCCCG 1652
Db AACCTATAGCCCCCAAACTGATAGCTTGTGTCAGACGACCCAGTCCCTACACCCCG 958
Qy CTTCTTGA 1660
Db CTTGAGGA 966
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RESULT 15

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DEFINITION mRNA sequence.
ACCESSION BI854754
VERSION BI854754.1 GI:15995501
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11987
High quality sequence stop: 775.
Location/Qualifiers
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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FEATURES

source

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Query: Match 41.1%; Score 734.4; DB 3; Length 883;
Best Local Similarity 96.1%; Pred. No. 2.1e-183;
Matches 786; Conservative 0; Mismatches 26; Indels 6; Gaps 3;
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ORIGIN
Query: Match 41.1%; Score 734.4; DB 3; Length 883;
Best Local Similarity 96.1%; Pred. No. 2.1e-183;
Matches 786; Conservative 0; Mismatches 26; Indels 6; Gaps 3;
Qy 1 CCGTCTCTTTCCAGTCTCTGAGCCCGGAGAGCCCTTCCGCGCACGCGGACATGGCGGCA 60
Db 65 CCGTCTCTTTCCAGTCTCTGAGCCCGGAGAGCCCTTCCGCGCACGCGGACATGGCGGCA 124
Qy 61 GCTTCAGAGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCGCCCTTGGGGCTGTCTTGTCTGCGC 120
Db 125 GCTTCAGAGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCGCCCTTGGGGCTGTCTTGTCTGCGC 184
Qy 121 TCGGCGTTGTCATGATCCCTCATGTCCTCCCTCATCAAGCAGCAGGTCTCAAGAATG 180
Db 185 TCGGCGTTGTCATGATCCCTCATGTCCTCCCTCATCAAGCAGCAGGTCTCAAGAATG 244
Qy 181 TCGGCGATAGACCCGAGCAGCCTGTCTCTTCGGGATGTGGAAGAGATCCCGTCCCTTTCT 240
Db 245 TCGGCGATAGACCCGAGCAGCCTGTCTCTTCGGGATGTGGAAGAGATCCCGTCCCTTTCT 304,
Qy 241 ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 300
Db 305 ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 364
Qy 301 CAGTAGTCCGGGAGCGTGGACCCCTATGTCTACAGGAGGTTTCAGACAAAGGTCAACATCA 360
Db 365 CAGTAGTCCGGGAGCGTGGACCCCTATGTCTACAGGAGGTTTCAGACAAAGGTCAACATCA 424
Qy 361 CTTTCAATGACAAACGACACCGCTGTCTCTTCGTGGAGAACCCGAGCCTCCATTTCCAGCCTG 420
Db 425 CTTTCAATGACAAACGACACCGCTGTCTCTTCGTGGAGAACCCGAGCCTCCATTTCCAGCCTG 484
Qy 421 ACAAGTCGATGCTCAGAGAGTGATACATTTGTACTGTGCCTAAACATCTTGTGCTCTGGGG 480
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Qy 481 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCCTGTGAGCTGATGATGATGATGATGATGAT 540
Db 545 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCCTGTGAGCTGATGATGATGATGATGATGAT 604
Qy 541 TCACCATGGGCCAGCGTGTCTTTTATGAACCG-CACAGTTGGTGAGATCTCTGTGGGGCTAT 599
Db 605 TCACCATGGGCCAGCGTGTCTTTTATGAACCCGACACAGTTGGTGAGATCTCTGTGGGGCTAT 664
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Db 725 AAATTTGGCCTGTGTGTTGGGATGAACTCGAATTTCTGGGGTCTTCACTGTCTTTCAC 784
Qy 717 ACGGGCGCTCCAGAAATTTTCAGCAGGATCCATCTGTGTGACAAATGGAACGGAC--TCAGCA 774
Db 785 CGGGCGTCCCAAAATTTTCAGCAGGAAACCATCTGTGGGCCCAATGGACGGGCTCCGCA 844
Qy 775 AGATCGAATATTGCGCATTCAGAGCAGGTGAACATGATC 812
Db 845 AAATCGAATATTGCGCTTCCAGAGCAGGTGTACTGGATC 882
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Search completed: February 24, 2006, 02:49:16

Job time : 7283.38 Secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Total number of hits satisfying chosen parameters: 2606114
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1785	100.0	1785	3	US-09-241-581B-7
4	1785	100.0	1785	3	US-09-385-799-3
5	1785	100.0	1785	6	PCT-US95-07721-7
6	1396.2	78.2	1825	2	US-08-890-980-3
7	1396.2	78.2	1825	3	US-08-890-979-3
8	1396.2	78.2	1825	3	US-09-032-894-3
9	1396.2	78.2	1825	3	US-09-031-626-3
10	1389.8	76.7	1788	2	US-08-559-505-1
11	1389.8	76.7	1788	2	US-08-749-907-1
12	1369.8	76.7	1788	3	US-09-241-581B-3
13	1369.8	76.7	1788	3	US-08-265-428-3
14	1369.8	76.7	1788	3	US-09-385-799-1
15	1369.8	76.7	1788	6	PCT-US95-07721-3
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19	1142.6	64.0	2630	3	US-09-031-626-1
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21	1141	63.9	2566	3	US-09-054-272-58
22	1141	63.9	2566	3	US-10-024-396-3
23	956.6	53.6	2595	3	US-09-949-016-2296
24	263.6	14.8	719	3	US-10-024-396-11

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Sequence 14038, A
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Sequence 2451, Ap
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Sequence 16, Appl
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Sequence 16, Appl
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Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-559-505-3
; Sequence 3, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; OTHER INFORMATION: encode the amino acid sequence for the murine Scavenger Recept

US-08-559-505-3

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Query Match      100.0%; Score 1785; DB 2; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CCGTCTCTTCCAGTCTCTGAGCCCGGAGAGCCCTTCCGCGCAGCGGACATGGGGGCA 60
QY 61 GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGGCGCCCTGAGGCTGCTGTTTCTGCGC 120
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DB 1741 ATGCCACAGCATGTGCAAAACAACTCAGGGACCGGAGACAGCC 1785
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RESULT 2

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US-08-749-907-3
; Sequence 3, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/749,907
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577
OTHER INFORMATION: /Function = "Nucleotides 51 through 1577"
OTHER INFORMATION: encode the amino acid sequence for the murine Scavenger Recept
US-08-749-907-3

Query Match 100.0%; Score 1785; DB.2; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGCTCTCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGCGACGCGGACATGGCGGCA	60
Db	1	CCGCTCTCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGCGACGCGGACATGGCGGCA	60
Qy	61	GCTCCAGGCGCGCTGGGTGCGCTTGGGGTTGGGCGCCCTGGGCTGCTGTTCTGCGC	120
Db	61	GCTCCAGGCGCGCTGGGTGCGCTTGGGGTTGGGCGCCCTGGGCTGCTGTTCTGCGC	120
Qy	121	TCGGCGTGTGATCATCTCTGAGTGTGCTTCCCTCATCAAGCAGCAGGTGCTCAAGATG	180
Db	121	TCGGCGTGTGATCATCTCTGAGTGTGCTTCCCTCATCAAGCAGCAGGTGCTCAAGATG	180
Qy	181	TCCGATAGACCGGAGCGCTGCTTCCGAGTGTGGAAGAGATCCCGTCCCTTTCT	240
Db	181	TCCGATAGACCGGAGCGCTGCTTCCGAGTGTGGAAGAGATCCCGTCCCTTTCT	240
Qy	241	ACTTGTCTGTCTACTTCTTGAAGTGTGTCACCCAAACGAGGTCTCAACGCGCAGAAC	300
Db	241	ACTTGTCTGTCTACTTCTTGAAGTGTGTCACCCAAACGAGGTCTCAACGCGCAGAAC	300
Qy	301	CAGTAGTCCGGAGCGTGAGCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA	360
Db	301	CAGTAGTCCGGAGCGTGAGCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA	360
Qy	361	CTTCAATGACACGACACCGCTGCTTGGGAGAACCGCAGCCTCCATTTCCAGCCTG	420
Db	361	CTTCAATGACACGACACCGCTGCTTGGGAGAACCGCAGCCTCCATTTCCAGCCTG	420
Qy	421	ACAAGTCCGATGGCTCAGAGAGTGAATACATTTGACTGCCTTAAACATTTGGTCTCGGGG	480
Db	421	ACAAGTCCGATGGCTCAGAGAGTGAATACATTTGACTGCCTTAAACATTTGGTCTCGGGG	480
Qy	481	GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGATGATGATG	540
Db	481	GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGATGATGATG	540
Qy	541	TCACCATGGGCGCGCTTTTATGACCGCAGTTGGTGAGATCCTGTGGGCGCTATG	600
Db	541	TCACCATGGGCGCGCTTTTATGACCGCAGTTGGTGAGATCCTGTGGGCGCTATG	600

Qy	601	ACGATCCCTTCGTGCATTTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGCA	660
Db	601	ACGATCCCTTCGTGCATTTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGCA	660
Qy	661	AATTTGGCGCTGTTTGTGGGATGAACAACCTCGAATCTGGGGTCTTCACTGTCTTCAAG	720
Db	661	AATTTGGCGCTGTTTGTGGGATGAACAACCTCGAATCTGGGGTCTTCACTGTCTTCAAG	720
Qy	721	CGCTCCAGAAATTTTCAGCAGGATCCATCTGCTGGAACAAATGGAACGACTCAGCAAGATCG	780
Db	721	CGCTCCAGAAATTTTCAGCAGGATCCATCTGCTGGAACAAATGGAACGACTCAGCAAGATCG	780
Qy	781	ATTATTGGCAATTCAGAGCAGTGAACATGATCAATGGGACTTCCGGGAGATGTGGGAC	840
Db	781	ATTATTGGCAATTCAGAGCAGTGAACATGATCAATGGGACTTCCGGGAGATGTGGGAC	840
Qy	841	CCTTCATGACACCGCAATCTCGCTGGAATTTCTCAGCCCGGAGGATGAGGTCATGA	900
Db	841	CCTTCATGACACCGCAATCTCGCTGGAATTTCTCAGCCCGGAGGATGAGGTCATGA	900
Qy	901	AGCTGACCTTCAACGAATCAAGGCTGTTGAAGGCAATTCACGATCGCTTCAACGCGCC	960
Db	901	AGCTGACCTTCAACGAATCAAGGCTGTTGAAGGCAATTCACGATCGCTTCAACGCGCC	960
Qy	961	CCGATCTCTGTTTGCACCGGCTCGTCTACCCACCAACGAGGCTTTCGCCATGCC	1020
Db	961	CCGATCTCTGTTTGCACCGGCTCGTCTACCCACCAACGAGGCTTTCGCCATGCC	1020
Qy	1021	GAGAGTCTGGCAATTCAGAAATGTCAGACCTTGCAGGTTTGGTGGGCTCTGTTCCTCCC	1080
Db	1021	GAGAGTCTGGCAATTCAGAAATGTCAGACCTTGCAGGTTTGGTGGGCTCTGTTCCTCCC	1080
Qy	1081	ACCCCACTTTTACACCGCGACCTGTGTGTGTCAGAAAGTGTTCCTGGTCTGAACCTTA	1140
Db	1081	ACCCCACTTTTACACCGCGACCTGTGTGTGTCAGAAAGTGTTCCTGGTCTGAACCTTA	1140
Qy	1141	ACCCAAAGAGCAATTCCTTGTCTGAGACATCAATCCGCTCACTGGGATCCCATGAAC	1200
Db	1141	ACCCAAAGAGCAATTCCTTGTCTGAGACATCAATCCGCTCACTGGGATCCCATGAAC	1200
Qy	1201	GTTCGTGAGATGACGCTGAGCTCTACATCAAACTGTCAAGGCGATCGGCAACAG	1260
Db	1201	GTTCGTGAGATGACGCTGAGCTCTACATCAAACTGTCAAGGCGATCGGCAACAG	1260
Qy	1261	GGAAGATCGAGCAGTAGTTCTGCGGTGTGTGTCGAAACAGAGCGAGCAATGGGTG	1320
Db	1261	GGAAGATCGAGCAGTAGTTCTGCGGTGTGTGTCGAAACAGAGCGAGCAATGGGTG	1320
Qy	1321	GCAAGCCCTTGACACGCTTCTACACGAGCTGGTGTGATGCCCCAGGTTCTTCACTACG	1380
Db	1321	GCAAGCCCTTGACACGCTTCTACACGAGCTGGTGTGATGCCCCAGGTTCTTCACTACG	1380
Qy	1381	CGCAGTATGTGCTGGGGCTTGGAGGCTCTGTGTGCTGGTGGCCCATCATCTGCCAAC	1440
Db	1381	CGCAGTATGTGCTGGGGCTTGGAGGCTCTGTGTGCTGGTGGCCCATCATCTGCCAAC	1440
Qy	1441	TGCGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGAGGCTCCCAAGATA	1500
Db	1441	TGCGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGAGGCTCCCAAGATA	1500
Qy	1501	AGGAGGCAATTCAGGCTCTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCGACGCTG	1560
Db	1501	AGGAGGCAATTCAGGCTCTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCGACGCTG	1560
Qy	1561	TGCAAGAGCCAGCTATAGGCTCTGAGACACTATAAGCCCGCCCAAACTGATAGCTT	1620
Db	1561	TGCAAGAGCCAGCTATAGGCTCTGAGACACTATAAGCCCGCCCAAACTGATAGCTT	1620
Qy	1621	GCTCAGACAGCAGCAGCTCCCTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAG	1680
Db	1621	GCTCAGACAGCAGCAGCTCCCTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAG	1680
Qy	1681	CCACAGTGCATGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGCGCACATGG	1740

Db 1681 CCACAGTGCAGTGGCTGAGCCGCCAGATGTACACCTGTCCGACGACGACATGG 1740
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Db 1741 ATGCCACGATGTGCAAAACAACTCAGGACGACGACGAC 1785
RESULT 3
US-09-241-581B-7
; Sequence 7, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241.581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through
; -1577 encode the amino acid sequence
; for the murine Scavenger Receptor
; Class BI."
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-241-581B-7
Query Match 100.0%; Score 1785; DB 3; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGGTCTCTTCAGGTCTGTAGCCCGGAGAGCCCTTCGGGCGACGCGGACATGGGGCGCA 60
Qy 61 GCTCCAGGCGCGTGGGTGGCTTGGGCGCCCTGGGCGCTGCTGTTGCTGCGC 120
Db 61 GCTCCAGGCGCGTGGGTGGCTTGGGCGCCCTGGGCGCTGCTGTTGCTGCGC 120
Qy 121 TCGCGTGTGATGATCCTCATGTGTCCTCCCTCATCAAGCAGAGGTCTCAAGAAATG 180
Db 121 TCGCGTGTGATGATCCTCATGTGTCCTCCCTCATCAAGCAGAGGTCTCAAGAAATG 180

Db 121 TCGCGTGTGATGATCCTCATGTGTCCTCCCTCATCAAGCAGAGGTCTCAAGAAATG 180
Qy 181 TCAGCATAGACCCGAGAGCCCTGTCTTCGGATGTGGAGAGAGATCCCGTCCCTTTCT 240
Db 181 TCAGCATAGACCCGAGAGCCCTGTCTTCGGATGTGGAGAGAGATCCCGTCCCTTTCT 240
Qy 241 ACTTGTCTGTCTACTTCTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGGCCAGAAC 300
Db 241 ACTTGTCTGTCTACTTCTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGGCCAGAAC 300
Qy 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Qy 361 CCTTCAATGACAAACGACACCGGTCTTCGAGAACCCGAGCCTCCATTTCCAGCCTG 420
Db 361 CCTTCAATGACAAACGACACCGGTCTTCGAGAACCCGAGCCTCCATTTCCAGCCTG 420
Qy 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCTTAACATCTTGGTCTCTGGGG 480
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Qy 481 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCTGAAGCTGATGATGATGATGATGATG 540
Db 481 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCTGAAGCTGATGATGATGATGATGATG 540
Qy 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTTCGTGTGAGATCCTGTGGGGTATG 600
Db 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTTCGTGTGAGATCCTGTGGGGTATG 600
Qy 601 AGCATCCCTTCGTGCAATTTTCTCAACACGTAACCTCCAGACATGCTTCCCATAAAGGGCA 660
Db 601 AGCATCCCTTCGTGCAATTTTCTCAACACGTAACCTCCAGACATGCTTCCCATAAAGGGCA 660
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Db 721 GGTCCAGAAATTCAGCAGGATCCATCTGTGTGACAAATGGAACGGACTCAGCAAGATCG 780
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Db 841 CTTTCATGACACCCGAAATCCTGTGGAATTTCTAGCCCGGAGGATGAGAGTCCATGA 900
Qy 901 AGCTGACCTACACGAAATCAAGGGTGTGGAAGGCAATCCACGATATCGCTTCAACGGCCC 960
Db 901 AGCTGACCTACACGAAATCAAGGGTGTGGAAGGCAATCCACGATATCGCTTCAACGGCCC 960
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Db 961 CCGATACTCTGTTTGCACACGGGTCCGTCTACCCACCCCAACGAGGCTTCTGCCCCATGCC 1020
Qy 1021 GAGAGTCTGGCATTCAGAAATGTCAGCACTGAGGTTTGGTGGCCCTCTGTGTTCTCTCCC 1080
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Db 1141 ACCCAAGGAGCATTCCTTGTCTTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1200
Qy 1201 GTTCTGTGAAGTGCAGTGCCTCTACATCAATCAATCTGTCAAGGGATCGGCAACAG 1260
Db 1201 GTTCTGTGAAGTGCAGTGCCTCTACATCAATCAATCTGTCAAGGGATCGGCAACAG 1260


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QY 781 ATTATTGGCAATCAGACAGTGTAAACATGATCAATGGAGCTTCGGGCGAGATGTGGGCAC 840
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QY 1021 GAGAGTCTGCAATCAGAAATGTCAGCACTGAGGTTTGTGGGCTCTGTCTCTCTCCC 1080
DB 1021 GAGAGTCTGCAATCAGAAATGTCAGCACTGAGGTTTGTGGGCTCTGTCTCTCTCCC 1080
QY 1081 ACCCCCACTTTTACAACGCGACCTGTGTTGTGAGAGCTGTTCTTGGTCTGAACCCCTA 1140
DB 1081 ACCCCCACTTTTACAACGCGACCTGTGTTGTGAGAGCTGTTCTTGGTCTGAACCCCTA 1140
QY 1141 ACCCAAAGGAGCAATCTCTGTTCTAGACATCCATCCGCTCACTGGGATCCCCATGAAC 1200
DB 1141 ACCCAAAGGAGCAATCTCTGTTCTAGACATCCATCCGCTCACTGGGATCCCCATGAAC 1200
QY 1201 GTTCTGTGAAGTGAAGTGAAGTCTTACATCAAAATCTGTAAGGGGATCGGGAAACAG 1260
DB 1201 GTTCTGTGAAGTGAAGTGAAGTCTTACATCAAAATCTGTAAGGGGATCGGGAAACAG 1260
QY 1261 GGAAGATCGAGCAGATGTTCTGCGTGTGTTGTTGTAACAGAGCGAGCAATGGGTG 1320
DB 1261 GGAAGATCGAGCAGATGTTCTGCGTGTGTTGTTGTAACAGAGCGAGCAATGGGTG 1320
QY 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGATGCCCCAGGTTCTTCACTACG 1380
DB 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGATGCCCCAGGTTCTTCACTACG 1380
QY 1381 GCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1440
DB 1381 GCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1440
QY 1441 TGGCAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
DB 1441 TGGCAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
QY 1501 AGGAGGCCATTACGGCTTACTCTGAGTCCCTGATGTCAACAGCTGCCCAGGGCAGCGTGC 1560
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QY 1561 TGCAGAGCAGCAGTATAGGGTCTGAAGACATATAAGCCGCCCCAAAACCTGATAGCTT 1620
DB 1561 TGCAGAGCAGCAGTATAGGGTCTGAAGACATATAAGCCGCCCCAAAACCTGATAGCTT 1620
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DB 1621 GGTTCAGACAGCCAGCCAGTCCCTACACCGGCTTCTTGGAGTCTCTCAGCGGACAGC 1680
QY 1681 CCACAGTGCATGGCTGAGCCGCCAGATGTACACCTGTGCGCAGCAGCGCACATGG 1740
DB 1681 CCACAGTGCATGGCTGAGCCGCCAGATGTACACCTGTGCGCAGCAGCGCACATGG 1740
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RESULT 5

PCT-US95-07721-7

; Sequence 7, Application PC/TUS9507721

; GENERAL INFORMATION:

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APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577
OTHER INFORMATION: /Function = "Nucleotides 51 through
OTHER INFORMATION: 1577 encode the amino acid sequence
OTHER INFORMATION: for the murine Scavenger Receptor
OTHER INFORMATION: Class BI."
PCT-US95-07721-7
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Query Match 100.0%; Score 1785; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 121 TCGGCGTTGTATGATCTCTATGTCCTTCCCTCTCATCAGCAGCAGGTGCTCAAGATG 180
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DB 241 ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCCTCAACGCGCAGAGC 300
QY 301 CAGTAGTCCGGGAGCGTGGACCCCTATGTCTACAGGGAGTTTCAGACAAAGGTTCAACATCA 360
DB 301 CAGTAGTCCGGGAGCGTGGACCCCTATGTCTACAGGGAGTTTCAGACAAAGGTTCAACATCA 360
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Db 110 CCCCTTCAGTCCCTGAGCCCGGAGCCCGGCGGCACACGCGGACATGCGGCGGACGCG 169
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Db 170 CAGGGCGGCTGGGTGGCTTGGGTTGGGGCGCCCTGGGGCTGCTGTTGCTCGCTCGG 229
QY 125 CGTGTGTCATGATCCTCATGCTGCGCTCCCTCATCAGCAGCAGGTGCTCAAGAATGTCG 184
Db 230 TGTGTTATGATCCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289
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Db 290 CATAGACCCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
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Db 350 GTCCGCTACTTCTTGAAGTGTCAACCAAGAGGTCTCAACGCGCAGAGCCAGT 409
QY 305 AGTCCGGGAGCGTGGACCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACCTT 364
Db 410 AGTCCGGGAGCGTGGACCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACCTT 469
QY 365 CAATGACACGACACCGTGTCTTGGGAGAACCGCAGCCTCAATTCAGCCTGACAA 424
Db 470 CAATGACAAATGATCTGTGCTTGTGGAGCACCGCAGCCTCAATTCAGCCTGACAA 529
QY 425 GTCCGATGCTCAGAGAGTCACTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACCTT 484
Db 530 GTCCGATGCTCAGAGAGTCACTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACCTT 589
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QY 1085 CCACTTTTACAGCCGACCTGTTGTTGTCAGAAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1144
Db 1190 TCACCTTCTACAAATGACAGACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1249

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Db 1370 GATCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
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QY 1505 GGCATTTCAGGCTACTCTGAGTCCCTGATGTCACAGCTGCCAGGCAACGGTGTCTGCA 1564
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QY 1625 AGACGACCAAGCTGCTTACACCCGCTTCTGAGGACTCTCTCAGCGGACAGCCAC 1684
Db 1730 AGACGACCAAGCTGCTTACACCCGCTTCTGAGGACTCTCTCAGCGGACAGCCAC 1789
QY 1685 CAGTGCATGGCTGAGCCCCCAGATGTCACACCTGT 1721
Db 1790 CAGTGCATGGCTGAG-CCCCAGATGTCACACCTGT 1825

RESULT 7

US-08-890-979-3
; Sequence 3, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 156..1682
US-08-080-979-3

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Query Match 78.2%; Score 1396.2; DB 3; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1;

5	CTCCTTCAGGTCCTGAGCCCGCAGAGCCCTTTCGGCGACACGCGGACATGGGCGGCGAGTC	64
110	CCGCTTCAGTCCCTTGAGCCCGCGAGCCCGCGCGCAACACGCGACATGGCGGCGAGCGC	169
65	CAGGGCGCGCTGGGTGCGCTTTGGGGTTGGGGCCCTGGGGCTGCTGTTTGTCTGGCTCGG	124
170	CAGGGCGCGCTGGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGCTGTGCTCGG	229
125	CGTTGTCAATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCCG	184
230	TGTGGTTATGATCCTCGTATGCCCTCGCTCATCAACAGCAGGTACTGAAGAAATGTCG	289
185	CATAGACCCGACGACGCTGTCTTCGGGATGTGGAAGAGATCCCGTCCCTTTCATCTT	244
290	CATAGACCCGACGACGCTGTCTTTGCAATTTGGAAGGAGATCCCTGTACCTTCTACTT	349
245	GTCTGTCTACTCTTTCGAAGTGGTCAACCCAAACGAGTCTCTCAACGCCACAGACCAGT	304
350	GTCCGICTACTTCTTCGAGGTGGTCAATCCACGCGAGATCCTAAAGGTGAGAACCCAGT	409
305	AGTCCGGAGCGTGGACCCCTATGTCTACAGGGAGTTCAGACAAAGGTCAAATCACCTT	364
410	AGTCCGGAGCGTGGACCCCTATGTCTACAGGGAATTCAGACATAAGGGCCAAATCACCTT	469
365	CAATGACAAACGACACCGGTGCTTCGTGGAGAACCGGACCTCCATTTCCAGCCCTGACAA	424
470	CAATGACAAATGATCTGTGCTCTTTGGAGACACCGCAGCCTCCATTTCCAGCCCGACAG	529
425	GTCCGATGGCTCAGAGAGTGACTACATTTGTACTGCCTAAACATCTTTGGTCTGGGGGGCTC	484
530	GTCCACGGCTCTGAGAGTGACTACATTTATCTGCTTAACATTTCTGGTCTTTGGGGGGCGC	589
485	GATATTGATGGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGACCTTTGGCGCTGGTCAAC	544
590	AGTAATGATGGAGAGCAAGTCTGCAGGCGCTGAAGCTGATGATGACCTTTGGGCGCTGGCCAC	649
545	CATGGGCCAGCTGCTTTTATGAACCGCACAGTTTGGTGAGATCCTGTGGGGCTATGACGA	604
650	CTTGGGCCAGCGTCCCTTATGAACCCGAAAGTTGGTGAGATCCTGTGGGGCTATGAGGA	709
605	TCCCTTCGTGCATTTTCTCAACAGTACTCCACAGCATGCTTCCCATAAAGGGGCAATTT	664
710	TCCCTTCGTGAAATTTTATCAACAAATACTTACACAGCATGTTTCCCATCAAGGGCAAGTT	769
665	TGGCGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAACGGCGGT	724
770	CGGCGCTGTTTGTGAGATGAACAACTCAGACTCTTGGGCTCTTCACTGTGTTTCAAGGGCGGT	829
725	CCAGAATTTCAGCAGGATCCATCTGGTGGACAAATGGAAACGGACTCAGCAAGATCGATTA	784
830	CCAGAACTTCAGCAAGATCCACTGGTGGACAGATGGNAATGGGCTCAGCAAGGTCAACTA	889
785	TTGGCAATTCAGACAGTGTAAATCATGATCAATGGGACTTCCGGGCGAGATGTGGGCAACCTTT	844
890	CTGGCAATTCAGACAGTGTAAATCATGATCAATGGCAATTTCCGGGCGAGATGTGGGCAACCTTT	949

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; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)
US-09-032-894-3

Query Match      78.2%; Score 1396.2; DB 3; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

Qy 5 CTCCTTCAGGTCTGAGCCCGAGAGCCCTTCGCGCAGCGGACATGCGGCGGAGCTC 64
Db 110 CCCCTTCAGTCCCTGAGCCCGAGCCCGGCGCGCACAGCGGACATGCGGCGGAGCGC 169

Qy 65 CAGGCGCGCTGGGTGGGCTTGGGGTGGGGCCCTGGGGCTGCTGTTGCTGGGCTCGG 124
Db 170 CAGGCGCGCTGGGTGGGCTTGGGGTGGGGCTGGGGCTGCTGTTGCTGGGCTCGG 229

Qy 125 CGTTGTGATGATCTCATGTGTCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCG 184
Db 230 TGTGTTATGATCTCTGATGCTGCTGCTCATCAAGCAGCAGGTGCTCAAGAAATGTCG 289

Qy 185 CATAGACCCGAGCAGCTGCTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTTACTT 244
Db 290 CATAGACCCGAGCAGCTGCTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTTACTT 349

Qy 245 GTCTGTCTACTTCTTCAAGTGTGTCACAGGAGTTCAGACAAAGGTCAACATCACCTT 304
Db 350 GTCCGTCTACTTCTTCAAGTGTGTCACAGGAGTTCAGACAAAGGTCAACATCACCTT 409

Qy 305 AGTCCGCGAGCGTGGACCTTATGCTACAGGAGTTCAGACAAAGGTCAACATCACCTT 364
Db 410 AGTCCGCGAGCGTGGACCTTATGCTACAGGAGTTCAGACAAAGGTCAACATCACCTT 469

Qy 365 CAATGACAAAGCAGCTGCTTCTGTTGGAAGACCGCAGCTCCATTTTCAGGCTTGACAA 424
Db 470 CAATGACAAAGCAGCTGCTTCTGTTGGAAGACCGCAGCTCCATTTTCAGGCTTGACAA 529

Qy 425 GTCCGAGGCTCAGAGAGTGTACTGCTTACTGCTTAACTCTTGGTCTGGGGGCTC 484
Db 530 GTCCGAGGCTCAGAGAGTGTACTGCTTACTGCTTAACTCTTGGTCTGGGGGCTC 589

Qy 485 GATATTGATGAGAGCAAGCTGTGAGCTGAGCTGATGATGACCTTGGGCTGGGTGAC 544
Db 590 GATATTGATGAGAGCAAGCTGTGAGCTGAGCTGATGATGACCTTGGGCTGGGTGAC 649

Qy 545 CATGGGCGAGGCTGTTTATGAAACCGCAGTTGTTGAGATCTGTTGGGCTTATGACGA 604
Db 650 CTTGGGCGAGGCTGTTTATGAAACCGCAGTTGTTGAGATCTGTTGGGCTTATGAGGA 709

Qy 605 TCCCTTGTGCTATTTCTCAACAGTGTCTCCAGACATGCTTCCCATAAAGGCAATT 664
Db 710 TCCCTTGTGATTTTATCAACAAATTTCTTACAGACATGTTCCCATCAAGGCAATT 769

Qy 665 TGGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCTACTGCTTTCAGGGCGT 724
Db 770 CGGCTGTTTGTGGGATGAACAACTCAGACTCTGGGCTCTTCTACTGTTTCAGGGCGT 829

Qy 725 CCAGAAATTCAGCAGGATCCATCTGTTGGGACAAATGGAACCGGATCAGCAGGATTCGATTA 784
Db 830 CCAGAAATTCAGCAGGATCCATCTGTTGGGACAAATGGAACCGGATCAGCAGGATTCGATTA 889

Qy 785 TTGGCATTTCAGCAGGATTCATGATGATCAATGGAACCTTCCGGGAGATGTTGGGACCTT 844
Db 890 CTTGGCATTTCAGCAGGATTCATGATGATCAATGGAACCTTCCGGGAGATGTTGGGACCTT 949

Qy 845 CATGACACCCGAAATCCTCGCTGGAAATTTCTTTCAGCCCGGAGGATGTCAGGTCCATGAAGCT 904
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Db 950 CATGACACCCAGTCTCGCTGGAAATTTCTTCACTCGGAAGCCTGCGAGTCTATGAAGCT 1009
Qy 905 GACCTACAAGCAATCAAGGTTTGAAGGCAATCCACGATATCGCTTCAAGGCCCCCGA 964
Db 1010 CACCTACCATGATTCAGGGGTGTTTGAAGGCAATCCACGATATCGCTTCAAGGCCCCTA 1069
Qy 965 TACTCTGTTTGGCAACGGGTTCGCTTACCCACCAAGGAGGCTTCCGCCATGCGGAGA 1024
Db 1070 AACTTTGTTTGCATGAGGTTCTGTTTACCCACCAATGAAGGTTTCTGCCCCGTGCTTGA 1129
Qy 1025 GTCTGCAATTCAGAAATGTCAGCACTGCAAGTTTGGTGGGCTCTGTTTCTCTCCACCC 1084
Db 1130 ATCCGCAATTCAAAATGTCAGCACTTGCAGGTTTGGTGCACCCCTGTTTCTGTGTCACACCC 1189
Qy 1085 CCACTTTTCAACGCCGACCTGCTGTTGTCAGAGCTGTTTGGTGTGACCCCTAACCC 1144
Db 1190 TCACTTTCAATGTCAGACCTGCTGATATCAGAAGCGGTTCTGGGTCGTGAACCTGACCC 1249
Qy 1145 AAGAGGAGCATTCCTTCTCTAGACATCCATCCGTCACCTGGGATCCCATGAACCTGTTTC 1204
Db 1250 AAGGAGCATTCCTTCTCTAGACATCCATCCGTCACCTGGGATCCCATGAACCTGTTTC 1309
Qy 1205 TGTGAAGATGCACTGAGCTCTTACATCAAACTGTCAAGGGCATCGGGCAACACAGGAA 1264
Db 1310 TGTGAAGTTGCAGATAAGCTCTTACATCAAGCTGTCAAGGGCATTTGGGCAACACAGGAA 1369
Qy 1265 GATCGAGCAGATGATGTTCTGCGGTTGCTGTTGTTGGAACAGAGCGGAGCAATGGTGGCAA 1324
Db 1370 GATCGAGCAGGTTGTTCTGCTTCCATTTGTTGTTGAGCAGAGCGTCCCATGGGCGGCA 1429
Qy 1325 GCGCTTGCAGCATGTTCTTACAGCAGCTGTTGCTGATGCGCCAGGTTCTTCACTACCGCA 1384
Db 1430 GCGCTTGCAGCATGTTCTTACAGCAGCTGTTGCTGATGATGATGATGATGATGATGATGAT 1489
Qy 1385 GTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
Db 1490 GTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
Qy 1445 CAGCAGGAGAAATGCTTTTGTGTTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1504
Db 1550 CAGCAGGAGAAATGCTTTTGTGTTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1609
Qy 1505 GGCATTCAGGCTTACTCTGAGTCCCTGATGTCACAGCTGCCAAGGCGACGCTGCTGCA 1564
Db 1610 GGCATTCAGGCTTACTCTGAGTCTCTGATGTCACAGCTGCCAAGGCGACGCTGCTGCA 1669
Qy 1565 AGAAGCCAAAGCTATAGGCTCTGAGACATTAAGCCCCCCCCCAACCTGATAGCTTTGGTC 1624
Db 1670 AGAAGCCAAAGCTATAGGCTCTGAGACATTAAGCCCCCCCCCAACCTGATAGCTTTGGTC 1729
Qy 1625 AGACAGCAGCAGGCTTCAACCCGCTTCTTGAAGGCTTCTGAGGAGCTCTGAGGAGCAGCCAC 1684
Db 1730 AGACAGCAGCAGGCTTCAACCCGCTTCTGAGGAGCTCTGAGGAGCAGGCTGAGGCTGAGG 1789
Qy 1685 CAGTGCATGCTGAGCCCCCAGGATGTCACCTCT 1721
Db 1790 CAGTGCATGCTGAG-CCCCAGATGTCACCTCT 1825
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RESULT 9

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US-09-031-626-3
; Sequence 3, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
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; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)
US-09-031-626-3

Query Match 78.2%; Score 1396.2; DB 3; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

QY 5 CTCCTTCAGGTCCTGAGCCCGAGAGCCCTTCGCGCAGCAGCGACATGGCGCAGCTC 64
DB 110 CCCCTTCAGTCCCTGAGCCCGAGCCCGGCGCGCAGCAGCGGACATGGCGCAGCGC 169

QY 65 CAGGCGCGCTGGGTGGCTTCCTGGGCTGGGCGCCCTGGGCGTGTCTGTGGCTCGG 124
DB 170 CAGGCGCGCTGGGTGGGCTGGGCGTGTGGGCGTGTGGCTCGGCTCGG 229

QY 125 CGTTGTATGATCTCTATGTGTCCTCTCCATCAAGCAGAGTGTCTCAAGATGTCG 184
DB 230 TGTGTTATGATCTCTGATGTCCTCGCTCATCAACAGCAGGTACTGAAGATGTCG 289

QY 185 CATAGACCCGAGCAGCTGCTTCGCGGATGTGAAGGATCCCGCTCCCTTCTACTT 244
DB 290 CATAGACCCGAGCAGCTGCTTCGCGGATGTGAAGGATCCCGCTCCCTTCTACTT 349

QY 245 GTCTGTCTACTTCTTCGAAGTGTCAACCCAAAGAGGTCTCAACCGCGCAGAGCCAGT 304
DB 350 GTCCGTCTACTTCTTCGAAGTGTCAACCCAGCGATCTTAAGGCTGGAAGCCAGT 409

QY 305 AGTCGGGAGGTGGACCTATGTCTACAGGAGTTGAGCAAAAGGTCAACATCACCTT 364
DB 410 AGTCGGGAGGTGGACCTATGTCTACAGGAGTTGAGCAAAAGGTCAACATCACCTT 469

QY 365 CAATGACACGACACCTGCTTCGCGGAGTGTGAAGGATCCCGCTCCCTTCTACTT 424
DB 470 CAATGACACGACACCTGCTTCGCGGAGTGTGAAGGATCCCGCTCCCTTCTACTT 529

QY 425 GTCCATGCTCTCAGAGTGTACTTACTTCTCAACATCTTGGTCTCGGCGGCTC 484
DB 530 GTCCATGCTCTCAGAGTGTACTTACTTCTCAACATCTTGGTCTCGGCGGCTC 589

QY 485 GATATGATGAGAGCAAGCTGTGAGCTGAGCTGAGCTGATGATGATGATGATGATG 544
DB 590 AGTAATGATGAGAGCAAGCTGTGAGCTGAGCTGAGCTGATGATGATGATGATGATG 649

QY 545 CATGGGCGAGGCTCTTTATGACCGCAGATGTTGGTGGATCTGTGGGCTATGACGA 604
DB 650 CTTGGGCGAGGCTCTTTATGACCGCAGATGTTGGTGGATCTGTGGGCTATGACGA 709

QY 605 TCCCTTCGTGATTTCTCAACAGTACTCTCCAGACATGCTTCCCATAAAGGCAAT 664
DB 710 TCCCTTCGTGATTTCTCAACAGTACTCTCCAGACATGCTTCCCATAAAGGCAAT 769

QY 665 TGGCTCTTTTGTGGGATGAACAACTCGAATTTGGGCTCTTCACTGTCTTTCAGGCGCT 724
DB 770 CGGCTCTTTTGTGGGATGAACAACTCGAATTTGGGCTCTTCACTGTCTTTCAGGCGCT 829

QY 725 CCAGATTTTCAGAGGATTCATCTGGTGGACAAATGGAACGAGATCGAGATCGATTA 784
DB 830 CCAGATTTTCAGAGGATTCATCTGGTGGACAAATGGAACGAGATCGAGATCGATTA 889

QY 785 TTGCAATTCAGAGGATGAACATGATGATGATGATGATGATGATGATGATGATGATG 844
DB 890 CTTGCAATTCAGAGGATGAACATGATGATGATGATGATGATGATGATGATGATGATG 949

QY 845 CATGACACCGGATTCCTCGCTGGAAATTTCTTCAGCCCGAGGAGCATGAGGTCCATGAAGCT 904

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QY 905 GACTATCAACGAATCAAGGTTTGAAGGATTTCCACGATATCGTTTACGCGCCCGCA 964
DB 1010 CACTTACCATGATTCAGGTTTGAAGGATTTCCACGATATCGTTTACGCGCCCGCA 1069
QY 965 TACTCTGTTTGGCAACGGGTCCTCTACCCACCAAGAGGCTTCTGCGCATGCGGAGA 1024
DB 1070 AACTTTGTTGCAATGGGTCCTGTTACCCACCAATGAAGTTTCTGCGCGTCTGGA 1129
QY 1025 GTCTGGCATTCGAATGTGAGCAGCTGAGGTTTGGTGGCTCTGTTTCTTCCACCC 1084
DB 1130 ATCCGCGATTCGAATGTGAGCAGCTTGGAGGTTTGGTGGACCCCTGTTTCTGTCACACCC 1189
QY 1085 CCACTTTTCAACCGCGACCCCTGTTGTCAGAAAGCTTCTTGGTCTGAACCCCTTAACCC 1144
DB 1190 TCACTTCAACGAGACCCCTGTTGTCAGAAAGCTTCTGCGTCTGAACCCCTTAACCC 1249
QY 1145 AAAGGAGCATTCCTGTTCTAGACATCCATCCGTCATCTGGGATCCCATGAATCTGTTT 1204
DB 1250 AAGGAGCATTCCTGTTCTGACATCCATCCGTCATCTGGGATCCCATGAATCTGTTT 1309
QY 1205 TGTGAAGTGCAGTGCAGCTCTACATCAATCTCTCAAGGAGTCTGGGCAACAGGAA 1264
DB 1310 TGTGAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1369
QY 1265 GATCGAGCAGTGTGCTGCGGTCGAAACGAGCGGAGCAATGGTGGCAA 1324
DB 1370 GATCGAGCAGTGTGCTGCGGTCGAAACGAGCGGAGCAATGGTGGCAA 1429
QY 1325 GCCCTTCAGCAGCTTCTACAGCAGTGTGCTGATGATGATGATGATGATGATGATGATG 1384
DB 1430 GCCCTTCAGCAGCTTCTACAGCAGTGTGCTGATGATGATGATGATGATGATGATGATG 1489
QY 1385 GTATGCTGCTGGGCTTGGAGGCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
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QY 1445 CAGCAGGAGAAATGCTTTTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTG 1504
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QY 1565 AGAAGCAGATGATGAGTCTGGAAGACATTAAGCCCCCAACCTGATAGTGTGCTGCTGCTG 1624
DB 1670 AGAAGCAGATGATGAGTCTGGAAGACATTAAGCCCCCAACCTGATAGTGTGCTGCTGCTG 1729
QY 1625 AGAAGCAGATGATGAGTCTGGAAGACATTAAGCCCCCAACCTGATAGTGTGCTGCTGCTG 1684
DB 1730 AGAAGCAGATGATGAGTCTGGAAGACATTAAGCCCCCAACCTGATAGTGTGCTGCTGCTG 1789
QY 1685 CAGTGCATGCTGAGCCCCCAGATGTCAACCTGT 1721
DB 1790 CAGTGCATGCTGAG-CCCCAGATGTCAACCTGT 1825

RESULT 10
US-08-559-505-1
; Sequence 1, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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; OTHER INFORMATION: encode the amino acid sequence for the Hamster Scavenger Receptor
US-08-559-505-1

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Query Match 76.7%; Score 1369.8; DB 2; Length 1788;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0

	Qy	5	CTCCTTCAGGTCCTCAGCGCCCGAGAGCCCCCTTCCGCCACCGCGGCATCATGGCGCGGCACTC	64
	Db	110		
	Qy	65	CAGGGCGCGCTGGGTGGCTTTGGGGCTTGGGGCCCTCGGGCTGTCTGTTCCTGCTGCGCTCCGG	124
	Db	170		
	Qy	125	CGTTGTCAATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATGTCTCG	184
	Db	230	TGTGGTTATGATCCTCGTGATGCCCTCGCTCATCAAACAGCAGGTACTGAAGAATAATTCGG	289
	Qy	185	CATPAGCCCGAGCAGCCTGTCTCTCGGATGTGGAAGAGATCCCCTGCTCCCTTTCTTCACTT	244
	Db	290	CATTAGACCAGCACCTGTCTTTGCMATGTGAAAGAGATCCCTGTACCCCTTCTTCACTT	349
	Qy	245	GTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAGGCACT	304
	Db	350	GTCCGTCTACTTCTTCGAGGTGGTCAATCCCGAGGAGATCCTAAAGGGTGAAGAAGCACT	409
	Qy	305	AGTCGGGAGCGTGACCCCTATGTCTACAGGGAGTTCAGACAAGAAGTCAACATCACTT	364
	Db	410		
	Qy	365	CAATGCAACCGACACCGTGTCTTCGTGGGAACCGCAGCCTCCATTTCCAGCGCTCGACAA	424
	Db	470	CAATGACAATGATATCTGTGTCTTTGTGGAGCACCGCAGCGCTCCATTTCCAGCCCGAGAC	529
	Qy	425	GTCGCATGGCTCAGAGATGTACTAATTTGTACTGCCTAA CATCTTGGTCTCTGGGGGGCTC	484
	Db	530	GTCCCCACGGCTCTGAGAGTGACTACATTTATTA TCTGCCTAA CATTCTTGGTCTTTGGGGGGCGC	589
	Qy	485	GATATTGATGGAGAGCAAGCCTGTGAGCGCTCAAGCTGATGATGACCTTGGCGCTGCTGCAC	544

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Db 1730 AGACGAGCCATCCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTC 1786

RESULT 11
US-08-749-907-1
; Sequence 1, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieser, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683
; OTHER INFORMATION: encode the amino acid sequence for the Hamster Scavenger Receptor
; OTHER INFORMATION: B-I."

US-08-749-907-1
Query Match 76.7%; Score 1369.8; DB 2; Length 1788;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 5 CTCCTTCAGGTCCTCAGAGCCCGAGAGCCCTTCCGCGCAGCGACATGGCGGAGCTC 64
Db 110 CCCCTTCAGTCCCTGAGCCCGCGAGCCCGGCGCGCACGCGACATGGCGGAGCTC 169
Qy 65 CAGGCGCGCTGGGTGGGCTTGGGGTGGGGCCCTGGGGTGGTGGTGGTGGTGGTGGT 124
Db 170 CAGGCGCGCTGGGTGGGCTTGGGGTGGGGCTGGGGTGGTGGTGGTGGTGGTGGT 229
Qy 125 CGTTGTATGATCTCTATGGTGGCCCTCCCTCATCAGCAGCAGCTGCTCAAGATGTCG 184
Db 230 TGTGGTATGATCTCTGATGGCCCTCGCTCATCAACAGCAGGACTGTAAGAAATGTCG 289
Qy 185 CATAGACCCGAGCAGCCTGTCTTTCGGGATGTGGAAGAGATGCCCGTCCCTTCTACTT 244

Db 290 CATAGACCCAGCAGCCTGTCTTTCGAATGTGGAAGAGATCCCTGTACCTTCTACTT 349
Qy 245 GTCTGTCTACTTCTTGAAGTGTCAACCAAGAGGTCTCAAGCGGCAGAGCCAGT 304
Db 350 GTCCGTCTACTTCTTGAAGTGTCAATCCAGGAGATCTTAAGGGTGAGAGCCAGT 409
Qy 305 AGTCCGGGAGCGTGGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCACC 364
Db 410 AGTGGGGAGCGTGGACCCCTATGTCTACAGGAAATCAGACATAAGGCCAACATCACC 469
Qy 365 CAATGACAAACGACACCGTGTCTTCTGAGAGACCGCAGCCTCCATTTCCAGCCTGCAA 424
Db 470 CAATGACAAATGATCTGTGTCTTGTGGAGACCGCAGCCTCCATTTCCAGCGCGCAG 529
Qy 425 GTCCGATGGCTCAGAGAGTCACTACATTTGACTGCTTAACTTGTCTTGGTCTTGGGGGCTC 484
Db 530 GTCCGAGGCTCTGAGAGTCACTACATTTACTTGTCTTAACTTGTCTTGGGGGCGC 589
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Db 590 AGTAATGATGAGAGCAAGTCTGAGCCTGGAAGCTGATGATGACCTTGGGGCTGGCCAC 649
Qy 545 CATGGGCCAGCGTGTCTTATGAAACCGCAGTGTGGTGGATCCTGTGGGGCTTATGACGA 604
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Qy 605 TCCCTTCGTGCTATTTCTCAACAGCTTACCTCCAGACATCTTCCCAATAAGGGCAAT 664
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GenCore version 5.1.7
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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134589005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1785	100.0	1785	3	US-09-148-012-3
2	1785	100.0	1785	6	US-10-178-611-3
3	1785	100.0	1785	6	US-10-164-863-3
4	1785	100.0	1785	6	US-10-176-073-3
5	1785	100.0	1785	9	US-10-933-037-3
6	1785	100.0	2496	7	US-10-322-281-564
7	1607	90.0	1607	8	US-09-882-945A-285
8	1607	90.0	1607	8	US-10-807-114-285
9	1459.4	81.8	2497	7	US-10-152-319A-1909
10	1396.2	78.2	1825	3	US-09-779-152-3
11	1396.2	78.2	1825	5	US-10-023-610-3
12	1396.2	78.2	1825	7	US-10-212-848-3
13	1369.8	76.7	1788	3	US-09-148-012-1
14	1369.8	76.7	1788	6	US-10-178-611-1
15	1369.8	76.7	1788	6	US-10-164-863-1
16	1369.8	76.7	1788	7	US-10-706-073-1
17	1369.8	76.7	1788	9	US-10-933-037-1
18	1142.6	64.0	2558	7	US-10-276-774-1032
19	1142.6	64.0	2630	3	US-09-779-152-1
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23	1141	63.9	2566	7	US-10-648-593-90

24	1141	63.9	2566	8	US-10-775-920-249	Sequence 249, App
25	1141	63.9	2566	8	US-10-794-198A-11	Sequence 11, Appl
26	1141	63.9	2566	9	US-10-956-157-1424	Sequence 1424, Ap
27	1133	63.5	2628	7	US-10-210-172-115	Sequence 115, App
28	1127.8	63.2	3144	7	US-10-322-281-567	Sequence 567, App
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30	959	53.7	2751	6	US-10-313-641-11	Sequence 11, Appl
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35	849	47.6	1240	7	US-10-210-172-117	Sequence 117, App
36	389.4	21.8	1400	9	US-10-956-157-6659	Sequence 6659, Ap
37	283.6	15.9	444	3	US-09-918-995-11387	Sequence 11387, A
38	263.6	14.8	719	6	US-10-024-396-11	Sequence 11, Appl
39	208.2	11.7	84252	7	US-10-322-281-563	Sequence 563, App
40	185.8	10.4	485	6	US-10-024-396-12	Sequence 12, Appl
41	166.6	9.3	599	9	US-10-450-763-22306	Sequence 22306, A
42	163	9.1	1938	7	US-10-152-319A-2060	Sequence 2060, Ap
43	163	9.1	2064	6	US-10-388-934-120	Sequence 120, App
44	162.2	9.1	2329	7	US-10-794-899-107	Sequence 107, App
45	161.2	9.0	1988	9	US-10-764-420-2465	Sequence 2465, Ap

ALIGNMENTS

RESULT 1
US-09-148-012-3
; Sequence 3, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51)..(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine
; OTHER INFORMATION: Scavenger Receptor Class BI
US-09-148-012-3

Query Match	100.0%;	Score 1785;	DB 3;	Length 1785;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	181	TCGCGGTGTGCATGATCTCTCATGTCCTTCCGCGCAGCGGACATGGGCGCA	240	
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Qy	241	ACTTGTCTGTCTACTTCTTCTGAAGTGTGTCAACCCAAACGAGGTCTCTCAACGGCCAGAACG	300
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Db	421	ACAAGTCGCATGGCTCAGAGAGTGACATACATTTGTACTGTCCCTAAACATCTTGGTCTCTGGGG	480
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; Publication No. US20030167475A1			
; GENERAL INFORMATION:			
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky			
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL			
; NUMBER OF SEQUENCES: 4			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory			
; STREET: 2800 One Atlantic Center			
; 1201 West Peachtree Street			
; CITY: Atlanta			
; STATE: Georgia			
; COUNTRY: USA			
; ZIP: 30309-3450			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/10/178,611			
; FILING DATE: 24-Jun-2002			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/749,907			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Pabst, Patrea L.			
; REGISTRATION NUMBER: 31,284			
; REFERENCE/DOCKET NUMBER: MIT/538			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (404) 873-8794			
; TELEFAX: (404) 873-8795			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1785 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			

QY 1321 GCAAGCCCCTGAGCACGTTCTACGCAGCTGGTGTGATGCCCCAGGTTCTTCACTACG 1380

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577
OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
encode the amino acid sequence for the murine Scavenger Receptor Class B1."
SEQUENCE DESCRIPTION: SEQ ID NO: 3;
US-10-178-611-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	181	TCCGATAGACCCGAGCAGCTGCTTCCGCGATGTGAAGAGATCCCGCTCCCTTCT	240
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Db	301	CAGTAGTCGGGAGCGTGGACCTATGTCTACAGGAGTTGAGACAAAGGTCAACATCA	360
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Db	421	ACAAGTCGATGGCTCAGAGAGTGACTACATTTGCTACCTTAACATCTTGGTCTGGGG	480
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RESULT 3

US-10-164-863-3
; Sequence 3, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863


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; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1

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Db	61	GCTCCAGGGCGCGCTGGGTGCCTTGGGGTTGGCGCCCTGGGGCTGCTGTTTCTCGGC	120	
Qy	121	TCGGCGTGTGTCATGATCCTCATGTCGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180	
Db	121	TCGGCGTGTGTCATGATCCTCATGTCGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180	
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Qy	361	CTTTCATGACAAACGACACCGCTGTCCTTCGTGGAGAACCGCAGCGCTCCATTTCCAGCCTG	420	
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Qy	421	ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGATCTGCCCTAACATCTTGTCTCTGGGG	480	
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Qy	481	GCTCGATATTTGATGGAGACGAGCCTGTGAGCCTGAAGCTCATGATGACCTTTGGGGCTGG	540	
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Qy	541	TCACATGGGCGCAGCGTCTTTTATGAACCCGACAGTTTGGTGAGATCTCTGTGGGGCTATG	600	
Db	541	TCACATGGGCGCAGCGTCTTTTATGAACCCGACAGTTTGGTGAGATCTCTGTGGGGCTATG	600	
Qy	601	ACGATCCCTTCGTGCATTTTCTCAACACGTAACCTCCCGACATGCTTCCCATTAAGGGCA	660	
Db	601	ACGATCCCTTCGTGCATTTTCTCAACACGTAACCTCCCGACATGCTTCCCATTAAGGGCA	660	
Qy	661	AATTTGGCCCTGTTTGTGGGATGAACAACCTCGAATTCCTGGGGCTTCTACTGCTTTCAGG	720	
Db	661	AATTTGGCCCTGTTTGTGGGATGAACAACCTCGAATTCCTGGGGCTTCTACTGCTTTCAGG	720	
Qy	721	CGGTCACAGAAATTCAGCAGGATCCATCTGGTGGACAAATGAACCGGATCTCAGCAAGATCG	780	
Db	721	CGGTCACAGAAATTCAGCAGGATCCATCTGGTGGACAAATGAACCGGATCTCAGCAAGATCG	780	

Qy	781	ATTATTGGCAATTCAGAGCAGTGTAAACATGATCAATGGGACTTCGGGGCAGATGTGGGCAC	840
Db	781		
Qy	781	ATTATTGGCAATTCAGAGCAGTGTAAACATGATCAATGGGACTTCGGGGCAGATGTGGGCAC	840
Db	781		
Qy	841	CCTTTCATGACACCCGGAATCCTCGCTCGAATTCTTCAGCCCGAGGAGCATGCAGTGCATGA	900
Db	841		
Qy	841	CCTTTCATGACACCCGGAATCCTCGCTCGAATTCTTCAGCCCGAGGAGCATGCAGTGCATGA	900
Db	841		
Qy	901	AGCTGACCTACAAAGAAATCAAGGGGTGTTGAAGGCATTCACAGTATCGCTTCACGGGCC	960
Db	901	AGCTGACCTACAAAGAAATCAAGGGGTGTTGAAGGCATTCACAGTATCGCTTCACGGGCC	960
Qy	961	CCGATACTCTGTTTGCACAGGGTCCGTCTAACCCACCCAAAGAGGCTTCCTGCCCATGCC	1020
Db	961	CCGATACTCTGTTTGCACAGGGTCCGTCTAACCCACCCAAAGAGGCTTCCTGCCCATGCC	1020
Qy	1021	GAGAGTCTGCATTCAGAAATGTCAGACCTGACAGTTTGGTGCGCTCTCTGTTCTCTCCC	1080
Db	1021	GAGAGTCTGCATTCAGAAATGTCAGACCTGACAGTTTGGTGCGCTCTCTGTTCTCTCCC	1080
Qy	1081	ACGCCCACTTTTACAAAGCCGACCTCTGTGTTGTTCAGAAAGCTGTTCTTGCTCTGAACCCCTA	1140
Db	1081	ACGCCCACTTTTACAAAGCCGACCTCTGTGTTGTTCAGAAAGCTGTTCTTGCTCTGAACCCCTA	1140
Qy	1141	ACCCAAAGGAGCAATCCTTGTGTTCTTAGACATCATCCGCTCCTGAGATCCCATGAACT	1200
Db	1141	ACCCAAAGGAGCAATCCTTGTGTTCTTAGACATCATCCGCTCCTGAGATCCCATGAACT	1200
Qy	1201	GTTCTGTGAAGATGTCAGCTGAGGCTCTACATCAAACTCTGTCAGAGGCATCGGGCAACAG	1260
Db	1201	GTTCTGTGAAGATGTCAGCTGAGGCTCTACATCAAACTCTGTCAGAGGCATCGGGCAACAG	1260
Qy	1261	GGAAAGATCGAGCCAGTAGTTCTCCGCTGCTGTGGTTTCGAAACAGAGCGGAGCAATGGGTG	1320
Db	1261	GGAAAGATCGAGCCAGTAGTTCTCCGCTGCTGTGGTTTCGAAACAGAGCGGAGCAATGGGTG	1320
Qy	1321	GCAAGCCCTGAGCAGCTTCTACACGCACTGTGTCTGATGCCCCAGGTTCTTCACTACG	1380
Db	1321	GCAAGCCCTGAGCAGCTTCTACACGCACTGTGTCTGATGCCCCAGGTTCTTCACTACG	1380
Qy	1381	CGCAGTATGTCTGCTGGGGCTTGGAGGCCCTCCTGTGCTGTGGTCCCATCATCTGCCAAC	1440
Db	1381	CGCAGTATGTCTGCTGGGGCTTGGAGGCCCTCCTGTGCTGTGGTCCCATCATCTGCCAAC	1440
Qy	1441	TGCGCAGCAGGAGAAATGCTTTTGTGTTGGAGTGGTAGTAAAGGGCTCCCAAGATA	1500
Db	1441	TGCGCAGCAGGAGAAATGCTTTTGTGTTGGAGTGGTAGTAAAGGGCTCCCAAGATA	1500
Qy	1501	AGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCACAGCTGCCAAGGGCAGCGTGC	1560
Db	1501	AGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCACAGCTGCCAAGGGCAGCGTGC	1560
Qy	1561	TGCAAGAAGCCAAAGCTATAGGGTCCCTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT	1620
Db	1561	TGCAAGAAGCCAAAGCTATAGGGTCCCTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT	1620
Qy	1621	GGTCAGACCAAGCCACCCAGTCCCTACACCCCGCTTCTTTGAGGACTCTCTCAGCGGACAGC	1680
Db	1621	GGTCAGACCAAGCCACCCAGTCCCTACACCCCGCTTCTTTGAGGACTCTCTCAGCGGACAGC	1680
Qy	1681	CCACCAAGTGCATGGCTGAGCCGCCAGATGTTCACACTCTGTCGACGCGCAGGCACATGG	1740
Db	1681	CCACCAAGTGCATGGCTGAGCCGCCAGATGTTCACACTCTGTCGACGCGCAGGCACATGG	1740
Qy	1741	ATGCCCAAGCTATGCAAAAACAACTCAGGGACCGAGGACAGACC	1785
Db	1741	ATGCCCAAGCTATGCAAAAACAACTCAGGGACCGAGGACAGACC	1785

RESULT 4
US-10-706-073-3
; Sequence 3, Application US/10706073

Publication No. US20040077526A1
GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
FILE OF INVENTION: In The Treatment Of Steroidal Overproduction
FILE REFERENCE: M178299
CURRENT APPLICATION NUMBER: US/10/706,073
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 09/148,012
PRIOR FILING DATE: 1998-10-04
PRIOR APPLICATION NUMBER: 60/057,943
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1785
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51)..(1577)
OTHER INFORMATION: Encodes the amino acid sequence for the murine
OTHER INFORMATION: Scavenger Receptor Class B1
US-10-706-073-3

Query Match 100.0%; Score 1785; DB 7; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGTCCTCTTCAGTCTCAGCCCGGAGAGCCCTTCGCGCGACGCGGACATGGCGGCA	60
Db	1	CCGTCCTCTTCAGTCTCAGCCCGGAGAGCCCTTCGCGCGACGCGGACATGGCGGCA	60
Qy	61	GCTCCAGGCGCGCTGGGCTGGGCTGGGCGCCCTGGGCGCTGCTGTTGCTGGC	120
Db	61	GCTCCAGGCGCGCTGGGCTGGGCTGGGCGCCCTGGGCGCTGCTGTTGCTGGC	120
Qy	121	TCGCGGTGTGTCATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAA	180
Db	121	TCGCGGTGTGTCATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAA	180
Qy	181	TCCGATAGACCCGAGCAGCTGCTTCCGCGATGTGAAGAGATCCCGCTCTTCT	240
Db	181	TCCGATAGACCCGAGCAGCTGCTTCCGCGATGTGAAGAGATCCCGCTCTTCT	240
Qy	241	ACTTGTCTGTCTACTTCTTCAAGTGGTCAACCCAAACGAGTCTCAACGCGCAGAGC	300
Db	241	ACTTGTCTGTCTACTTCTTCAAGTGGTCAACCCAAACGAGTCTCAACGCGCAGAGC	300
Qy	301	CAGTAGTCCGCGAGCGTGGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA	360
Db	301	CAGTAGTCCGCGAGCGTGGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA	360
Qy	361	CCTTCAATGACAAACGACACCGTGTCTTGTGAGAGACCGCAGCTCCATTTCCAGGCTG	420
Db	361	CCTTCAATGACAAACGACACCGTGTCTTGTGAGAGACCGCAGCTCCATTTCCAGGCTG	420
Qy	421	ACAAAGTCCGATGGCTCAGAGAGTGAATGATGTTGCTTAAATCTTGTCTCTGGGG	480
Db	421	ACAAAGTCCGATGGCTCAGAGAGTGAATGATGTTGCTTAAATCTTGTCTCTGGGG	480
Qy	481	GCTCGATATTGATGGAGAGCAAGCTGTGAGCTGAAGCTGATGATGATGATGATGATG	540
Db	481	GCTCGATATTGATGGAGAGCAAGCTGTGAGCTGAAGCTGATGATGATGATGATGATG	540
Qy	541	TCACCATGGCGCAGCTGCTTTTATGAACCGCAGATGTTGGTGGGCTATG	600
Db	541	TCACCATGGCGCAGCTGCTTTTATGAACCGCAGATGTTGGTGGGCTATG	600
Qy	601	ACGATCCCTTCGTGATTTCTCAACACGATCTCCGAGACATGTTCCCATTAAGGGCA	660
Db	601	ACGATCCCTTCGTGATTTCTCAACACGATCTCCGAGACATGTTCCCATTAAGGGCA	660

Qy	661	AATTTGGCTGTTTGGTGGAGTGAACAACTCGAATTTCTGGGCTCTTCACTGTCTTACGG	720
Db	661	AATTTGGCTGTTTGGTGGAGTGAACAACTCGAATTTCTGGGCTCTTCACTGTCTTACGG	720
Qy	721	CGGTCCAGAAATTTTCAGCAGGATCCATCTGTGGGCAAAATGGAACGAGTCTCAGCAAGATCG	780
Db	721	CGGTCCAGAAATTTTCAGCAGGATCCATCTGTGGGCAAAATGGAACGAGTCTCAGCAAGATCG	780
Qy	781	ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGCGAGATGTGGGCAC	840
Db	781	ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGCGAGATGTGGGCAC	840
Qy	841	CCTTCATGACACCCGAAATCTCGTGGAAATTTCTTCAGCCCGGAGGCAATGCAAGTTCATGA	900
Db	841	CCTTCATGACACCCGAAATCTCGTGGAAATTTCTTCAGCCCGGAGGCAATGCAAGTTCATGA	900
Qy	901	AGCTGACCTCAACGAATCAAGGCTGTTTGAAGGCAATTCACGATATCGCTTTCAGGCCC	960
Db	901	AGCTGACCTCAACGAATCAAGGCTGTTTGAAGGCAATTCACGATATCGCTTTCAGGCCC	960
Qy	961	CCGATACTCTGTTTGGCAACGGGTCCTGTACCCACCCAAACGAAGGCTTCTGCCCATGCC	1020
Db	961	CCGATACTCTGTTTGGCAACGGGTCCTGTACCCACCCAAACGAAGGCTTCTGCCCATGCC	1020
Qy	1021	GAGAGTCTGGCAATTCAGAAATGTGACACCTGACAGTGTGGTGGCTCTGTTTCTCTCCC	1080
Db	1021	GAGAGTCTGGCAATTCAGAAATGTGACACCTGACAGTGTGGTGGCTCTGTTTCTCTCCC	1080
Qy	1081	ACCCCACTTTTACAAACCGCCGCTGTGTGTCAGAGCTGTTTCTTGGTCTGAACCTTA	1140
Db	1081	ACCCCACTTTTACAAACCGCCGCTGTGTGTCAGAGCTGTTTCTTGGTCTGAACCTTA	1140
Qy	1141	ACCCAAAGGAGCAATTCCTGTTTCTTACATCAATCCATCCGCTCACTGGGATCCCATGAAC	1200
Db	1141	ACCCAAAGGAGCAATTCCTGTTTCTTACATCAATCCATCCGCTCACTGGGATCCCATGAAC	1200
Qy	1201	GTTCTGTGAAGATGACAGCTGAGCTCTTACATCAATCTGTCAAGGGCATCGGGCAACAG	1260
Db	1201	GTTCTGTGAAGATGACAGCTGAGCTCTTACATCAATCTGTCAAGGGCATCGGGCAACAG	1260
Qy	1261	GGAGATCGAGCCAGTGTCTGCGTGTGTTGTCAGACAGAGCGGAGCAATGGGTG	1320
Db	1261	GGAGATCGAGCCAGTGTCTGCGTGTGTTGTCAGACAGAGCGGAGCAATGGGTG	1320
Qy	1321	GCAAGCCCTTGAGCAGCTGTTTACACGAGCTGTTGTCAGTCCCGCAGGCTCTTCACTACG	1380
Db	1321	GCAAGCCCTTGAGCAGCTGTTTACACGAGCTGTTGTCAGTCCCGCAGGCTCTTCACTACG	1380
Qy	1381	CGCAGTATGCTCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTCCCATCATCTGCCAAC	1440
Db	1381	CGCAGTATGCTCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTCCCATCATCTGCCAAC	1440
Qy	1441	TGGCAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1500
Db	1441	TGGCAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1500
Qy	1501	AGGAGGCTTTCAGGCTTCTGAGTCCCTGATGTCACAGCTGTCACAGGCGACGCTGTC	1560
Db	1501	AGGAGGCTTTCAGGCTTCTGAGTCCCTGATGTCACAGCTGTCACAGGCGACGCTGTC	1560
Qy	1561	TGCAAGAGCAAGCTATAGGGCTCTGAAGACACTATAAGCCCCCCCCCACTGATAGCTT	1620
Db	1561	TGCAAGAGCAAGCTATAGGGCTCTGAAGACACTATAAGCCCCCCCCCACTGATAGCTT	1620
Qy	1621	GGTCAGACAGCCAGCTCCCTTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1680
Db	1621	GGTCAGACAGCCAGCTCCCTTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1680
Qy	1681	CCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
Db	1681	CCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
Qy	1741	ATGCCACGCAATGTGCAAAAAACAACTCAGGGACCCAGGGACAGACC	1785

Db 1741 ATGCCACGATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1785
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RESULT 5

US-10-933-037-3
; Sequence 3, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004

CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:

NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; encode the amino acid sequence for the murine Scavenger Receptor Class B1.
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-933-037-3

Query Match 100.0%; Score 1785; DB 9; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTCTCTCAGTCTGAGCCCGGAGAGCCCTTCGGCGCAGCGGACATGGGGCGCA 60
Db 1 CCGTCTCTCAGTCTGAGCCCGGAGAGCCCTTCGGCGCAGCGGACATGGGGCGCA 60
Qy 61 GCTCCAGGGCGCTGGGTGGCTTGGGTGGCGCCCTGGGGCTGCTGTTTCTCGGC 120
Db 61 GCTCCAGGGCGCTGGGTGGCTTGGGTGGCGCCCTGGGGCTGCTGTTTCTCGGC 120
Qy 121 TCGGGTGTTCATGATCCTCATGTGGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 180
Db 121 TCGGGTGTTCATGATCCTCATGTGGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 180
Qy 181 TCCGCATAGACCCGAGCAGCTGCTTCCGTGGGATGTGAAGGAGATCCCGTCCCTTCT 240
Db 181 TCCGCATAGACCCGAGCAGCTGCTTCCGTGGGATGTGAAGGAGATCCCGTCCCTTCT 240

Qy 241 ACTTGTCTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAGC 300
Db 241 ACTTGTCTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAGC 300
Qy 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTTCAGACAAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTTCAGACAAAAGGTCAACATCA 360
Qy 361 CCTTCAATGACAACGACACCGTGTCTCTGTGAGAAACCGCAGCCTCCATTTCCAGCCTG 420
Db 361 CCTTCAATGACAACGACACCGTGTCTCTGTGAGAAACCGCAGCCTCCATTTCCAGCCTG 420
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Qy 781 ATTATTGGCATTCAGACGAGTGTAAATGAGGACTTCCCGGCGAGATGTGGGCGAC 840
Db 781 ATTATTGGCATTCAGACGAGTGTAAATGAGGACTTCCCGGCGAGATGTGGGCGAC 840
Qy 841 CTTTCATGACACCCGAATCTCTGCTGGAATTTCTAGCCCGGAGGATGAGGATGTCATGA 900
Db 841 CTTTCATGACACCCGAATCTCTGCTGGAATTTCTAGCCCGGAGGATGAGGATGTCATGA 900
Qy 901 AGCTGACCTACACGAAATCAAGGGTGTGTTGAAGCATTCCTCAGTATCGCTTCAACGGCCC 960
Db 901 AGCTGACCTACACGAAATCAAGGGTGTGTTGAAGCATTCCTCAGTATCGCTTCAACGGCCC 960
Qy 961 CCGATACTCTGTTTGCACACGGGTCCGTCTTACCCACCAACGAAAGCTTCTGCCCATGCC 1020
Db 961 CCGATACTCTGTTTGCACACGGGTCCGTCTTACCCACCAACGAAAGCTTCTGCCCATGCC 1020
Qy 1021 GAGAGTCTGGCATTCAGAATGTGAGCACTGAGGTTTGGTGGCGCTCTGTTTCTCTCCC 1080
Db 1021 GAGAGTCTGGCATTCAGAATGTGAGCACTGAGGTTTGGTGGCGCTCTGTTTCTCTCCC 1080
Qy 1081 ACCCCACATTTTACAGCGGACCCCTGTGTCGAAGCTGTTCTTGGTCTCAACCCCTA 1140
Db 1081 ACCCCACATTTTACAGCGGACCCCTGTGTCGAAGCTGTTCTTGGTCTCAACCCCTA 1140
Qy 1141 ACCCAAGGAGCATTCCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
Db 1141 ACCCAAGGAGCATTCCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
Qy 1201 GTTCTGTGAAGATGACAGCTGAGCCTTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Db 1201 GTTCTGTGAAGATGACAGCTGAGCCTTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Qy 1261 GGAAGATCGAGCCAGTAGTTCTGCGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
Db 1261 GGAAGATCGAGCCAGTAGTTCTGCGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
Qy 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGTGTGCTGATGCCCCAGGTTCTTCACTACG 1380

Qy	1381	CGCAGTATGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGTGGCCCATCATCTGCCAAC	1440
Db	1523	CGCAGTATGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGTGGCCCATCATCTGCCAAC	1582
Qy	1441	TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTAGTAAAGGGCTCCACAGATA	1500
Db	1583	TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTAGTAAAGGGCTCCACAGATA	1642
Qy	1501	AGGAGGCCATTACAGGCCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCGCACGGTGC	1560
Db	1643	AGGAGGCCATTACAGGCCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCGCACGGTGC	1702
Qy	1561	TGCAGAAGCCAGCTATAGGGTCTCAAGACACTATAAGCCCCCAAACTGATAGCTT	1620
Db	1703	TGCAAGAAGCCAGCTATAGGGTCTCAAGACACTATAAGCCCCCAAACTGATAGCTT	1762
Qy	1621	GGTCAAGCAGGCCACCCAGTCCCTACACCCGCTTCTTTGAGGACTCTCTCAGCGGCACGC	1680
Db	1763	GGTCAAGCAGGCCACCCAGTCCCTACACCCGCTTCTTTGAGGACTCTCTCAGCGGCACGC	1822
Qy	1681	CCACCACTGCCATGGCCCTGAGCCCCCAGATGTTCACACTGTGCCAGCGCACGCACATGG	1740
Db	1823	CCACCACTGCCATGGCCCTGAGCCCCCAGATGTTCACACTGTGCCAGCGCACGCACATGG	1882
Qy	1741	ATGCCCAAGCATGTGCAAAAACAACTCAGGGACCAAGGACAGACC	1785
Db	1883	ATGCCCAAGCATGTGCAAAAACAACTCAGGGACCAAGGACAGACC	1922

RESULT 7

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US-09-882-945A-285
; Sequence 285, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 285
; LENGTH: 1607
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-882-945A-285

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Query Match	90.0%;	Score 1607;	DB 3;	Length 1607;
Best Local Similarity	77.3%;	Pred. No. 0;		
Matches 1243;	Conservative 364;	Mismatches 0;	Indels 0;	Gaps 0
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Db	1	GCUCAAGAUGCCGCAUNGACCCGAGCAGCGUCCUUCGGAGUGUGNAGGAGAUCC	60	
Qy	230	CGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGAAGTGGTCAACCCAAAACGAGGTCTCTCAA	289	
Db	61	CGUCCUUCUACUUGUGUGUCUACUUCUUCGAAUGUGGUCAACCCAAAACGAGGUGUCCUCAA	120	
Qy	290	CGGCGCAAGACCGAGTAGTCCGSGGACGCTGGACCCCTATGTCTACAGGAGATTACAGACAAA	349	
Db	121	CGGCGCAAGACCCAGUAGUCGSGGACGUGGACCCUUAUGUCUACAGGAGGUUCAGACAAA	180	
Qy	350	GGTCAACATCATTCTCAATGACAACGACACCGTGTCTCTTCGTGGAGNACCGGAGCCTCCA	409	
Db	181	GGUCAACAUCUUCUUAUGACAACGACACCGUGUCCUUCUGUGAGAACCGCAGCUCUCA	240	
Qy	410	TTTTCAGCCTCGACAAGTCGCATGGCTCAGAGAGTGACTCATTTGTACTCGCTAAACTCTT	469	

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
6938.932 Million cell updates/sec

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Perfect score: 1785
Sequence: 1 CCGTCTCTTCAGGTCTCTGA.....TCAGGACCGAGGACAGACC 1785

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubnpa/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubnpa/US11_NEW_PUB.seq.*
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- 14: /cgn2_6/ptodata/1/pubnpa/US11_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1455.6	82.1	2497	12	US-11-136-527-2943
2	1369.8	76.7	1788	12	US-11-128-061-1074
3	1369.8	76.7	1788	12	US-11-128-049-1074
4	1291.2	72.3	1531	9	US-11-222-745-3
5	1142.6	64.0	2569	8	US-10-821-234-66
6	1141	63.9	2566	9	US-11-072-175-90
7	1141	63.9	2566	12	US-11-055-309A-11
8	1048.4	58.7	1530	9	US-11-222-745-8
9	694.6	38.9	1400	12	US-11-136-527-7039
10	513.2	28.8	600	12	US-11-128-061-4716
11	513.2	28.8	600	12	US-11-128-049-4716
12	163.8	9.2	2076	12	US-11-136-527-1803
13	127	7.1	1400	12	US-11-136-527-5899
14	97.2	5.4	496	12	US-11-128-061-2632
15	97.2	5.4	496	12	US-11-128-061-2632
16	97.2	5.4	496	12	US-11-128-049-2632
17	97.2	5.4	496	12	US-11-128-049-6274
18	82.2	4.6	506	6	US-09-925-065A-51554
19	69.6	3.9	2675	12	US-11-136-527-2950
20	64.8	3.6	1910	12	US-11-128-061-1101

21	64.8	3.6	1910	12	US-11-128-049-1101	Sequence 1101, Ap
22	58.6	3.3	2216	8	US-10-909-125-1747	Sequence 1747, Ap
23	57.8	3.2	645	6	US-09-925-065A-675492	Sequence 675492, Ap
24	43.6	2.4	586	6	US-09-925-065A-593691	Sequence 593691, Ap
25	43.6	2.4	586	6	US-09-925-065A-593692	Sequence 593692, Ap
26	43.6	2.4	595	6	US-09-925-065A-840891	Sequence 840891, Ap
c 27	43	2.4	2024	12	US-11-004-762-21	Sequence 21, Appl
28	41.4	2.3	2718	6	US-09-925-065A-701020	Sequence 701020, Ap
c 29	41.4	2.3	2828	12	US-11-004-762-22	Sequence 22, Appl
30	41	2.3	4192	7	US-10-826-585-36	Sequence 36, Appl
31	41	2.3	4646	8	US-10-775-169-198	Sequence 198, Appl
32	41	2.3	4646	12	US-11-045-578-5	Sequence 5, Appl
c 33	38.8	2.2	6264	12	US-11-075-185-58	Sequence 58, Appl
c 34	38.8	2.2	78869	12	US-11-075-185-1	Sequence 1, Appl
35	38.2	2.1	2060	12	US-11-122-329-8	Sequence 8, Appl
36	38.2	2.1	2060	12	US-11-169-041-66	Sequence 66, Appl
37	37.8	2.1	1400	12	US-11-128-061-4097	Sequence 4097, Ap
38	37.8	2.1	1400	12	US-11-128-049-4097	Sequence 4097, Ap
39	37.8	2.1	3958	12	US-11-128-061-455	Sequence 455, App
40	37.8	2.1	3958	12	US-11-128-049-455	Sequence 455, App
41	36.8	2.1	2043	12	US-11-000-688-1033	Sequence 1033, Ap
42	36.8	2.1	2048	12	US-11-226-701-16	Sequence 16, Appl
43	36.6	2.1	6615	12	US-11-052-554A-518	Sequence 518, App
44	36.4	2.0	564	6	US-09-925-065A-331637	Sequence 331637, Ap
45	36.4	2.0	564	6	US-09-925-065A-331639	Sequence 331639, Ap

ALIGNMENTS

RESULT 1
US-11-136-527-2943
; Sequence 2943, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2943
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2943

Query Match	82.1%	Score	1465.6	DB	12	Length	2497
Best Local Similarity	88.6%	Pred. No.	0				
Matches	1558	Conservative	23	Mismatches	177	Indels	0
Gaps	0						
Qy	1	CCGTCCTCTTCAGTCTCTGAGCCGAGAGCCCTTCGCGCGCAGCGGACATGGCGGCA	60				
Db	153	CGGTCTCTTCAGTCTCTGAGCCGAGAGCTTCGCGCGCAGCGGACATGGCGGCA	212				
Qy	61	GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTTGGGCGCCCTGGGGCTGCTGTTGCTGCGC	120				
Db	213	GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTTGGGCGCTGCTGTTGCTGCGC	272				
Qy	121	TCGCGGTGTCATGATCTCTGATGTCCTTCCTTCATCAAGCAGCAGGCTCTCAAGATG	180				
Db	273	TCGCGGTGTCATGATCTCTGATGTCCTTCCTTCATCAAGCAGCAGGCTCTCAAGATG	332				
Qy	181	TCGCGATAGACCCGAGCAGCTGCTCTTCGGGATGTGAAGGAGATCCCGTCTCTTCT	240				
Db	333	TCGCGATAGACCCGAGCAGCTGCTCTTCGGGATGTGAAGGAGATCCCGTCTCTTCT	392				
Qy	241	ACTTGTCTGCTACTTCTTCGAAGTGGTCAACCAACAGAGGTCTCTCAACGCGCAGAAC	300				


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Qy 185 CATAGACCCGAGCAGCCCTGCTCTTGGGATGTGGAAGAGATCCCCGTCCTCTTCTACTT 244
Db 290 CATAGACCCGAGCAGCCCTGCTCTTGGCAATGTGGAAGAGATCCCTGTACTT 349
Qy 245 GTCTGTCTACTTCTTGAAGTGTCAACCCAAAGAGGTCTCTAA CGGCCAGAACCCAGT 304
Db 350 GTCCGCTACTTCTTTCGAGGTGTGTCATCCAGCAGATCTTAAAGGTTGGAAGCCAGT 409
Qy 305 AGTCCGGAGGTGGAACCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCACTT 364
Db 410 AGTCCGGAGGTGGAACCTATGTCTACAGGAAATTCAGACAAAGGCCAACATCACTT 469
Qy 365 CAATGACACGACACCGGTGCTCTTCTGAGAGAACCGCAGCCTCTCAATTTCCAGCCTGACAA 424
Db 470 CAATGACAAATGATACTGTGTCTTGTGGAGACCGCAGCCTCAATTTCCAGCCGAGACAG 529
Qy 425 GTCCATGGCTCAGAGAGTGACTATGTAATGTGCTTAAACATCTTGTGCTCTGAGGAGCTC 484
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Qy 485 GATATTGATGAGAGCAAGCTGTGAGCCTGMAAGTCTGATGATGACCTTGGGCTGTGTCAC 544
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Qy 545 CATGGGCCAGCGTCTTTTATGAAACCGACAGATTGTGTGAGATCTCTGTGGGCTATGACGA 604
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Qy 725 CCAGAAATTTCAAGAGTCACTCTGTGTGGAACAAATGGAACGGACTCAGCAAGATCGAATTA 784
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Qy 845 CATGACACCCGAACTCTGCTGGAATTTCTCAGCCCGAGGCATGCAAGTCCATGAAGCT 904
Db 950 CATGACACCCGAACTCTGCTGGAATTTCTCAGTCCGGAAGCCTGCAAGGCTCATGAAGCT 1009
Qy 905 GACCTACAAAGAAATCAAGGGTGTGGAAGGCAATTTCCACAGTATCGCTTCAAGGCCCCCGA 964
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Db 1250 AAGGAGCAATTCCTGTTTCTTGAATCAATCCATCCGCTCACTGGGATCCCATGAATCTTTC 1309
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Db 1430 GCCCTTGAACACAGCTTCTACACGAGCTGTGTGATGCCCCAGGTCTTCTACGTATGCA 1489
Qy 1385 GTATGTGCTGCTGGGCTTGGAGCCTCTCTGTTGCTGGTGGCCCATCATCTGCCAACTGCG 1444
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Qy 1445 CAGCCAGGAAATGCTTTTGTGAGTGTGTAGTAAAGGGCTCCAGAGTAAGGA 1504
Db 1550 CAGCCAGGAAATGCTTTTATTTGAGTGTGTAGTAAAGGGCTCCAGAGTAAGGA 1609
Qy 1505 GGCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGCAAGGCTGCTGCA 1564
Db 1610 GGCATTCAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGCAAGGCTGCTGCA 1669
Qy 1565 AGAAGCAAGCTATAGGCTCTGGAAGACACTATAAGCCCCCCCCAACTGATAGCTTGGTC 1624
Db 1670 AGAAGCAAGCTATAGGCTCTGGAAGACACTATAAGCCCCCCCCAACTGATAGCTTGGTC 1729
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Db 1730 AGACCAAGCAGCAGCCTTACACCCCGCTTCTTGAAGACTCTCTCAGGGGACAGTC 1786

RESULT 4
US-11-222-745-3
; Sequence 3, Application US/11222745
; Publication No. US20060035834A1
; GENERAL INFORMATION:
; APPLICANT: Karin, Nathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30441
; CURRENT APPLICATION NUMBER: US/11/222,745
; CURRENT FILING DATE: 2005-09-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-222-745-3

Query Match 72.3%; Score 1291; DB 9; Length 1531;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1381; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy 50 CATGGGGGAGCTCCAGGGCGGCTGGGTGGGCTTGGGGTGGGGCCCTGGGGCTGTCT 109
Db 1 CATGGGGGAGCTCCAGGGCACCTGGGTGGGCTTGGGGCTGGGGCTTCTAGGGCTGT 60
Qy 110 GTTGTGCTGCGCTGGGCTGTGATGATCTCATGTGTGCGCTCCCTCATCAAGCAGCAGGT 169
Db 61 GTGTGCTGCGCTGGGCTGTGATGATCTCATGTGTGCGCTCCCTCATCAAGCAGCAGGT 120
Qy 170 GCTCAAGAAATGTCGCGATAGACCCGAGCAGCTGTCTTCCGGATGTGGAAGAGATCCC 229
Db 121 GCTCAAGAAATGTCGCGATAGACCCGAGCAGCTGTCTTCCGGATGTGGAAGAGATCCC 180
Qy 230 CGTCCCTTTCTACTGTGTCTACTTCTTCGAAGTGGTCAACCCAAACAGGCTCCCAA 289
Db 181 TGTTCCTTTCTACTGTGTGTCTACTTCTTCGAAGTGGTCAACCCAAACAGGCTCCCAA 240
Qy 290 CGGCCAGAGCCAGTAGTCCGGAGGTGAGACCTATGTCTACAGGAGTTTCAGACAAA 349
Db 241 TGGCCAGAGCCAGTAGTCCGGAGGTGAGACCTATGTCTACAGGAGTTTCAGACAAA 300
Qy 350 GGTCAACATCACCTTCAATGACACCAACCGGTGTCTTCTGTGGAGAACCGGAGCTCCA 409
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554 GCCTGCTTTATGAACCGCAGCTGGTGAGATCTCTGTGGGGCTATGACGATCCCTTCGT 613
1997 ACCTGCTTTATGAACCGCAGCTGGTGAGATCATGTGGGGCTACAGGACCCCTTGT 1938
614 GCATTTTCTCAACACGCTACCTCCGACAGATGCTTCCCATAAAGGGCAAAATTTGGCCTGTT 673
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1757 CGATCAGTGCAACATGATCAATGGGACTTCTGGGCAATGCGGCGCTTTCATGACTCC 1698
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1574 GCTATAGGCTCTTGAACACTATTAAGCCCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCT 1633
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1634 ACCCAGTCTCTTACACCCCGCTTCTTGGAGTCTCTCTCAGCGGACAGCCCACTGCTCAT 1693

917 CCCAGCCCTTACACCCCGCTTCTCCGGAATCTCCAGGACAGAGCCCGCCAGCCAC 858
1694 GGCCTGAGCCCC 1706
857 AGCCTGAGCCTCC 845
RESULT 6
US-11-072-175-90
; Sequence 90, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 2566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-90
Query Match 63.9%; Score 1141; DB 9; Length 2566;
Best Local Similarity 79.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 345; Indels 0; Gaps 0;
QY 14 GTCTCAGCGCCGAGAGCCCTTCCGCGCACGCGGACATGGGCGGCGAGCTCCAGGGCGCG 73
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QY 74 CTGGGTGGCTTGGGGTGGGGCTTGGGGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCT 133
DB 93 CTGGGTGGCTGCGGGGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152
QY 134 GATCCTCATGTTGCCCTCCCTCATCAAGCAGCAGGCTGCTCAAGAAAGTCCGATAGACCC 193
DB 153 GATCGTGAATGGTGGCTGCTCATCAAGCAGCAGGCTGCTTAAGAAAGTCCGATAGACCC 212
QY 194 GAGCAGCTGCTCTTCCGGATGTGGAAGAGATCCCGCTTCTTCTTCTTCTTCTTCTTCT 253
DB 213 CAGTAGCCTGCTTCAACATGTGGAAGAGATCCCTATCCCTTCTTCTTCTTCTTCTTCT 272
QY 254 CTTCTTCAAGTGGTCAACCCAAACGAGTCTCAACCGGCGAGAGCAGTGTCCGGGA 313
DB 273 CTTCTTCAAGTGGTCAACCCAAACGAGTCTCAACCGGCGAGAGCAGTGTCCGGGA 332
QY 314 GCGTGAACCTTGTCTTACAGGAGTTCAGACAAAGGTCACATCAACCTTCAATGACAA 373
DB 333 GCCTGGGCTTGTGAGTGTACAGGAGTTCAGGCAAAAGCAATCAACCTTCAACAA 392
QY 374 CAGACCGTGTCTTCTTGGAGAACCGGAGCTTCCATTTCCAGCCTGACAAAGTCCGATGG 433
DB 393 CGACCGTGTCTTCTTGGAGTACCGGCTTCCAGTTCAGGCTTCCAGCTTCCAGCTCC 452
QY 434 CTGAGAGTGTACTAATTGTACTGCTTAACATCTTGGTCTTGGGGGCTTGGATTTGAT 493
DB 453 CTGAGAGTGTACTAATTGTACTGCTTAACATCTTGGTCTTGGGGGCTTGGATTTGAT 512
QY 494 GAGAGCAACCTTGTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 553
DB 513 GGAGATAAGCCCATGACCTGAACTCATATGATCTTGGCATTCACCACTTCCGCGA 572
QY 554 GCCTGCTTTTATGAACCGCAGCTTGTGAGATCTCTTGGGGCTTATGACGATCCCTTCGT 613

Qy 494 GGAGAGCAAGCCTGTGACGCTGAGCTGATGATGACCTTGGCGTGTGTCACCATGGGCCA 553
Db 513 GGAGAAAGCCCATGACCTTGAAGCTCATCATGACCTTGGCATTCACCAACCCCTCGSCGA 572
Qy 554 GCGTGTCTTTATGAACCGCACAGTTGTGTGATCTCTGTGGGGCTATGACGATCCCTTCGT 613
Db 573 ACGTGCCTTCATGAACCGCACAGTTGTGGGTGATCATGTGGGGCTTACAAAGGACCCCTTGT 632
Qy 614 GCATTTTCTCAACAGCTACCTCCAGACATGCTTCCCATAAAGGGCAAAATTTGSCCTGTT 673
Db 633 GAATCTCATCAACAGTACTTTCAGGCATGTTCCCTTCAAGGACAAAGTTCGATTAAT 692
Qy 674 TGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTTCACGGGCGTCCAGAAATTT 733
Db 693 TGCTGAGCTCAACAACTCCGACTTGGGCTCTTACGGTCTTACGGGGGTCCAGAACAT 752
Qy 734 CAGCAGGATCCATCTGTGGGCAAAATGGACCGGACTCAGCAAGATCAATTAATTTGGCAATC 793
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Qy 794 AGACAGTGTAAACATGATCAATGGGACTTCGGGCGAGATGGGCGACCTTTCATGACACC 853
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Db 873 TGAGTCTCGCTGGAGTTCTTAAAGGCAATCCACGATATCGCTTCTGGCTCCCAAAACCCCTGTT 932
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Db 1113 CAACGCCAGCCTGTGTGTGTAAGGCAATCCACGATATCGCTTTCACGGGCGGCTTTCATGCTGTCAT 1172
Qy 1154 TTCTTGTCTTACACATCCATCCGTCACCTGGGATCCCATGAACTTCTGTGGAAT 1213
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Qy 1214 GCAGCTGAGCCTTACATCAAACTCTGCAAGGGCATCGGGCAACAGGGAAGATCGAGCC 1273
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Qy 1334 CACGTTTACAGCAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1393
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Qy 1394 GCTGGGCTTGGAGGCTCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453
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Db 1473 GAAATGCTTTTGTGTAAGGCAATCGGGCAACAGGGAAGATCGAGCC 1532
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Qy 1574 GCTATAGGGTCTGAGACACTATAAGCCCGCCCAAACTGATAGCTTGGTTCAGACCAAGCC 1633

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Db 1653 CCCACCGCTTACACCGCTTCTTCCCGGACTTCCAGCAGACAGCCCCCAGCCCCAC 1712
Qy 1694 GGCTGAGCCCC 1706
Db 1713 AGCTGAGCTCC 1725

RESULT 8
US-11-222-745-8
; Sequence 8, Application US/11222745
; Publication No. US20060035834A1
; GENERAL INFORMATION:
; APPLICANT: Karin, Nathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AN
; FILE REFERENCE: 30441
; CURRENT APPLICATION NUMBER: US/11/222,745
; CURRENT FILING DATE: 2005-09-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-222-745-8

Query Match 58.7%; Score 1048.4; DB 9; Length 1530;
Best Local Similarity 80.3%; Pred. No. 7e-289;
Matches 1229; Conservative 0; Mismatches 301; Indels 0; Gaps 0;

Qy 51 ATGGGGCGGAGCTCCAGGGCGGCTGGGTGGCTTGGGGTGGGGCTTGGGGCTGCTG 110
Db 1 ATGGGCTGTCTCCGCCAAAGCGGCTGGGCTGGCGGGCGCTGGGGCTGCTGCTG 60
Qy 111 TTTGCTGGCTGGGCTGTGTCATGATCTTGGTGGCTTGGGGTGGGGCTTGGGGCTGCTG 170
Db 61 TGGGCTGTGCTGGGCTGTGTCATGATCTGTCATGTCGTCGTCGTCATCAAGCAGGTC 120
Qy 171 CTCAGAAATGTCGCGATAGACCCGAGCAGCTGCTCTTGGGATGTGGAGGAGATCCCC 230
Db 121 CTTAAGAACGTGGGATCGACCCAGTAGCTGCTCTTCAACATGTGGAAGGAGATCCCT 180
Qy 231 GTCCTTTCTACTGTGTCTACTTCTTGAAGTGGTCAACCCCAACGAGGTCCTCAAC 290
Db 181 ATCCCTTCTATCTCTCCGCTACTTCTTTGAGCTCATGAACCCAGCGAGATCCTGAAG 240
Qy 291 GGCAGAGCAGTAGTCGGGAGCGTGGACCTATGTCTACAGGGAGTTTCAGACAAAG 350
Db 241 GGCAGAGCAGTAGTCGGGAGCGCGGGCTTACGTGTACAGGGAGTTCAGGCAAAA 300
Qy 351 GTCAACATCACCTTCAATGACACGACACGTCGCTCTTGGTGGAGAACCGACGCTCCAT 410
Db 301 AGCAACATCACCTTCAACACGACACCGTCGCTCTTCTCGAGTACCGACCTTCAG 360
Qy 411 TTCAGCCTGACAAGTTCGATGGCTCAGAGGTGACTTACTTGTCTGCTTAACATCTTG 470
Db 361 TTCAGCCTTCAAGTTCGACCGCTCGGAGCGACTACATCGTCATGCCCAACATCTG 420
Qy 471 GTCTGGGGGCTCGATATTTGATGGAGAGCAAGCTGTGTAGGCTTGAAGCTGATGAGCC 530
Db 421 GTCTGGGGGCTCGATATTTGATGGAGAGCAAGCTGTGTAGGCTTGAAGCTGATGAGCC 480
Qy 531 TTGGGCTGTGTACCATGGGCGGCTGCTTTTATGAACCGCAGTGTGTGAGATCTG 590
Db 481 TTGGGCTGTGTACCATGGGCGGCTGCTTTTATGAACCGCAGTGTGTGAGATCTG 540
Qy 591 TGGGGCTGTGTACCATGGGCTGCTTTTCTCAACACGTCACCTCCAGACATGCTTCCC 650

541	Db	TGGGGCTCAAGGACCCCTTTGTGAAATCTCATCAACAAAGTACTTTTCCAGGCGATGTTCCCC	600
651	Qy	ATAAGGGCAAAATTTGGCGCTGTTTGTGGATGAACCAACTCGAAATCTTGGGGCTCTTCACT	710
601	Db	TTCAAGGACAAATTCGATTTATTTGCTGAGCTCAACAACTCCGACTCTGGGCTCTTCAAG	660
711	Qy	GTCTTACGGGGCTGCAGAAATTTTCAGCAGAGATTCATCTGTGTGGAACAATGGAAACGGACTC	770
661	Db	GTGTTCACGGGGGTCCAGAAATCATCAGCAGGATCCACTCGTGTGGAACAATGGAAACGGGCTG	720
771	Qy	AGCAAGATCGATTTATTCGCAATTCAGACAGTGTAACATGATCAATGGGACTTTCGGGCGAG	830
721	Db	AGCAAGGTTGACTTCTGGCATTCGATCAGTGCAACATGATCAATGGAACTTCTGGGGCAA	780
831	Qy	ATGTGGGACACCTTTTCATGACACCCGGAATTCCTCGCTGGAAATCTTTCAGCCCGGAGGCATGC	890
781	Db	ATGTGGCGCGCTTTCATGACTCTCTGAGTCTCGCTGGAGTTCTACAGCCCGGAGGCGCTGC	840
891	Qy	AGGTCCATGAAGCTGACTCAACAGAAATCAAGGGTGTTTGAAGGCAATTCACACGTATCGC	950
841	Db	CGATCCATGAAGCTTAATGTACAAGGAGTCAGGGGTGTTTGAAGGCATCCCCACCATATCGC	900
951	Qy	TTCAAGGCCCCCGATATCTGTGTTTGCACACGGGTCGCTCTACCCACCCCAACGAAGGCTTC	1010
901	Db	TTGCTGGCTCCCAAAACCTGTGTTGCCAACGGGTCCATCTACCCACCCCAACGAAGGCTTC	960
1011	Qy	TGCCCATGCGGAGAGTCTGGCATTTCAGAAATGTCAGACACTTCGACGGTTTGTGCGCCCTCTG	1070
961	Db	TGCCCGTGCGTGAGTCTCGAAATTCAGAAATTCAGAACGTCAGCACCTGCAGGTTTCAGTGCCCTTG	1020
1071	Qy	TTTTCTCCCAACCCCACTTTTACAAAGCCGACCTGTGTGTGTCAGAAAGCTGTGTTCTGGT	1130
1021	Db	TTTTCTCTCCCATCTCTCACTTCTCTCAACGCCGACCCGGTTCTGGCAGAAAGCGGTGACTGGC	1080
1131	Qy	CTGAACCTTAACCCAAAGGAGCATTCCTGTGTTCTTAGACATCCATCCGCTCACTGGGATC	1190
1081	Db	CTGCAACCTTAACAGGAGGACATCTCTTGTGTTCTTCGACATCCACCCGCTCAACGGGAATC	1140
1191	Qy	CCCATGAATGTTCTGTGAAGATGACAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATC	1250
1141	Db	CCCATGAATGCTCTGTGAAACTGCAGCTGAGCCTCTACATGAAATCTGTGCGAGGCATT	1200
1251	Qy	GGGCAACAGGGAGATCGAGCAGTAGTTTCTGCGGTTGCTGTGGTTTTCGAACAGAGCGGA	1310
1201	Db	GGAACAACTGGGAAGATTTGAGCCCTGTGGTCTCTGCGCCTGCTCTGGTTTTCGACAGAGCGGG	1260
1311	Qy	GCAATGGGTGGCAAGCCCTCTGAGCACGTTCTTACACGACGCTGGTGTGATGCCCCAGGTT	1370
1261	Db	GCCATGGAGGGGAGATCTTTCACACATTTACACTCAGCTGTGTTGTATGCCCCAAGGTG	1320
1371	Qy	CTTTCATACGCGCAGTAGTGTCTGTCTGGGGCTTCGAGGCCCTCTCTGTTGCTGGTGCCTCATC	1430
1321	Db	ATGCACTATGCCCCAGTAGTCTCTCTGCGCGCTGGGGCTCGGCTCTGCTGCTGCTCCCTGTC	1380
1431	Qy	ATCTGCCAACTGCGCAGCAGGAGAAATGCTTTTTTGTGTTTGGAGTGTGTATTAAGGGC	1490
1381	Db	ATCTGCCAAATTCGGAGCCCAAGAAATGCTATTATTTTGGAGTAGTAGTAAAGGGC	1440
1491	Qy	TCCCAGGATTAAGGAGGCCATTTACGGCCTACTCTCTGAGTCCCTGTGATGTACACAGCTGCCAAG	1550
1441	Db	TCAAGGATTAAGGAGGCCATTTACGGCCTATTCTGAAATCCCTGTATGACATCAAGCTCCCAAG	1500
1551	Qy	GGCACGGTGTGCAAGAGCCAAAGCTATAG	1580
1501	Db	GGCTCTGTGCTGCAGGAAGCAAACTGTAG	1530

RESULT 9

RESULT 9
US-11-136-527-7039

03-11-138-327-7033 ; Sequence 7039, Application US/11136527

Sequence 7032, Application 03/1
; Publication No. US20050287570A1

; COLLECTION NO: 0020
; GENERAL INFORMATION:

APPLICANT: Wyeth

Db 781 CGGCACATAGTGTGCGGAACACTCAKGGACCA 813

RESULT 10

```

US-11-128-061-4716
; Sequence Filing No. US20060003958A1
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128.061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4716
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-4716

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D_b 541 CAGACCAGCCATCCAGCCCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC 598

RESULT 11

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US-11-128-049-4716
; Sequence 4716, Application US/11128049
; Publication No. US20060010513A1
;
GENERAL INFORMATION:
;
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
;
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
;
TITLE OF INVENTION: MAKING AND USING SAME
;
FILE REFERENCE: 01997.027700
;
CURRENT APPLICATION NUMBER: US/11/128,049
;
CURRENT FILING DATE: 2005-05-11
;
PRIOR APPLICATION NUMBER: US 60/570,425
;
PRIOR FILING DATE: 2004-05-11
;
NUMBER OF SEQ ID NOS: 7285
;
SOFTWARE: Patentin version 3.3
;
SEQ ID NO 4716
;
LENGTH: 600
;
TYPE: DNA
;
ORGANISM: Cricetus griseus
;
US-11-128-049-4716

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Db 541 CAGACCACCATCCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC 598

RESULT 12
US-11-136-527-1803
; Sequence 1803, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1803
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1803

Query Match 9.2%; Score 163.8; DB 12; Length 2076;
Best Local Similarity 47.1%; Pred. No. 2.3e-36;
Matches 572; Conservative 2; Mismatches 629; Indels 12; Gaps 2;

Qy 97 CCCGCGGCTGCTGTTGCTGCGCTCGCGGTGTCATGATCCTCATGGTGCCTCCCTCA 156
Db 271 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
Qy 157 TCAAGCAGCAGGTGCTCAAGAAATGTCGCGATAGACCCGAGCAGCTGTCTTCGGGATG 216
Db 331 TGGACACAGCATCAGAGAGATATGTTATCAAAATGGTACCAAGTCTTTGATTCCT 390
Qy 217 GGAAGGAGATCCCGTCCCTTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276
Db 391 GGGAGAGCCCCCTCTACTCTGTACATCCAGTTTATTTCTCAATGTCCACCAATCCAG 450
Qy 277 ACAGGTCTCTCAAGCGCAGAGCCAGTGTGCGGAGCGTGGACCTGTCTACAGGG 336
Db 451 AGGAGATCTCTCAAGGAGAAATCCCTGCTAGAGAGTGGGCGGTACACCTACAGGG 510
Qy 337 AGTTTCAGACAAAGGTCAACATCACTTCAATGACACACGACCGTGTCTTCGTGAGA 396
Db 511 AGCTCAGNACAGGCAACGCTTCAAGTTGAGAAATGGAAACCAATATCTCCGCTCA 570
Qy 397 ACCGAGCCTCCATTTCCAGCTGACAAAGTCGATGGCTCAGAGAGTCACTACATTGTAC 456
Db 571 CCAATAGGCATATATTTTGAACGAAACCACTGTGTTGGAGACCCCTACCGTTGACTTGA 630
Qy 457 TGCCTAACATCTGGTCTCGGGGGCTCGATATTGATGGAGAGACAGCTGTGAGCCCTGA 516
Db 631 TTGAACAATAAATATTTCTCTGTTGACTGTGTGGAATGGCCAGCAGCGCTTCTCTCA 690
Qy 517 AGCTGATGATGACCTTGGCGCTGTCTACCATGGCGCGTCTTTTATGACCGCAGAG 576
Db 691 GGGAGATCATCGAGCCATGCTGAAGCTTATCAGCAGACGCTGTTGTCTACTCACACTG 750
Qy 577 TTGCTGAGATCCTGTGGGGCTATGACGATCCCTTCGTGCATTTTCTCAACAGCTACCTCC 636
Db 751 TACATGAATCTCTCTGGGGCTTACAAAGATGAGGCTTGTGCTGCTCATATTTTCAGAC 810
Qy 537 CAGACATGCTTCCCATTAAGGGCAATTTGGCCGTGTTGGTGGATGAACTCGAATT 696
Db 811 CTGACGTCTCCCC-----TAACTTGGCCTGTTCTATGAGAGAAATGGAATAATG 861
Qy 697 CTGGGCTCTTCACTGCTCTTACGGCGCTCCAGAAATTTTCAGCAGGATCCATCTGCTGACA 756
Db 862 ATGGGGAGTATGTTTTCTGACTGGAGAGCAATTTACCTGAACTTTTACAAAATTTGG 921
Qy 757 AATGGAACGGACTCAGCAAGATCGATTATTGGCATTTCAGAGCAGTGTAAATGATCAATG 816

Db 922 AGTGGATGAAAAACGTCGCTGGACTGGTGGACGAGCACAGTGCATATGATCAACG 981
Qy 817 GGAATTCGCGGAGATGTGGGCAACCTTTCATGACACCCGAATCTGCTCGAATTTCTTCA 876
Db 982 GGCAGAGGAGATCTTTTTCACCCATTATAAGCAAGATGAGACCTGTACATCTTCC 1041
Qy 877 GCCCGAGGAGATGAGGTTCATGAGCTGACCTACACGAATCAAGGCTGTTTGAAGGCA 936
Db 1042 CATCTGACTTCTCGAGTCTGCTATATAACTTTTTCAGTAGCTTTGAGAACGTAGAGGAC 1101
Qy 937 TTCCAGTATGCTTTCACGCGCCCGCATACTCTGTTTCCAGCGGTCCGTCTACCCAC 996
Db 1102 TGCTGCTTTTTCGGTATAAGGTGCTGSCAGAAATAGCAAAATTCCTCCGAAAACGCTG 1161
Qy 997 CCAAC---GAAGGCTTCTGCCATGCCGAGAGTCTGCATTCAGAAATGTCAGCACTGCA 1053
Db 1162 GCTTCTGTATACCGGAGGAAATGTCATGACGCGGGAGTCTGACGTGACGATTTGCA 1221
Qy 1054 GGTTCGCTGCTGCTGCTTCTCTCCACCCCACTTTTACACGCGGACCTGTGTGTGT 1113
Db 1222 AGAATGCTGCGCCATTTATCATGCTTCTTCCACACTTTTACCAAGCGGACGAGAAGTTCG 1281
Qy 1114 CAGAGCTGTTCTGCTGAAACCTTAACCCAAAGGAGCATTCCTGTTTCTTAGACATCC 1173
Db 1282 TTTTGGCCATAAAGGCGATCGTCCAAACAAAGGAAGAACATGAGTCAATTTTGTGGACATTA 1341
Qy 1174 ATCCGCTCAGTGGATCCCATGAACTGTTCTGTGAAGATGACAGCTGAGCTCTTACATCA 1233
Db 1342 ATCTTTGACAGAAATTTTAAAGGGSCTAAGAGATTCCAAATCAACACGTCATGTTA 1401
Qy 1234 AATCTGTCAAGGATCGGGCAACAGGGAAGATCGAGCCAGTAGTTTCTCCGTTGCTGT 1293
Db 1402 AGAAGCTGGATGACTTTGTGAAACGGAACATTTAGGCTATGKTTCCTCCAGTGT 1461
Qy 1294 GGTTCGACAGAGCG 1308
Db 1462 ATCTCAATGAGAGTG 1476

RESULT 13
US-11-136-527-5899
; Sequence 5899, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5899
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5899

Query Match 7.1%; Score 127; DB 12; Length 1400;
Best Local Similarity 49.9%; Pred. No. 6.3e-26;
Matches 375; Conservative 2; Mismatches 362; Indels 12; Gaps 2;

Qy 561 TTTATGAACCGCAGTGTGTGAGATCTCTGTGGGCTATGACGATCCCTTCGTGCAATTT 620
Db 59 TTTGTCACTCACACTGTACATGAACCTGCTGTGGGCTTACAAAGATGAGGTCTTGTGCTC 118
Qy 621 CTCACACGCTACCTCCAGACATGCTTCCATTAAGGGAATTTGGCCTGTTTGTGGG 680
Db 119 GTCCATATTTTCAGACCTGACGCTCCCC-----TAACTTGGCCTGTTCTATGAG 169

QY 681 ATGAACAACCTCGAATCTTGGGGTCTTCACTGTCTTCCACGGCGCTCAGAAATTTTCAGCAGG 740
Db 170 AGAAATGGAACATAATGATGGGAGTATGTTTTCTGACTGGAGAGGACAATTAACCTGAAC 229
QY 741 ATCCATCTGGTGGCAAAATGGAACGGACTCAGCAGATGCAATTAATGGCAATTCAGAGCAG 800
Db 230 TTTTACAAAAATTTGGAGTGGAAATGGAATAACCGTCTGGACTGGTGGAGCAGCGACAG 289
QY 801 TGTAAATGATCAATGAGACTTCCGGGCAGATGTGGSCACCTTCATGACACCCGGAATCC 860
Db 290 TGCATATGATCAACGGGACAGCGGAGATCTTTTCCACCAATTAATAAGCAAGGATGAG 349
QY 861 TCGCTGGAATTTCTTACGCCCGGAGCATGAGGTCCATGAAGTGAAGCTTCAACAGCAATCA 920
Db 350 ACCCTGTACATCTTCCCATCTGACTTCTGCAGGTCCGCTATATATACTTTTCAGTAGCTTT 409
QY 921 AGGTGTTTGAAGCATTCACAGTATCGCTTTCAGGCCCGCCGATCTCTGTTTGGCCCAAC 980
Db 410 GAGAACGTAGAGGACTGCTCTGCTTTTTCGGTATAAGGTGCTGCAGAAATACTAGCCAAAT 469
QY 981 GGTCCGTCTACCCACCCCAAC---GAGGGCTTCTGCCCATGCCGAGAGTCTGGCATTTCA 1037
Db 470 TCCTCCGAAACGCTGGCTTCTGTATACCGAGGAAACTGSCATGGACGGGAGTCTG 529
QY 1038 AATGTACGACCTCTGAGGTTTGGTGGCCCTCTGTTTCTCTCCACCCCCCACTTTTACAAC 1097
Db 530 AAGCTCAGCATTTGCAAGATGTTGGCCGCTATATCATGCTTTTCCACACTTTTACCA 589
QY 1098 GCCGACCTGTGTTGTGAGAGCTGTTCTTGGTCTGAACCTTAACCCAAAGGAGCATTC 1157
Db 590 GCCGACGAGAAGTTGTTTGGCCCATAAAGGCGTGGTCCAAACAGGAAGAACATGAG 649
QY 1158 TTGTTCTAGACATCCATCGGTCTGCTGAGTCCCATGAGTCTTCTGTGAGATGCG 1217
Db 650 TCAATTTGGACATTAATCTTTTACAGGAATTAATTTAAGAGGSCCAAGAGATTCCAA 709
QY 1218 CTGAGCCTCTACATCAAAATCTGTCAAGGCGATCGGCAAAACAGGGAAGATCGAGCCAGTA 1277
Db 710 ATCAACAGTACGTTAAGAGCTGATGACTTTGTGGAAACGGGAACATTAGMCTATG 769
QY 1278 GTTCTGCGTGTGTTGGTTCGAACAGCG 1308
Db 770 KTTTTCCAGTGATGTCTCAATGAGAGTG 800

RESULT 14
US-11-128-061-2632
; Sequence 2632, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2632
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-2632

Query Match 5.4%; Score 97.2; DB 12; Length 496;
Best Local Similarity 87.8%; Pred. No. 1.4e-17;
Matches 130; Conservative 0; Mismatches 13; Indels 5; Gaps 2;
QY 1638 AGTCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGCCACCGATGGCC 1697
Db 1 AGCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGTCCGCCAGTGGCC 60
QY 1698 TGAGCCCCCAGATGTCAACCTCTCGCACGCGACATGGATGCCACCGCATGTGCA 1757
Db 61 TGAGCCCCCAGATGTCAACCTCTCTGTC----TGCACAGCACATGCGCCCGGCGTGTGCA 116
QY 1758 AAAACAACCTCAGGACCGAGGACAGACC 1785
Db 117 AATC-ACTCAGGACCGAGGACAGACC 143
RESULT 15
US-11-128-061-6274
; Sequence 6274, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6274
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-6274

Query Match 5.4%; Score 97.2; DB 12; Length 496;
Best Local Similarity 87.8%; Pred. No. 1.4e-17;
Matches 130; Conservative 0; Mismatches 13; Indels 5; Gaps 2;
QY 1638 AGTCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGCCACCGATGGCC 1697
Db 1 AGCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGTCCGCCAGTGGCC 60
QY 1698 TGAGCCCCCAGATGTCAACCTCTCGCACGCGACATGGATGCCACCGCATGTGCA 1757
Db 61 TGAGCCCCCAGATGTCAACCTCTCTGTC----TGCACAGCACATGCGCCCGGCGTGTGCA 116
QY 1758 AAAACAACCTCAGGACCGAGGACAGACC 1785
Db 117 AATC-ACTCAGGACCGAGGACAGACC 143

Search completed: February 23, 2006, 18:46:02
Job time : 549.539 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 23, 2006, 12:34:44 ; Search time 152 Seconds
 (without alignments)
 1471.341 Million cell updates/sec

Title: US-08-765-108-8
 Perfect score: 2681
 Sequence: 1 MGSSRRARWALGALGALL.....YSESIMSPAAGTGLQEAHL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*

1: Geneseqp1980s:*
 2: Geneseqp1990s:*
 3: Geneseqp2000s:*
 4: Geneseqp2001s:*
 5: Geneseqp2002s:*
 6: Geneseqp2003as:*
 7: Geneseqp2003bs:*
 8: Geneseqp2004s:*
 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	2	AAW93575 Mouse sca
2	2681	100.0	509	2	AAW93575 Mouse sca
3	2681	100.0	509	5	Abb57092 Mouse isc
4	2681	100.0	509	5	Aae21525 Murine sc
5	2681	100.0	509	8	ADJ53337 Murine SR
6	2681	100.0	509	9	ADZ13455 Murine ca
7	2681	100.0	509	9	AEB03940 Murine Sc
8	2681	100.0	519	8	ABO84950 Murine ca
9	2681	100.0	519	8	ADR67033 Murine ca
10	2677	99.9	509	8	ADU51468 Mouse sca
11	2504	93.4	509	8	ADU51466 Rat scave
12	2504	93.4	510	7	ADE56446 Rat Prote
13	2504	93.4	510	7	ADE56442 Rat Prote
14	2479	92.5	509	7	ADE55241 Rat Prote
15	2468	92.1	506	9	ADZ13453 Murine ca
16	2447	91.3	509	2	AAW93575 Mouse sca
17	2447	91.3	509	2	AAW93574 Hamster s
18	2447	91.3	509	2	AAW93574 Hamster s
19	2447	91.3	509	5	ABG33056 Hamster S
20	2447	91.3	509	5	Aae21523 Murine s
21	2447	91.3	509	6	ABO27241 Human sca
22	2447	91.3	509	6	ADJ46121 Human sca
23	2447	91.3	509	8	ADJ53335 Hamster S
24	2447	91.3	509	8	ADU51467 Hamster s

25	2296	85.6	509	9	AEB03938 Hamster S
26	2200	82.1	509	6	ABO27240 Human sca
27	2200	82.1	509	8	ADJ46119 Human sca
28	2200	82.1	509	9	ADZ13464 Human can
29	2200	82.1	509	9	ADZ13458 Human can
30	2200	82.1	514	9	ADZ13466 Human can
31	2193	81.8	509	2	AAW97899 Human SR-
32	2193	81.8	509	2	AAW97899 Human SR-
33	2193	81.8	532	4	ABE12012 Human SR-
34	2193	81.8	532	7	ABE09273 Novel pro
35	2192	81.8	509	2	AAW49573 Human CLA
36	2192	81.8	509	2	AAW49573 Human CLA
37	2192	81.8	509	8	ADL61106 Human CD3
38	2192	81.8	510	7	ADL61106 Human CD3
39	2192	81.8	510	7	ADL61106 Human CD3
40	2160	80.6	509	7	ADL61106 Human CD3
41	2068.5	77.2	537	4	ABG22317 Novel hum
42	2051	76.5	481	7	ABG22317 Novel hum
43	2022.5	75.4	552	6	ABR62035 Human SR-
44	2022.5	75.4	552	7	ABR62035 Human SR-
45	2022.5	75.4	552	8	ADP23287 PRO polyp

ALIGNMENTS

RESULT 1

AAW93575
 ID AAW93575 standard; protein; 509 AA.
 XX
 AC AAW93575;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Mouse scavenger receptor class B-I protein.
 XX

Scavenger receptor class B type I; mouse; steroid production; HDL; cholesterol; cholesteryl ester transport; high-density lipoprotein; lipoprotein; liver; steroidogenic tissue; SR-BI; contraception; treatment; disorder; overproduction; underproduction; menopause; breast cancer; prostate cancer; endometriosis; fibroid tumour.

Mus sp.

WO9911288-A1.

11-MAR-1999.

04-SEP-1998; 98WO-US018463.

05-SEP-1997; 97US-0057943P.

(MASI) MASSACHUSETTS INST TECHNOLOGY.

Krieger M;

WPI; 1999-204984/17.

N-PSDB; AAX23404.

Modification of steroid production in mammals - by administering modulator of SR-BI expression or activity.

Disclosure; Page 81-82; 86pp; English.

This invention describes a method for modifying steroid production in a mammal which comprises administering a compound that alters cholesterol or cholesteryl ester transport from high-density lipoprotein (HDL) or other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger receptor class B type I). This method is useful for female contraception, for treating disorders characterised by overproduction of steroids, for treating disorders characterised by underproduction of steroids, especially menopause, for treating disorders that can be treated by decreasing steroid production, especially breast cancer, prostate cancer,

CC endometriosis or fibroid tumours

XX Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFYLSVYFFVNVNPNVNLNGQKVPVRRGYPVYRERFRQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFFVNVNPNVNLNGQKVPVRRGYPVYRERFRQKVNITFNDNDTVSFVENRSLH 120
 QY 121 FQPKSHGSES DYIVLPNII VLGGSILMESKPVSLKLMNTLALVTMGQRAFMNRTVGEIL 180
 Db 121 FQPKSHGSES DYIVLPNII VLGGSILMESKPVSLKLMNTLALVTMGQRAFMNRTVGEIL 180
 QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 QY 241 SKIDYWHSEQNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
 Db 241 SKIDYWHSEQNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
 Db 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
 QY 361 LNPMPKHSFLFDIHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVPVLLWPFQSG 420
 Db 361 LNPMPKHSFLFDIHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVPVLLWPFQSG 420
 QY 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGLLLVPIICQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGLLLVPIICQLRSQEKCFLFWSGSKG 480
 QY 481 SQDKEAIQAYSESILMSPAAGTGLVQEAAL 509
 Db 481 SQDKEAIQAYSESILMSPAAGTGLVQEAAL 509

RESULT 2

AAY44020
 ID AAY44020 standard; protein; 509 AA.

AC AAY44020;

XX 18-JAN-2000 (first entry)

DE Mouse Scavenger receptor class BI protein.

XX Hamster; scavenger receptor; modulation; cholesterol transport; lipid;
 KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;
 KW high density lipoprotein; ester; blood.

OS Mus sp.

XX US5962322-A.

XX 05-OCT-1999.

XX 15-NOV-1996; 96US-00749907.

XX 15-NOV-1996; 96US-00749907.

XX (UTPE-) UNIV PENNSYLVANIA.

FA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M, Rigotti A, Kozarsky K;
 PI

XX WPI; 1999-589717/50.
 DR N-PDB; AA230616.

XX Modulating cholesterol transport for the control of cholesterol levels in blood.

PS Disclosure; Col 29-32; 23pp; English.

XX This sequence represents the mouse scavenger receptor class BI (SR-BI) which is used in a method of modulating cholesterol transport. The method comprises selectively altering the transport of lipid, cholesterol and/or lipoproteins (or their components) into and out of mammalian cells to alter plasma cholesterol levels, by administering a compound which alters the expression or activity of the SR-BI scavenger protein receptor. This alters the rate of clearance of the protein component of high density lipoprotein (HDL) as compared to the ester component of HDL. The method may be used to control cholesterol levels in the blood plasma of mammals

XX Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFYLSVYFFVNVNPNVNLNGQKVPVRRGYPVYRERFRQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFFVNVNPNVNLNGQKVPVRRGYPVYRERFRQKVNITFNDNDTVSFVENRSLH 120
 QY 121 FQPKSHGSES DYIVLPNII VLGGSILMESKPVSLKLMNTLALVTMGQRAFMNRTVGEIL 180
 Db 121 FQPKSHGSES DYIVLPNII VLGGSILMESKPVSLKLMNTLALVTMGQRAFMNRTVGEIL 180
 QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 QY 241 SKIDYWHSEQNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
 Db 241 SKIDYWHSEQNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
 Db 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
 QY 361 LNPMPKHSFLFDIHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVPVLLWPFQSG 420
 Db 361 LNPMPKHSFLFDIHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIEPVPVLLWPFQSG 420
 QY 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGLLLVPIICQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGLLLVPIICQLRSQEKCFLFWSGSKG 480
 QY 481 SQDKEAIQAYSESILMSPAAGTGLVQEAAL 509
 Db 481 SQDKEAIQAYSESILMSPAAGTGLVQEAAL 509

RESULT 3

ABB57092

ID ABB57092 standard; protein; 509 AA.

XX ABB57092;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:202.
 DE Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX Krieger M, Rigotti A, Kozarsky K;
 PI

vasospastic ischaemia; ischaemic condition; ischaemic disease.

Mus musculus.

WO200188188-A2.

22-NOV-2001.

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

WPI; 2002-034733/04.

N-PSDB; AB199330.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

Claim 2; Page 576-579; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in AB57020 to AB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention

Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVWILMPSLIKQVILKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVWILMPSLIKQVILKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSSSDYILVNLVLGSSILMESKPVSLKLMNTLALVTMGORAFMNTVGEIL 180
Db 121 FQPKSHGSSSDYILVNLVLGSSILMESKPVSLKLMNTLALVTMGORAFMNTVGEIL 180
Qy 181 WGYDDPFVHFLNTLYLPMPLPIKGFGLFVGWNNNSGVFTVFTGVQNPRIHLVDKNLGL 240
Db 181 WGYDDPFVHFLNTLYLPMPLPIKGFGLFVGWNNNSGVFTVFTGVQNPRIHLVDKNLGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPMPTPESSLEPSPPEACHSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPMPTPESSLEPSPPEACHSMKLTYNESRVFEGIPYR 300
Qy 301 FTAPDTLAFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLAFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKXHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIIEPVVPLPLWFEQSG 420

Db 361 LNPMPKXHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGIQGTGKIIEPVVPLPLWFEQSG 420
Qy 421 AMGGKPLSTFTYTLVLMPOVLHYAQYVLLGIGLLLVPIICQLRSQEKCFLFWSGSKKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQYVLLGIGLLLVPIICQLRSQEKCFLFWSGSKKG 480
Qy 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509
Db 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509

RESULT 4

AAE21525

ID AAE21525 standard; protein; 509 AA.

AC AAE21525;

DT 16-JUL-2002 (first entry)

DE Murine scavenger receptor type B-I (SR-BI).

KW Scavenger receptor protein type BI; low density lipoprotein; LDL; murine; SR-BI.

OS Mus sp.

FN US6350859-B1.

PD 26-FEB-2002.

PF 02-FEB-1999; 99US-00241581.

PR 23-JUN-1994; 94US-00265428.

PR 27-MAR-1997; 97US-00765108.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Krieger M, Acton SL, Rigotti A;

DR WPI; 2002-314680/35.

DR N-PSDB; RAD33917.

PT Antibody specific for scavenger receptor protein type BI useful for detection, characterization or isolation of receptor proteins, as well as inhibiting scavenger protein binding to low density lipoprotein.

PS Claim 1; Col 49-52; 41pp; English.

CC The invention relates to an antibody specific for scavenger receptor protein type B-I (SR-BI) derived from murine and hamster. Antibodies of the invention are useful for detection, characterisation and isolation of receptor proteins and for inhibiting scavenger protein binding to low density lipoprotein (LDL). The present sequence is murine SR-BI protein Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 5; Length 509;

Best Local Similarity 100.0%; Pred. No. 3.8e-261;

Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVWILMPSLIKQVILKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVWILMPSLIKQVILKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSSSDYILVNLVLGSSILMESKPVSLKLMNTLALVTMGORAFMNTVGEIL 180
Db 121 FQPKSHGSSSDYILVNLVLGSSILMESKPVSLKLMNTLALVTMGORAFMNTVGEIL 180
Qy 181 WGYDDPFVHFLNTLYLPMPLPIKGFGLFVGWNNNSGVFTVFTGVQNPRIHLVDKNLGL 240

Db 181 WGYDDPFVHFLNTYLPDMLPIKGRGLFVGWNNNSGVFTFTGVQFNSRIHLVDKWNGL 240
 QY 241 SKIDYWHSEQCNNMNGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 Db 241 SKIDYWHSEQCNNMNGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 QY 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKIGQGTGKIEBPVVLPLLWPFQSG 420
 Db 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKIGQGTGKIEBPVVLPLLWPFQSG 420
 QY 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 Db 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 QY 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509
 Db 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509

RESULT 5

ADJ53337
 ID ADJ53337 standard; protein; 509 AA.

XX AC ADJ53337;

XX DT 06-MAY-2004 (first entry)

XX DE Murine SR-BI scavenger receptor polypeptide.

XX KW Mouse; SR-BI; scavenger receptor; HDL receptor; lipid; cholesterol;
 KW lipoprotein; bile acid; steroid hormone; vitamin A; atherosclerosis;
 KW adipocyte fat uptake; endocrine disorder; antiarteriosclerotic; receptor;
 KW scavenger receptor class BI.

XX OS Mus sp.

XX FN US2003167475-A1.

XX PD 04-SEP-2003.

XX PF 24-JUN-2002; 2002US-00178611.

XX PR 15-NOV-1996; 96US-00749907.

XX PR 30-AUG-1999; 99US-00385799.

XX PA (KOZA/) KOZARSKY K.

XX PA (RIGO/) RIGOTTI A.

XX PA (KRIE/) KRIEGER M.

XX PI Kozarsky K, Rigotti A, Krieger M;

XX DR WPI: 2004-246237/23.

XX DR N-PSDB; ADJ53336.

XX FT Screening for agents that influence lipid transport, useful e.g. for
 FT treating or preventing atherosclerosis, based on modulation of the SR-BI
 FT scavenger receptor.

XX PS Disclosure; SEQ ID NO 4; 22pp; English.

XX CC The invention relates to a method for screening compounds that alter
 CC transport of lipids, cholesterol, lipoproteins or their components,
 CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
 CC homologue. The test compound is administered to an animal and cholesterol
 CC or bile acid levels, production levels of steroid hormones or alterations
 CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
 CC hormones, bile acids and vitamin A is measured. Agents that alter
 CC transport of lipids, cholesterol or lipoproteins are potentially useful

CC for the treatment or prevention of atherosclerosis, fat uptake by
 CC adipocytes and some endocrine disorders. This sequence represents the
 CC murine SR-BI scavenger receptor of the invention.

XX SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 8; Length 509;

Best Local Similarity 100.0%; Pred. No. 3.8e-261;

Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMIIMVPSLIKQVLKNVRIDPSSLSFGMMKEIP 60

Db 1 MGSSRRARWALGALGALLFAALGVVMIIMVPSLIKQVLKNVRIDPSSLSFGMMKEIP 60

QY 61 VPYLSVYFEVYNPNEVLNGQKPVYRERGYPYVYRFRQKVNITFENDNIVSVFVNRSLH 120

Db 61 VPYLSVYFEVYNPNEVLNGQKPVYRERGYPYVYRFRQKVNITFENDNIVSVFVNRSLH 120

QY 121 FQDKSHGSES DYIVLPNIIIVLGGSIIMESKPVSLKLMMTLALVTMGQRAFMNRTVGEIL 180

Db 121 FQDKSHGSES DYIVLPNIIIVLGGSIIMESKPVSLKLMMTLALVTMGQRAFMNRTVGEIL 180

QY 181 WGYDDPFVHFLNTYLPDMLPIKGRGLFVGWNNNSGVFTFTGVQFNSRIHLVDKWNGL 240

Db 181 WGYDDPFVHFLNTYLPDMLPIKGRGLFVGWNNNSGVFTFTGVQFNSRIHLVDKWNGL 240

QY 241 SKIDYWHSEQCNNMNGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300

Db 241 SKIDYWHSEQCNNMNGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300

QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360

Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360

QY 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKIGQGTGKIEBPVVLPLLWPFQSG 420

Db 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKIGQGTGKIEBPVVLPLLWPFQSG 420

QY 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480

Db 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480

QY 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509

Db 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509

RESULT 6

ADZ13455

ID ADZ13455 standard; protein; 509 AA.

XX AC ADZ13455;

XX DT 16-JUN-2005 (first entry)

XX DE Murine cancer-associated protein #109.

XX KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

XX KW cytosolic.

XX OS Mus sp.

XX PN WO2005031001-A2.

XX PD 07-APR-2005.

XX PF 23-SEP-2004; 2004WO-US031617.

XX PR 23-SEP-2003; 2003US-00669920.

XX PA (CHIR) CHIRON CORP.

XX PI Morris DW, Malandro MS;

XX WPI; 2005-273395/28.
DR N-PSDB; ADZ13454.
XX
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
XX Disclosure; SEQ ID NO 975; 198pp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a murine cancer-associated protein of
CC the invention.
XX
XX Sequence 509 AA;
SQ
Query Match 100.0%; Score 2681; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSRRARWALGIGLGLLFAALGVMLVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Db 1 MGSRRARWALGIGLGLLFAALGVMLVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Qy 61 VPFFLSVFFVFNPNVNLGQKPVRRPGVYVREPRQKNITFNDNDTVSFVENRSLH 120
Db 61 VPFFLSVFFVFNPNVNLGQKPVRRPGVYVREPRQKNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMNTLALVTMGQAFMNRVTGSEIL 180
Db 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMNTLALVTMGQAFMNRVTGSEIL 180
Qy 181 WGYDDPFVHNTLYPDMLPIKGFGLVGMNNSGVFTFTGQNFSTRHLVDKWNGL 240
Db 181 WGYDDPFVHNTLYPDMLPIKGFGLVGMNNSGVFTFTGQNFSTRHLVDKWNGL 240
Qy 241 SKIDYWHSEQCNMNGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYWHSEQCNMNGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
Qy 301 FTPADTLFANGSVYPPNFGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVIG 360
Db 301 FTPADTLFANGSVYPPNFGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVIG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVKQQLSLYKSVKIGIQTKIEPVVPLPLWFQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVKQQLSLYKSVKIGIQTKIEPVVPLPLWFQSG 420
Qy 421 AMGGKPLSTFTQVLMPQVLYHAYVLLGGLLLVPIICQLRSQEKCFLWGSKKG 480
Db 421 AMGGKPLSTFTQVLMPQVLYHAYVLLGGLLLVPIICQLRSQEKCFLWGSKKG 480
Qy 481 SODKEAIOAYSESLMSPAAGTGVLEAKL 509

Db 481 SODKEAIOAYSESLMSPAAGTGVLEAKL 509
RESULT 7
AEB03940
ID AEB03940 standard; protein; 509 AA.
XX AEB03940;
AC AEB03940;
XX
XX 25-AUG-2005 (first entry)
XX Murine Scavenger Receptor Class B-1, SEQ ID 4.
XX Antilipemic; transgenic animal; Scavenger Receptor Class B-1;
XX high density lipoprotein receptor; cholesterol; lipid.
XX Mus sp.
XX US2005136005-A1.
XX 23-JUN-2005.
XX 02-SEP-2004; 2004US-00933037.
XX 23-JUN-1994; 94US-00265428.
XX 19-JUN-1995; 95WO-US007721.
XX 15-NOV-1996; 96US-00749907.
XX 27-MAR-1997; 97US-00765108.
XX 30-AUG-1999; 99US-00385799.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Kozarsky K, Rigotti A, Krieger M;
XX
XX WPI; 2005-457475/46.
XX N-PSDB; AEB03939, AEB03942.
XX
XX New genetically engineered mouse or derivative cells with inactivated SR-
XX BI gene expression or activity, useful as a model for designing drugs
XX that can modulate cholesterol transport.
XX
XX Disclosure; SEQ ID NO 4; 21pp; English.
XX
XX The present invention relates to a novel genetically engineered mouse, or
XX cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene
XX expression or SR-BI activity has been inactivated. SR-BI is a high
XX density lipoprotein (HDL) receptor. It was found that estrogen
XX downregulates SR-BI under conditions of upregulation of the low density
XX lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
XX adrenal membranes and other non-placental steroidogenic tissues from
XX animals treated with estrogen, but not in other non-placental non-
XX steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
XX tissue causes a decrease in blood cholesterol levels. The animal is
XX useful as a model for designing drugs that can modulate cholesterol
XX transport or that can stimulate or inhibit the binding to and lipid
XX movements mediated by SR-BI and redirect uptake and metabolism of lipids
XX and cholesterol by cells. The present sequence is SR-BI, which was used
XX to illustrate the invention. Note: The SEQ ID 3 given in the sequence
XX listing (the sequence shown in AEB03939) is stated to be 1785 nucleotides
XX in length. However, there appears to be a 1 to 3 nucleotide deletion at
XX the end of each line of the sequence shown in the sequence listing.
XX resulting in a sequence that is 1761 nucleotides in length. Therefore a
XX corrected version of the sequence has been produced with Ns added to
XX replace the missing nucleotides (the sequence shown in AEB03942). SEQ ID
XX 3 is stated to encode SEQ ID 4 (given in AEB03940).
SQ Sequence 509 AA;
Query Match 100.0%; Score 2681; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
DB 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFVVPNEVNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
DB 61 VPFLSYVFFVVPNEVNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
QY 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMMTLALVTMGORAFMNRVTGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMMTLALVTMGORAFMNRVTGEIL 180
QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
DB 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
DB 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQTKIIEPVVLPILLWFEQSG 420
DB 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQTKIIEPVVLPILLWFEQSG 420
QY 421 AMGKPLSTFTYTLVMPQVLYHQAQVYLLGLGILLVPIICQLRSQEKCFLFWGSKKG 480
DB 421 AMGKPLSTFTYTLVMPQVLYHQAQVYLLGLGILLVPIICQLRSQEKCFLFWGSKKG 480
QY 481 SODKEATQAYSESILMSPAKGTVLQEA 509
DB 481 SODKEATQAYSESILMSPAKGTVLQEA 509

RESULT 8
AB084950
ID AB084950 standard; protein; 519 AA.
XX AC AB084950;
XX DT 18-NOV-2004 (first entry)
XX DE Murine cancer-associated protein (CAP) MP07-081.
XX KW Mouse; cancer-associated protein; CAP; cancer; cytostatic.
XX OS Mus musculus.
XX FN WO2004058146-A2.
XX PD 15-JUL-2004.
XX PF 15-DEC-2003; 2003WO-US040081.
XX PR 17-DEC-2002; 2002US-00322281.
XX PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Malandro MS;
XX DR WPI; 2004-499109/47.
XX DR N-ESDB; ABD33431.
XX PT Novel human cancer associated protein encoded within open reading frame
XX PT of cancer associated gene, useful as targets for diagnosing cancer.
XX PS Disclosure; SEQ ID NO 565; 182pp; English.
XX CC The invention relates to cancer-associated proteins (CAP) and the cancer-

CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a murine CAP of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 519 AA;
Query Match 100.0%; Score 2681; DB 8; Length 519;
Best Local Similarity 100.0%; Pred. No. 3.9e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
DB 11 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 70
QY 61 VPFLSYVFFVVPNEVNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
DB 71 VPFLSYVFFVVPNEVNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 130
QY 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMMTLALVTMGORAFMNRVTGEIL 180
DB 131 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMMTLALVTMGORAFMNRVTGEIL 190
QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
DB 191 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 250
QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
DB 251 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 310
QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
DB 311 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 370
QY 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQTKIIEPVVLPILLWFEQSG 420
DB 371 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQTKIIEPVVLPILLWFEQSG 430
QY 421 AMGKPLSTFTYTLVMPQVLYHQAQVYLLGLGILLVPIICQLRSQEKCFLFWGSKKG 480
DB 431 AMGKPLSTFTYTLVMPQVLYHQAQVYLLGLGILLVPIICQLRSQEKCFLFWGSKKG 490
QY 481 SODKEATQAYSESILMSPAKGTVLQEA 509
DB 491 SODKEATQAYSESILMSPAKGTVLQEA 519
RESULT 9
ADR67033
ID ADR67033 standard; protein; 519 AA.
XX AC ADR67033;
XX DT 18-NOV-2004 (first entry)
XX DE Mouse cancer associated protein sequence SEQ ID NO:79.
XX KW cancer; cancer associated nucleic acid; cancer associated gene;
XX KW cancer associated protein; CAP; cytostatic; vaccine; gene therapy;
XX KW lymphoma; leukaemia; mouse.

OS Mus sp.
 FN WO2004074321-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US005000.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 23-SEP-2003; 2003US-00669920.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 FA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652915/63.
 DR N-PSDB; ADR67031, ADR67032.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS Disclosure; SEQ ID NO 79; 166pp; English.
 XX
 CC The present invention describes an isolated cancer associated (CA)
 CC nucleic acid (I). Also described: (1) an expression vector comprising (I)
 CC ; (2) a host cell comprising (I) or the expression vector; (3) a
 CC microarray for detecting a CA nucleic acid; (4) an isolated cancer
 CC associated protein (CAP) polypeptide, encoded within an open reading
 CC frame of a CA sequence; (5) an isolated antibody, or its antigen binding
 CC fragment, that binds to the above polypeptide; (6) a hybridoma that
 CC produces the above monoclonal antibody; (7) a pharmaceutical composition
 CC comprising the above antibody and a pharmaceutical excipient; (8) a kit
 CC for detecting cancer cells, comprising the (monoclonal) antibody
 CC described above; (9) methods for diagnosing cancer or for detecting the
 CC presence or absence of cancer cells in an individual; (10) a method for
 CC inhibiting growth of cancer cells in an individual; (11) a method for
 CC delivering a therapeutic agent to cancer cells in an individual; (12) an
 CC electronic library comprising the above polynucleotide or polypeptide, or
 CC their fragments; (13) methods of screening for anticancer activity or for
 CC a bioactive agent capable of modulating the activity of a CAP; (14)
 CC methods for detecting cancer associated with expression of a polypeptide
 CC in a test cell sample, or with the presence of an antibody in a test
 CC serum sample; (15) a method for treating cancers; and (16) a method for
 CC inhibiting the expression of CA gene in a cell. The CA sequences have
 CC cytostatic activity, and can be used in vaccines, and in gene therapy.
 CC The composition and methods are useful for detecting, diagnosing,
 CC preventing and treating cancers, especially lymphoma and leukaemia. They
 CC may also be used in screening for agents that modulate cancer. The
 CC present sequence represents a cancer associated protein (CAP) sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 519 AA;

Query Match 100.0%; Score 2681; DB 8; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3,9e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKKEIP 60
 Db 11 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKKEIP 70
 Qy 61 VPFYLSVYFFVFNVEVNGKPVVRERGPVVRERGPVVRERGPVVRERNDTTSFVENRSLH 120
 Db 71 VPFYLSVYFFVFNVEVNGKPVVRERGPVVRERGPVVRERGPVVRERNDTTSFVENRSLH 130
 Qy 121 FOPDKSHGSESDYIVLPNVLVGGSLMESKPSVSLKMTLALVTMGORAFNNRTVGAIL 180
 Db 131 FOPDKSHGSESDYIVLPNVLVGGSLMESKPSVSLKMTLALVTMGORAFNNRTVGAIL 190
 Qy 181 WGYDDPFFVHFLNTLPDMLPIKGFGLFVGNNNSGVFTFTGTQVNFPSRIHLVDKWNGL 240

Db 191 WGYDDPFFVHFLNTLPDMLPIKGFGLFVGNNNSGVFTFTGTQVNFPSRIHLVDKWNGL 250
 Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
 Db 251 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 310
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 311 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 370
 Qy 361 LNPKEHSLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQOTGKIPIPVLPILWFQSG 420
 Db 371 LNPKEHSLFLDIHPVTGIPMNCVVMQSLYIKSVKGIQOTGKIPIPVLPILWFQSG 430
 Qy 421 AMGGKPLSTFTQVLMPQVLYHAYVLLGLGGLLLVPIICQLRSQEKCLFWSGSKG 480
 Db 431 AMGGKPLSTFTQVLMPQVLYHAYVLLGLGGLLLVPIICQLRSQEKCLFWSGSKG 490
 Qy 481 SQDKEAIOAYSESLMSPAAGTGLVQEA 509
 Db 491 SQDKEAIOAYSESLMSPAAGTGLVQEA 519

RESULT 10
 ADUS1468
 ID ADUS1468 standard; protein; 509 AA.
 XX
 AC ADUS1468;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Mouse scavenger receptor class B type I-related protein - SEQ ID 3.
 XX
 KW Monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 KW SR-BI; spermatogenesis.
 XX
 OS Mus musculus.
 XX
 PN JP2004331633-A.
 XX
 PD 25-NOV-2004.
 XX
 PF 29-MAY-2003; 2003JP-00152800.
 XX
 PR 10-MAR-2003; 2003JP-00063407.
 XX
 FA (UYKA-) UNIV KANAZAWA TLO YG.
 XX
 DR WPI; 2004-810031/80.
 XX
 PT Novel monoclonal antibody which belongs to mouse IgG1/kappa subclasses and
 PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 PT rat origin, useful for functional analysis of SR-BI.
 XX
 PS Disclosure; SEQ ID NO 3; 21pp; Japanese.
 XX
 CC The invention comprises a monoclonal antibody that belongs to the mouse
 CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI
 CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a mouse SR-BI-related protein.
 XX
 SQ Sequence 509 AA;

Query Match 99.9%; Score 2677; DB 8; Length 509;
 Best Local Similarity 99.8%; Pred. No. 9,6e-261;
 Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKKEIP 60
 Db 11 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKKEIP 60

Db 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQOVLKKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFLSVYVFEVNPNEVLNGOKPVVREGRGYVYVREGRQKVNITFNDNDTVSFVENSLH 120
 Db 61 VPFLSVYVFEVNPNEVLNGOKPVVREGRGYVYVREGRQKVNITFNDNDTVSFVENSLH 120
 QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
 QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLDKWNGL 240
 Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLDKWNGL 240
 QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMLTYNESRVFEGIPTYR 300
 Db 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 QY 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIQGTGKIHPVVLPLLWFQSG 420
 Db 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIQGTGKIHPVVLPLLWFQSG 420
 QY 421 AMGKPLSTFTYQLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLWFGSKKG 480
 Db 421 AMGKPLSTFTYQLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLWFGSKKG 480
 QY 481 SQDKAIOAYSLSLMSPAKGTVLQEAKL 509
 Db 481 SQDKAIOAYSLSLMSPAKGTVLQEAKL 509

RESULT 11
 ADU51466
 ID ADU51466 standard; protein; 509 AA.
 AC ADU51466;
 DT 10-FEB-2005 (first entry)
 DE Rat scavenger receptor class B type I (SR-BI)-related protein - SEQ ID 1.
 KW monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 KW SR-BI; spermatogenesis.
 OS Rattus norvegicus.
 PN JP2004331633-A.
 XX 25-NOV-2004.
 XX 29-MAY-2003; 2003JP-00152800.
 XX 10-MAR-2003; 2003JP-00063407.
 XX (UYKA-) UNIV KANAZAWA TILO YG.
 XX WPI; 2004-810031/80.
 PT Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
 PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 PT rat origin, useful for functional analysis of SR-BI.
 XX Disclosure; SEQ ID NO 1; 21pp; Japanese.

The invention comprises a monoclonal antibody that belongs to the mouse
 CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI

CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a rat SR-BI-related protein.
 XX Sequence 509 AA;
 SQ
 Query Match 93.4%; Score 2504; DB 8; Length 509;
 Best Local Similarity 92.3%; Pred. No. 2.9e-243;
 Matches 470; Conservative 23; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQOVLKKNVRIDPSSLSFGMWKEIP 60
 Db 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQOVLKKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFLSVYVFEVNPNEVLNGOKPVVREGRGYVYVREGRQKVNITFNDNDTVSFVENSLH 120
 Db 61 VPFLSVYVFEVNPNEVLNGOKPVVREGRGYVYVREGRQKVNITFNDNDTVSFVENSLH 120
 QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
 QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLDKWNGL 240
 Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLDKWNGL 240
 QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMLTYNESRVFEGIPTYR 300
 Db 241 SEVNYHSEOCNMGNTAGQWAPFMTPESSLEFFSPACRSMLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 QY 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIQGTGKIHPVVLPLLWFQSG 420
 Db 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIQGTGKIHPVVLPLLWFQSG 420
 QY 421 AMGKPLSTFTYQLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLWFGSKKG 480
 Db 421 MMGKTLNTFTYQLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLWFGSKKG 480
 QY 481 SQDKAIOAYSLSLMSPAKGTVLQEAKL 509
 Db 481 SQDKAIOAYSLSLMSPAKGTVLQEAKL 509

RESULT 12
 ADE56446
 ID ADE56446 standard; protein; 510 AA.
 AC ADE56446;
 XX 29-JAN-2004 (first entry)
 XX Rat Protein D89655, SEQ ID NO 2299.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 DE Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 PN WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

QY	421	AMGGKPLSTFTYQLVLPQVLYHQAQYVLGGGLLLVPIICOLRSQEKCFLWMSGKKG	480
DB	421	MMGGKTLTFTYQLVLPQVLYHQAQYVLGGGLLLVPIIYQLRSQEKCFLWMSGKKG	480
QY	481	SQDKEAIOAYSLSLMSPAKGTVLQEAKL	509
DB	481	SQDKEAMQAYSLSLMSPAKGTVLQEAKL	509
RESULT 13			
ID	AD856442		
ID	AD856442	standard; protein; 510 AA.	
XX	AC	AD856442;	
XX	DT	29-JAN-2004 (first entry)	
XX	XX	Rat Protein D89655, SEQ ID NO 2295.	
DE	DE		
XX	XX		
XX	XX		
KW	XX	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;	
KW	XX	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.	
OS	OS	Rattus norvegicus.	
XX	XX		
PN	PN	WO2003016475-A2.	
XX	XX		
PD	PD	27-FEB-2003.	
XX	XX		
PF	PF	14-AUG-2002; 2002WO-US025765.	
XX	XX		
PR	PR	14-AUG-2001; 2001US-0312147P.	
PR	PR	01-NOV-2001; 2001US-0346382P.	
PR	PR	26-NOV-2001; 2001US-0333347P.	
XX	XX		
PA	PA	(GCHO) GEN HOSPITAL CORP.	
PA	PA	(FARB) BAYER AG.	
XX	XX		
PI	PI	Woolf C, D'urso D, Befort K, Costigan M;	
XX	XX		
XX	XX	WPI; 2003-268312/26.	
DR	DR	GENBANK; D89655.	
XX	XX		
XX	XX	New composition comprising two or more isolated polypeptides, useful for	
PT	PT	preparing a medicament for treating pain in an animal.	
PS	PS	Claim 1; Page; 1017pp; English.	
XX	XX		
CC	CC	The invention discloses a composition comprising two or more isolated rat	
CC	CC	or human polynucleotides or a polynucleotide which represents a fragment,	
CC	CC	derivative or allelic variation of the nucleic acid sequence. Also	
CC	CC	claimed are a vector comprising the novel polynucleotide, a host cell	
CC	CC	comprising the vector, a method for identifying a nucleotide sequence	
CC	CC	which is differentially regulated in an animal subjected to pain and a	
CC	CC	kit to perform the method, an array, a method for identifying an agent	
CC	CC	that increases or decreases the expression of the polynucleotide sequence	
CC	CC	that is differentially expressed in neuronal tissue of a first animal	
CC	CC	subjected to pain, a method for identifying a compound which regulates	
CC	CC	the expression of a polynucleotide sequence which is differentially	
CC	CC	expressed in an animal subjected to pain, a method for identifying a	
CC	CC	compound that regulates the activity of one or more of the	
CC	CC	polynucleotides, a method for producing a pharmaceutical composition, a	
CC	CC	method for identifying a compound or small molecule that regulates the	
CC	CC	activity in an animal of one or more of the polypeptides given in the	
CC	CC	specification, a method for identifying a compound useful in treating	
CC	CC	pain and a pharmaceutical composition comprising the one or more	
CC	CC	polypeptides or their antibodies. The polynucleotide or the compound that	
CC	CC	modulates its activity is useful for preparing a medicament for treating	
CC	CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	
CC	CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene	
CC	CC	therapy). The sequence presented is a rat protein (shown in Table 2 of	
CC	CC	the specification) which is differentially expressed during pain. Note:	
CC	CC	The sequence data for this patent did not form part of the printed	
CC	CC	specification, but was obtained in electronic form directly from WIPO at	

GENEANK; D096935.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at

Db 421 MWGGKTLNFTYQLVLMPOVHLHYAQYVLLGGLLVPILYQLRSQKCFLWGSKGG 480
Qy 481 SODKEAIQAYSESLMSPAAGKTVLQEAKL 509
Db 481 SODKEAMQAYSESLMSPAAGKTVVQEAKL 509

RESULT 15
ADZ13453
ID ADZ13453 standard; protein; 506 AA.
XX AC ADZ13453;
XX 16-JUN-2005 (first entry)
XX Murine cancer-associated protein #108.
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasia;
KW cytostatic.
XX Mus sp.
XX WO2005031001-A2.
XX 07-APR-2005.
XX 23-SEP-2004; 2004WO-US031617.
XX 23-SEP-2003; 2003US-00669920.
XX (CHIR) CHIRON CORP.
XX Morris DW, Malandro MS;
XX WPI; 2005-273395/28.
XX N-PSDB; ADZ13452.
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX Disclosure; SEQ ID NO 973; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a murine cancer-associated protein of the invention.

Seq Sequence 506 AA;
Query Match 92.1%; Score 2468; DB 9; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIILWVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMIILWVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYFFEVVNPNEVANGQKPVVREGRGPVYVREKQVNTITFNDNDTVSFVENSLH 120
Db 61 VPFYLSVYFFEVVNPNEVANGQKPVVREGRGPVYVREKQVNTITFNDNDTVSFVENSLH 120
Qy 121 FQDKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGORAFMNTVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGORAFMNTVGEIL 180
Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNSGVFTVFTGVQVFSRIHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNSGVFTVFTGVQVFSRIHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFPSPSEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFPSPSEACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFAANGSVYPPNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFAANGSVYPPNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKEHSLFLDIHPVTGIPMNCVVMQVLSLYIKSVKIGQGTGKIEPVPVLLPLWFQSG 420
Db 361 LNPMPKEHSLFLDIHPVTGIPMNCVVMQVLSLYIKSVKIGQGTGKIEPVPVLLPLWFQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVHLHYAQYVLLGGLLVPILYQLRSQ 467
Db 421 AMGGKPLSTFTYQLVLMPOVHLHYAQYVLLGGLLVPILYQLRSQ 467

Search completed: February 23, 2006, 12:40:06
Job time : 153.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 12:40:25 ; Search time 26 Seconds
(without alignments)
1883.628 Million cell updates/sec

Title: US-08-765-108-8
Perfect score: 2881
Sequence: 1 MGGSSRRARWALGALGALL.....YSESLMSPAAGTGLQAKL 509
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: PIR.80.*
- 2: PIR1.*
- 3: PIR2.*
- 4: PIR3.*
- 5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2484	92.7	529	2 JC5533	scavenger receptor
2	2447	91.3	509	1 A53920	scavenger receptor
3	2192	81.8	509	1 A48528	membrane glycoprot
4	742.5	27.7	478	1 A56525	lysosomal integral
5	734	27.4	478	1 JH0241	85K lysosomal memb
6	732	27.3	478	2 JC5670	lysosomal membrane
7	677	25.3	472	1 A54870	cell adhesion rece
8	662	24.7	472	2 I49590	CD36 antigen - mou
9	645	24.1	472	1 A47402	fatty acid binding
10	633	23.6	519	1 S38957	epithelial membran
11	587	21.9	457	1 S43137	D-CD36 protein - f
12	490.5	18.3	534	2 T27054	hypothetical prote
13	472	17.6	525	2 A59259	sensory neuron mem
14	401	15.0	536	2 T24000	hypothetical prote
15	393	14.7	531	2 T20763	hypothetical prote
16	379	14.1	590	2 T20537	hypothetical prote
17	363.5	13.6	552	2 T27424	hypothetical prote
18	345	12.9	562	2 T15396	hypothetical prote
19	115.5	4.3	1573	2 T50113	3-dehydroquinatate s
20	105.5	3.9	592	2 E70488	cytochrome-c oxida
21	104.5	3.9	924	2 B95192	hypothetical prote
22	104	3.9	1003	2 T05898	hypothetical prote
23	101.5	3.8	1026	2 T18220	chitin synthase (E
24	99.5	3.7	570	2 T38489	helicase - fission
25	99.5	3.7	924	2 G38058	hypothetical prote
26	98	3.7	303	2 AC1087	PTS system mannose
27	98	3.7	303	2 AB1451	PTS system mannose
28	96.5	3.6	273	2 AB1551	hypothetical prote
29	96.5	3.6	1835	2 S46082	urea carboxylase (

30 3.6 224 2 AP0851 secretory protein
31 96 955 2 T39765 probable nuclear m
32 95 224 2 T11207 spa protein - Sal
33 95 224 2 S37308 spa protein - Sal
34 95 695 2 D90468 copper-transportin
35 94.5 411 2 H69158 LPS biosynthesis R
36 94.5 3.5 2211 1 KPB05 coagulation factor
37 94 3.5 366 2 C89875 hypothetical prote
38 94 3.5 670 2 T32221 hypothetical prote
39 94 3.5 1661 2 S64800 probable membrane
40 93 901 2 T03726 capsid polypeptide
41 92.5 3.5 605 2 AC1139 internalin protein
42 92 3.4 398 2 S74347 hypothetical prote
43 92 3.4 427 2 C87232 probable integral
44 92 3.4 448 2 T44869 probable membrane
45 92 3.4 543 2 F91067 hypothetical prote

ALIGNMENTS

RESULT 1

JC5533

scavenger receptor class B type I precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004

C;Accession: JC5533

R;Mizutani, T.; Sonoda, Y.; Minegishi, T.; Wakabayashi, K.; Miyamoto, K.

Biochem. Biophys. Res. Commun. 234, 499-505, 1997

A;Title: Cloning, characterization, and cellular distribution of rat scavenger receptor (

A;Reference number: JC5533; MUID:97320450; PMID:9177301

A;Accession: JC5533

A;Molecule type: mRNA

A;Residues: 1-529 <MTZ>

A;Cross-references: UNIPROT:P97943; UNIPARC:UPI0000177A34

A;Experimental source: ovary

C;Comment: This protein is a specific receptor for high density lipoprotein. It plays a

to ovarian theca interna cells or to corpus luteum.

C;Genetics:

A;Gene: srbi

C;Superfamily: lysosomal integral membrane protein II

F;1-25/Domain: signal sequence #status predicted <Sig>

F;466-482/Domain: transmembrane #status predicted <TM>

Query Match 92.7%; Score 2484; DB 2; Length 529;

Best Local Similarity 88.8%; Pred. No. 2.8e-188;

Matches 470; Conservative 23; Mismatches 16; Indels 20; Gaps 1;

Qy 1 MGGSSRRARWALGALGALLFAALGVVMILMFSLIKQQLKNVRIDPSSLSFGMWKEIP 60

Db 1 MGVSRRARWALGALGVLGLLCAALGVIMILMFSLIKQQLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPVLSYVFPEVNPNEVLNGQXVVRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120

Db 61 VPVLSYVFPEVNPNEVLNGQXVVRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120

Qy 121 FQPDKSHGSSDYVLNPNILVGLSSILLESKPSVSLKLMMTLALVTMGORAFMNTVGEIL 180

Db 121 FQPDKSHGSSDYVLNPNILVGLSSILLESKPSVSLKLMMTLALVTMGORAFMNTVGEIL 180

Qy 181 WGVDPPVPHFLNTYLPDMLPIKGFGLFVGNNNSNGSVFTVFTGVQFNRHLVDKNGL 240

Db 181 WGVEDPVPNLSKYFPDMFIKGFGLFVGNNSSSGVFTVFTGVQFNRHLVDKNGL 240

Qy 241 SKIDYWHSEQCNNMNGTSGQWAPFMTPESSLSBFFSPSEACRSKMLTYNESRVFEGIPYR 300

Db 241 SEVNYWHSEQCNNMNGTAGQWAPFMTPESSLSBFFSPSEACRSKMLTYQESRVFEGIPYR 300

Qy 301 FTAPDPTLFPANGSVYPNPEGPCPCRESGIONVYCRFCGAPLFLSHPHFYNDPVLSEAVLG 360

Db 301 FTAPDPTLFPANGSVYPNPEGPCPCRESGIONVYCRFCGAPLFLSHPHFYNDPVLSEAVLG 360

Qy 361 -----LNPNPKHSLFLDHPVTGIPMNCVKNQSLSLYKSVKGI 400


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Db 301 FVAPKTLFANGSIYPPNPGFCPCLESIGQNVSTCRFSAPLFLSHPHFLNADPVLAEAVTG 360
Qy 361 LNPFPKHSLELDHPVTGIPMNCVKMQLSLYKSKVGIGTGKIEPVLPLLMFQSG 420
Db 361 LHPNQEAHSLFDHPVTGIPMNCVKQLSLYKSKVAGIGTGKIEPVLPLLMFAESG 420
Qy 421 AMGKPLSTFTTQVLMPQVLAHYQVLLGLGGLLVPITICQURSQBKCFLFWGSKKG 480
Db 421 AMEGETLFTTQVLMPQVLAHYQVLLGLGGLLVPITICQURSQBKCFLFWGSKKG 480
Qy 481 SODKEAIOAYSESLMSPAAGTQVLQEA 509
Db 481 SKDKEAIOAYSESLMTSAPKGVQLQEA 509

RESULT 4
A56525
Lysosomal integral membrane protein II - human
N:Alternate names: lgs85; LIMP II; lysosomal membrane 85K sialoglycoprotein
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: A56525; JQ1523
R:Calvo, D.; Dopazo, J.; Vega, M.A.
Genomics 25, 100-106, 1995
A:Title: The CD36, CLA-1 (CD36L1), and LIMP II (CD36L2) gene family: cellular distribution
A:Reference number: A56525; MUID:95293360; PMID:7539776
A:Accession: A56525
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-478 <CAL>
A:Cross-references: UNIPROT:Q14108; UNIPARC:UPI000017423A
R:Fujita, H.; Takata, Y.; Kono, A.; Tanaka, Y.; Takahashi, T.; Himeno, M.; Kato, K.
Biochem. Biophys. Res. Commun. 184, 604-611, 1992
A:Title: Isolation and sequencing of a cDNA clone encoding the 85KDa human lysosomal sialoglycoprotein in rat
A:Reference number: JQ1523; MUID:92246940; PMID:1374238
A:Accession: JQ1523
A:Molecule type: mRNA
A:Residues: 1-83, 'E', 85-478 <FUJ>
A:Cross-references: UNIPARC:UPI0000032D38; GB:D12676; NID:g219702; PIDN:BA02177.1; PID:
A:Experimental source: pancreatic islet
R:Sandoval, I.V.; Arredondo, J.J.; Alcalde, J.; Noriega, A.G.; Vandekerckhove, J.; Jimen
J. Biol. Chem. 269, 6622-6631, 1994
A:Title: The residues Leu(11e)(475)-Ile(Leu, Val, Ala) (476), contained in the extended c
somes.
A:Reference number: A57905; MUID:94165051; PMID:7509809
A:Contents: annotation; sorting signal
C:Genetics:
A:Gene: GDB:CD36L2
A:Map position: 4pter-4qter
A:Superfamily: lysosomal integral membrane protein II
C:Keywords: glycoprotein, lysosome, transmembrane protein
F:2-478/Product: lysosomal membrane 85K sialoglycoprotein #status predicted <LYS>
F:2-3/Domain: intracellular #status predicted <CYT1>
F:4-26/Domain: transmembrane #status predicted <TR1>
F:27-432/Domain: lysosomal lumenal #status predicted <LLUM>
F:433-458/Domain: transmembrane #status predicted <TR2>
F:459-478/Domain: intracellular #status predicted <CYT2>
F:475-476/Region: endosomal/lysosomal sorting signal
F:45, 68, 105, 206, 224, 249, 304, 325, 412, 430/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 27.7%; Score 742.5; DB 1; Length 478;
Best Local Similarity 32.6%; Pred. No. 8.9e-51;
Matches 156; Conservative 103; Mismatches 190; Indels 29; Gaps 9;

Qy 15 GALLFLFAALGVMMIL--MVPSLIKQVLKXNRIDPSSLSFGMKKEIPVPFYLSPYFVFEV 72
Db 10 GTLSLLLLVTSVTLVARVQKAVDQSLTEKKIVLRNGTEAFDSWEKPLPVYTTQYFVNV 69
Qy 73 VNPNEVLNGQKPVVRERGFYVRPRQKNITFDND--DTVSFVNRSRLSHFQPDKSHGS-E 130
Db 70 TNPBEILRGETPRVQEVGFTYTRLRNKNITQFGDNGTTISAVSNKAYVFRDQSVGDPK 129
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Qy 131 SDYIVLPIIIVLGSILMSEKPSVSLKLMMTLALVTMQRAPMNTVGEILLWGYDDPFWHF 190
Db 130 IDLIRTLNIPVL--TVIEWQVHPLREIIEAMLKAYQKQLFVTHVDELLWGYKDEILSL 187
Qy 191 LNTVLPDMLPIKKGKGLFVGMNNSNSGVFTVFCQVQNFPSRIHLVDKNGLSKIDYWHSEQ 250
Db 188 IHVFRPDISY---FGLFYKNGTNDGDYVFLTGEDSYLNFTKIVENWNGKTSLDWJITDK 244
Qy 251 CNMINTSGQWMAFPMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYRFTAPDTILFAN 310
Db 245 CNMINTGDSFHLITKDEVLYVFPDSFRCRSVYITFSDYESVQGLPAFRYKVPABILAN 304
Qy 311 GSVYPPNEGFC---PCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSSAVLGLNPNPK 366
Db 305 TS---DNAGFCIPEGNCLGSGVLNVISCKNGAPIIMSFPHFYQADERFVSAIEGMHPNQE 361
Qy 367 EHSPLFDHPVTGIPMNCVKMQLSLYKSKVGIGTGKIEPVLPLLMFQSGAMGKPK 426
Db 362 DHETFDINPLTGLILKAARKFQINIVYKKLDDPVETGDIRTMVFPVYMLNESVHI-DKE 420
Qy 427 LSTFYTQLVMPQVLAHYQVLLGLGGLLVPITICQURSQBKCFLFWGSKGSKQDK 484
Db 421 TASRLKSMINTLIITNPIIIMALGVFFGLV-----FTWLACKGQSGSMD 466

RESULT 5
JH0241
85K lysosomal membrane sialoglycoprotein - rat
N:Alternate names: 74k lysosomal membrane protein LIMP
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Nov-1991 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: JH0241; PH0212; A41180
R:Fujita, H.; Ezaki, J.; Noguchi, Y.; Kono, A.; Himeno, M.; Kato, K.
Biochem. Biophys. Res. Commun. 178, 444-452, 1991
A:Title: Isolation and sequencing of a cDNA clone encoding 85KDa sialoglycoprotein in rat
A:Reference number: JH0241; MUID:91315465; PMID:1859403
A:Accession: JH0241
A:Molecule type: mRNA
A:Residues: 1-478 <FUJ>
A:Cross-references: UNIPROT:P27615; UNIPARC:UPI0000167995; GB:D10587; NID:g222
A:Note: the authors translated the codon CCT for residue 59 as Lys, TAT for residue 278 a
somes.
A:Molecule type: protein
A:Residues: 2-9, 49-67, 116-121, 228-234, 283-294, 355-373 <FUZ>
A:Cross-references: UNIPARC:UPI000017423B; UNIPARC:UPI000017423C; UNIPARC:UPI000017423D;
A:Experimental source: liver
R:Vega, M.A.; Segui-Real, B.; Garcia, J.A.; Cales, C.; Rodriguez, F.; Vandekerckhove, J.
J. Biol. Chem. 266, 16818-16824, 1991
A:Title: Cloning, sequencing, and expression of a cDNA encoding rat LIMP II, a novel 74-k
A:Reference number: A41180; MUID:91358482; PMID:1715871
A:Accession: A41180
A:Molecule type: mRNA
A:Residues: 1-478 <VEG>
A:Cross-references: UNIPARC:UPI0000167995; GB:M68965; NID:g205206; PIDN:AAA41531.1; PID:
A:Note: parts of this sequence, including the amino end of the mature protein, were confi
R:Sandoval, I.V.; Arredondo, J.J.; Alcalde, J.; Noriega, A.G.; Vandekerckhove, J.; Jimen
J. Biol. Chem. 269, 6622-6631, 1994
A:Title: The residues Leu(11e)(475)-Ile(Leu, Val, Ala) (476), contained in the extended ce
somes.
A:Reference number: A57905; MUID:94165051; PMID:7509809
A:Contents: annotation; sorting signal
C:Superfamily: lysosomal integral membrane protein II
C:Keywords: glycoprotein, transmembrane protein
F:2-478/Product: 85K lysosomal membrane sialoglycoprotein #status experimental <MAT>
F:2-3/Domain: intracellular #status predicted <CYT1>
F:4-26/Domain: transmembrane #status predicted <TR1>
F:27-432/Domain: lysosomal lumenal #status predicted <LYS>
F:433-458/Domain: transmembrane #status predicted <TR2>
F:459-478/Domain: intracellular #status predicted <CYT2>
F:475-476/Region: endosomal/lysosomal sorting signal
F:45, 68, 105, 122, 206, 224, 249, 304, 325, 412, 430/Binding site: carbohydrate (Asn) (covalent) #
```


191 191 -----PYPVTTTGLFYFYNNTADGVYKVFNGKDNISKVAIIDTYGKRNLSWYES-HCD 244

253 253 MINGTSGQWAPFMTPESSLEFFPEACRSKMLTYNESRVFEGIPYTRFTAPDTLFANGS 312

245 245 MINGTDAASFPPFVEKSOVLQFFSSDICSRIYAVFESDVLNKGIPYRVFVLPSKAFASPV 304

313 313 VYPNNEGFCP-----CRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLGNLNP 365

305 305 ENPDNYCFCTEKIISKNTSYGVLDDICKCKEGRPVYISLPHFLYASPDVSEPIDGLNPNE 364

366 366 KEHSLFLDIHPVTGIPMNCVSKMQLSIYKSVKIGQTGKIE-PVVLPLLWPFQSGAMGC 424

365 365 ESHRTYLDIEPTTGTLQFAKRLQVNLVLVPSSEKIQVLKNLKNRYIVPILWLNETGTIGD 424

425 425 KPLSTFTYQLVLMPOVLHYAQVLLGLGGILLLVPII--CQLRSQ 467

425 425 EXANFRSQVTKINLGLIEWILLSGVVMFVAFMISYCACRSK 469

RESULT 8

149590

C:36 antigen - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49590

R:Endmann, G.; Stanton, L.W.; Madden, K.S.; Bryant, C.M.; White, R.T.; Protte

J. Biol. Chem. 268, 11811-11816, 1993

A:Title: CD36 is a receptor for oxidized low density lipoprotein.

A:Reference number: I49590; MUID:93280144; PMID:7685021

A:Accession: I49590

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-472 <RES>

A:Cross-references: UNIPROT:Q08957; UNIPARC:UPI00000018D7; GB:L23108; NID:9567

C:Superfamily: lysosomal integral membrane protein II

Query Match 24.7%; Score 662; DB 2; Length 472;

Best Local Similarity 30.5%; Pred. No. 2e-44;

Matches 142; Conservative 104; Mismatches 195; Indels 24; Gaps 10

QY 17 IGLLFAALGVNMLVPSLIHQVQLKNVRIDPSLSFGMKKEIPVFPYLSVYFVFNPN 76

DB 15 IGAVLAVFGGILPVPDMLIEKTKREVLVEEGTAFKNVKTGTTVYRQFMIFDVQNP 74

QY 77 EYL-NGQKPVVRERGPPYVR--EPRQKNITFNDD--TVSFVENRSLHFQDKSHGESDY 133

DB 75 DVAKNSKKIKVKQRPYTRVRYLAKENITQDPEDHTVSPVQNGAIFBPSLSVSGTDDN 134

QY 134 IYLPNILLGSGIILMESKPSVLKMLMTLALVTMGORA-FMNRVTGELLWGYDDPFFVHFLN 192

DB 135 FTVLNLVAAPHIYQNSFVQVNLN---SLIKKSKSMFQTRSLKELLWGYKDPFSLV- 190

QY 193 TYLPDMLPIKKGFLGVGMNNSGVPTFTGVQVNSRIHLVDKNGLSKIDYVHSEQC 252

DB 191 -----PYPISTATVGVPYNDVDGVTVKVFNGKDNISKVAIISYKGRNLSWYPS-YCD 244

QY 253 MINGTSGQWAPFMTPESSLEFFPEACRSKMLTYNESRVFEGIPYTRFTAPDTLFANGS 312

DB 245 MINGTDAASFPPFVEKSGTLFQFAKRLQVNLVLVPSSEKIQVLKNLKNRYIVPILWLNETGTIGD 424

QY 313 VYPNNEGFCP-----CRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLGNLNP 365

DB 305 QNPDNHCFTCTBKVINNCTSYGVLDDICKCKEGRPVYISLPHFLHASEPDVSEPIEGLHPNE 364

QY 366 KEHSLFLDIHPVTGIPMNCVSKMQLSIYKSVKIGQTGKIE-PVVLPLLWPFQSGAMGC 424

DB 365 DEHRTYLDVEPTTGTLQFAKRLQVNLVLVPSSEKIQVLKNLKNRYIVPILWLNETGTIGD 424

QY 425 KPLSTFTYQLVLMPOVLHYAQVLLGLGGILLLVPII--CQLRSQ 467

DB 425 EXAENFTQVTKIKLGLVEMALLIGVVMFVAFMISYCACRSK 469

RESULT 9

A47402
fatty acid binding/transport protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A47402
R;Abumrad, N.A.; El-Maghrabi, M.R.; Amri, E.Z.; Lopez, E.; Grimaldi, P.A.
J. Biol. Chem. 268, 17665-17668, 1993
A;Title: Cloning of a rat adipocyte membrane protein implicated in binding or transport
F;460-482/Domain: intracellular #status predicted <TM2>
F;483-519/Domain: intracellular #status predicted <CYT2>
A;Reference number: A47402
A;Molecule type: mRNA
A;Residues: 1-472 <ABU>
A;Cross-references: UNIPROT:Q07969; UNIPARC:UPI000015568; GB:L19658; NID:g310112; PIDN:

C;Superfamily: lysosomal integral membrane protein II
C;Keywords: glycoprotein; transmembrane protein
F;2-6/Domain: intracellular #status predicted <CYT1>
F;7-30/Domain: transmembrane #status predicted <TM1>
F;31-439/Domain: extracellular #status predicted <EXT>
F;440-466/Domain: transmembrane #status predicted <TM2>
F;467-472/Domain: intracellular #status predicted <CYT2>
F;79,102,134,205,220,235,247,417/Binding site: carboxydrate (Asn) (covalent) #status pre

Query Match 24.1%; Score 645; DB 1; Length 472;
Best Local Similarity 30.3%; Pred. No. 4.4e-43;
Matches 145; Conservative 91; Mismatches 192; Indels 50; Gaps 10;

Qy 17 LGLFAALGVVMIILVPSLIKQVLKNVRIDPSLSFGMMKEIPVPYLSVYFEVNVN 76
Db 15 IGAVLAVFGGILMPGVGLLIEKTIKREVLLEGGTIAFKNVKGTGTVYRQFWVFDVQNP 74

Qy 77 EVL-NGQKPVVRERGPYVR-BFRQKNITFNDND-TVSFVNRSLHFQDKSHGESDY 133
Db 75 EVAKNSSKIKVIRGPYTYRVYLAKENITQDPKDSVSFQPNCAIFEPSSLSVGTENDN 134

Qy 134 IVLNLIIVLG-----GSTLMESKPVSLKMLMTLALVTMGQAFMNRVTGEI 179
Db 135 FTVNLAVAAAPHYIYNSFVGVNLNLSKSK-----SNFQTRSLKEL 178

Qy 180 LMGYDDPFVHPLNTYLPDLPIKGFGLVGMNNSGVFTFTGQVNFRIHLVDKWN 239
Db 179 LMGYKDPFLSLV-----PYEISTTVGVFPYNNVGVKVSNGKDNISKVAIIDTYKG 232

Qy 240 LSKIDYHSEOCNMGTSQGMWAPMTPESSLEFPSPACRSKMLIYNSRVFEGIPY 299
Db 233 KRNLISYWS-YCDMINGTDAASFPLGKSKRTLRFSSDICRSIYAVFSEVNLKGPVY 291

Qy 300 RFTAPDTLTFANGSVYPPNEGFCP-----CRESGIENVSTCRFGAPLFLSHPHFYNA 352
Db 292 RFVLPAANAFAPLQNPNDNHCFTBEKVISNNCTSYGVLDIGCKEKGKPVYNSLPFLHASP 351

Qy 353 VLSBAVLGLNPNKHESLFLDIHPTVTGPMNCVQMLSLYKSVKGIQGTGKIE-PVVL 411
Db 352 DVSEPIEGLNTEDEHRYLDVEPIITGTLQFSKRLQVNLVLPARKIEALKNLKRPVIV 411

Qy 412 PLLMFEQSGANGKPLSTFTYTLVMPQVTLHYAQLVIGLIGGLLLVPIL--COLRSQ 467
Db 412 PILMLNETGTIGDEKAEMFRQVTKIKLLGLVEMVLLGVGVFMVAFMISYCACRSK 469

RESULT 10

S38957
epithelial membrane protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S38957
R;Hart, K.; Wilcox, M.
J. Mol. Biol. 234, 249-253, 1993
A;Title: A Drosophila gene encoding an epithelial membrane protein with homology to CD36
A;Reference number: S38957; MUID:94047068; PMID:7693949
A;Accession: S38957
A;Molecule type: mRNA
A;Residues: 1-519 <HAR>

A;Cross-references: UNIPROT:Q24336; UNIPARC:UPI00000774AD; EMBL:X73332; NID:g429163; PIDN:
C;Genetics:
A;Gene: FlyBase:FBgn0010435
A;Cross-references: FlyBase:FBgn0010435
C;Superfamily: lysosomal integral membrane protein II
C;Keywords: transmembrane protein
F;2-19/Domain: intracellular #status predicted <CYT1>
F;20-39/Domain: transmembrane #status predicted <TM1>
F;460-482/Domain: transmembrane #status predicted <TM2>
F;483-519/Domain: intracellular #status predicted <CYT2>

Query Match 23.6%; Score 633; DB 1; Length 519;
Best Local Similarity 31.5%; Pred. No. 4.5e-42;
Matches 161; Conservative 92; Mismatches 214; Indels 44; Gaps 14;

Qy 6 RARWALGALGALLLPAAL---GVVMILMPSLIQOVLKNVRIDPSSLSFGMMKEIPVP 62
Db 18 RKWWTI-----VAAALIIGGIIVVACEFTVLIDAVDRMVVALREFGAKTFGWWAKPPVE 71

Qy 63 FYLSVYFFEVVNPVNL-NGQKPVVRERGPYVR-BFRQKNITFNDND-TVSFVNRSLHF 121
Db 72 PRISLYIYNNVTNADDFLSNGSKAIVDEVPYVYSETWEKVNIVENDNGHLSYNLRKIYSF 131

Qy 122 QPDKSHGESDYIVLNPILVGLSGIILMESKPVSLKMLMTLALVTMGQAFMNRVTGEILW 181
Db 132 REDLSVGPEDDVIVVNIPLMSATSSQSKHAARFLRLAMASINDILKIKPQVQSVGQLLW 191

Qy 182 GYDDPPVHPLNTYLP--DMLPIKGFGLVGMNNSGVFTFTGQVNFRIHLVDKWN 239
Db 192 GYEDPILKLAKDVVPKEQKLPYE-BFGLLYGKNGTSSDRVTNTVTDITRRYGIIDNFNG 250

Qy 240 LSKIDYHSEOCNMGTSQGMWAPMTPESSLEFPSPACRSKMLTY-NESRVFEGIPT 298
Db 251 RTHLPHTWTADACNTLAGTDSIFPPHIDHRIHLVYDKLCRLLLPLVFEKEVMTSNEVPG 310

Qy 299 YRFTAPDTLTFANGSVYPPNE-----GFCPCRESGIENVSTCRFGAPLFLSHPHFYNA 352
Db 311 YRFTTVGVFRCCQ--PPGQHVLSRGKSPSCPNGLFNVLSCQYDSPIMLSPPHFLADE 368

Qy 353 VLSBAVLGLNPNKPE-HSLFLDIHPTVTGPMNCVQMLSLYKSVKGIQGTGKIEPVVL 411
Db 369 SLRTQVEGISPPMKKEKHQFFDQPKMGTTLRVARIQINLAVSQVFDIKQVANFPDIIIF 428

Qy 412 PLLMFEQSGANGKPLSTFTYTLV---LMPQVLYHAQVY-LLAGLGLLLVPIICOLR- 465
Db 429 PILWFE-----GIDNLPDEVTLMMRFAEQPPKIRVALIVGLCALGVILLLLLTCLIRN 484

Qy 466 SQEKCFLFMWSG-----KGSQDK 485
Db 485 SHRQSTLHLEGSNYLATAQVDNMKNQKQNDQ 515

RESULT 11

S43137
D-CD36 protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S43137; S43136

R;Franc, N.; Dimarcq, J.; Hoffmann, J.; Laqueux, M.

submitted to the EMBL Data Library, March 1994

A;Description: d-CD36 : a second Drosophila gene related to the CD36 family of cell adhes

A;Reference number: S43136

A;Accession: S43137

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-457 <FRA>

A;Cross-references: UNIPROT:Q27367; UNIPARC:UPI000016BB39; EMBL:Z31583; NID:g468537; PIDN:

C;Genetics:

A;Gene: FlyBase:croquemort

A;Cross-references: FlyBase:FBgn0015924

C;Superfamily: lysosomal integral membrane protein II

Query Match 21.9%; Score 587; .DB 1; Length 457;

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 23, 2006, 12:35:04 ; Search time 147.5 Seconds
 (without alignments)
 2434.671 Million cell updates/sec
 Title: US-08-765-108-8
 Perfect score: 2681
 Sequence: 1 MGGSSRRWALGALGALL.....YSESLMSPAAGTVLQEAQL 509

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	2681	100.0	509	1	SCRB1_MOUSE	Q61009 mus musculus
2	2681	100.0	509	2	Q4FK30_MOUSE	Q4fk30 mus musculus
3	2504	93.4	509	1	SCRB1_RAT	P97943 rattus norv
4	2484	92.7	509	2	Q5SR83_RAT	Q5sr83 rattus norv
5	2479	92.5	509	2	Q88548_RAT	Q88548 rattus norv
6	2447	91.3	509	1	SCRB1_CRIGR	Q80417 cricetus
7	2275.5	84.9	506	2	Q6B417_RAT	Q6b417 rattus norv
8	2215	82.6	509	1	SCRB1_FIG	Q8eqcl sus scrofa
9	2212	82.5	509	2	Q6T8F1_TUPGB	Q6t8f1 tupia glis
10	2200	82.1	509	2	Q52L25_HUMAN	Q52l25 homo sapien
11	2180	81.3	509	1	SCRB1_BOVIN	O18824 bos taurus
12	2148	80.1	509	2	Q6WIW9_RABIT	Q6wiw9 oryctolagus
13	2022.5	75.4	552	1	SCRB1_HUMAN	Q8wtv0 homo sapien
14	2022.5	75.4	581	2	Q59FM4_HUMAN	Q59fm4 homo sapien
15	1970	73.5	501	2	Q6WIW8_RABIT	Q6wiw8 oryctolagus
16	1401.5	52.3	460	2	Q4S1T9_TETNG	Q4s1t9 tetraodon n
17	1311	48.9	457	2	Q7ZYX0_BRARE	Q7zyx0 brachydanio
18	768	28.6	2096	2	Q4SJ33_TETNG	Q4sj33 tetraodon n
19	746	27.8	532	2	Q64HW6_ONCMY	Q64hw6 oncorhynch
20	741.5	27.7	477	1	SCRB2_HUMAN	Q14108 homo sapien
21	741.5	27.7	478	2	Q53Y63_HUMAN	Q53y63 homo sapien
22	734	27.4	477	1	SCRB2_RAT	P27615 rattus norv
23	732	27.3	477	1	SCRB2_MOUSE	Q35114 mus musculus
24	729	27.2	483	2	Q5XH33_XENLA	Q5xh33 xenopus lae
25	727.5	27.1	531	2	Q8JGR8_BRARE	Q8jgr8 brachydanio
26	722.5	26.9	484	2	Q7ZTL6_XENLA	Q7ztl6 xenopus lae
27	721	26.9	522	2	Q7Q950_ANOGA	Q7q950 anopheles g
28	709	26.4	465	2	Q6DHC7_BRARE	Q6dhc7 brachydanio
29	695	25.9	460	2	Q4SAC1_TETNG	Q4sac1 tetraodon n
30	687	25.6	472	2	Q5BKES_RAT	Q5bkes rattus norv
31	684.5	25.5	601	2	Q8IGY0_DROME	Q8igy0 drosophila

32	682.5	25.5	520	2	Q7KVF1_DROME	Q7kvf1 drosophila
33	682.5	25.5	551	2	Q9WOX0_DROME	Q9wox0 drosophila
34	678	25.3	471	1	CD36_MESAU	P70110 mesocricetu
35	678	25.3	472	2	Q925W0_RAT	Q925w0 rattus norv
36	677.5	25.3	471	2	Q5ZL18_CHICK	O5z18 gallus gall
37	677	25.3	471	1	CD36_HUMAN	P16671 h platelet
38	677	25.3	472	2	Q6IMX5_RAT	Q6imx5 rattus norv
39	675	25.2	472	2	Q6J512_MACMU	Q6j512 macaca mula
40	675	25.2	472	2	Q4R6B4_MACFA	Q4r6b4 macaca fasc
41	668	24.9	469	2	Q8SZV3_DROME	Q8szv3 drosophila
42	663	24.7	472	2	Q357S4_RAT	O357s4 rattus norv
43	662	24.7	471	1	CD36_MOUSE	Q88857 mus musculu
44	659	24.6	472	2	Q8C6Z4_MOUSE	Q8c6z4 mus musculu
45	645	24.1	471	1	CD36_RAT	Q07969 rattus norv

ALIGNMENTS

RESULT 1
 SCRB1_MOUSE STANDARD; PRT; 509 AA.
 AC Q61005; Q9CWJ7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
 GN Name=Scarb1; Synonyms=Srbl;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96152374; PubMed=8560269;
 RA Acton S., Rigotti A., Landschulz K.T., Xu S., Hobbs H.H., Krieger M.;
 RT "Identification of scavenger receptor SR-BI as a high density
 lipoprotein receptor."
 RL Science 271:518-520(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Dalla E., Dragani T.A., Fletcher C.F., Choithia C., Corbani L.R., Cousins S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16989-16993(2002).
 CC -!- FUNCTION: Receptor for different ligands such as phospholipids,
 CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
 CC cells. Probable receptor for HDL, located in particular region of
 CC the plasma membrane, called caveolae. Facilitates the flux of free
 CC and esterified cholesterol between the cell surface and
 CC extracellular donors and acceptors, such as HDL and to a lesser
 CC extent, apoB-containing lipoproteins and modified lipoproteins.
 CC Probably involved in the phagocytosis of apoptotic cells, via its
 CC phosphatidylserine binding activity (By similarity).
 CC -!- SUBUNIT: The C-terminal region binds to PDZK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
 CC localized to cholesterol and sphingomyelin-enriched domains within
 CC the plasma membrane, called caveolae (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed primarily in liver and nonplacental
 CC steroidogenic tissues.
 CC -!- PTM: N-glycosylated (By similarity).
 CC -!- SIMILARITY: Belongs to the CD36 family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL; U37799; AAC52378.1; -; mRNA.
 DR EMBL; AK010622; BAB27068.1; -; mRNA.
 DR EMBL; AK028191; BAC25802.1; -; mRNA.
 DR EMBL; AK033114; BAC28157.1; -; mRNA.
 DR EMBL; BC004656; AA04656.1; -; mRNA.
 DR Ensembl; ENSMUSG0000037936; Mus musculus.
 DR MGI; MGI:923578; Scarb1.
 DR GO; GO:0016599; C:cytosolic membrane; IDA.
 DR GO; GO:0000299; C:integral to membrane of membrane fraction; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR InterPro; IPR005428; CD36 antigen.
 DR PANTHER; PTHR11923; CD36; 1.
 DR Pfam; PF01130; CD36; 1.
 DR PRINTS; PR01610; CD36ANTIGEN.
 DR PRINTS; PR01609; CD36FAMILY.
 DR Glycoprotein; Receptor; Transmembrane.
 KW Glycoprotein; Receptor; Transmembrane.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 440 Extracellular (Potential).
 FT TRANSMEM 441 461 Potential.
 FT TOPO_DOM 462 509 Cytoplasmic (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD

FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 288 288 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 396 396 S -> F (in Ref. 2; BAB27068).
 FT CONFLICT 468 509 EKCFLWSSGKSGQKEAIQAYSESLSMSPAAGTVOLEAK
 FT L -> GPEDTISPNLIAWSDDPPSPYTPLEDSLSGQPTS
 FT AMA (in Ref. 2; BAB27068).
 SQ SEQUENCE 509 AA; 56754 MW; 5CFCD62DD6ECB1C CRC64;
 Query Match 100.0%; Score 2681; DB 1; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSSRRARWVAGLGGALGALLFAALGVVMIIMVPSLIKQVLLKNVRIDPSSLSFGMKKEIP 60
 DB 1 MGSSRRARWVAGLGGALGALLFAALGVVMIIMVPSLIKQVLLKNVRIDPSSLSFGMKKEIP 60
 QY 61 VPYLSYVFPEVVPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVNSLH 120
 DB 61 VPYLSYVFPEVVPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVNSLH 120
 QY 121 FQPKSHGSESDYIVLPNLLVGGSTILMSKPVSLKMMTLALVTMGQAFMNRVTGEIL 180
 DB 121 FQPKSHGSESDYIVLPNLLVGGSTILMSKPVSLKMMTLALVTMGQAFMNRVTGEIL 180
 QY 181 WGYDDDFVPHNTYLPDMLPIKGFGLFVGMNNSGVSFTVFTGVQNFSLHLVDKWNGL 240
 DB 181 WGYDDDFVPHNTYLPDMLPIKGFGLFVGMNNSGVSFTVFTGVQNFSLHLVDKWNGL 240
 QY 241 SKIDYWHSECNNINGTSGOMWAPFMTPESSLSFFSPEACRSKMLTYNESRVFEGIPTYR 300
 DB 241 SKIDYWHSECNNINGTSGOMWAPFMTPESSLSFFSPEACRSKMLTYNESRVFEGIPTYR 300
 QY 301 FTAPDITLFGANGVYPNNEGCPRESGIONVSTCRGAPLFLSHPHFYNADPVLSEAVLG 360
 DB 301 FTAPDITLFGANGVYPNNEGCPRESGIONVSTCRGAPLFLSHPHFYNADPVLSEAVLG 360
 QY 361 LNPXKHSFLDTHPVTGIPMNCVMQSLYIKSVKIGQTKIEPVPVPLLWFPQSG 420
 DB 361 LNPXKHSFLDTHPVTGIPMNCVMQSLYIKSVKIGQTKIEPVPVPLLWFPQSG 420
 QY 421 AMGKPLSTFTYTLQVLMPOVLYHYAVYVLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
 DB 421 AMGKPLSTFTYTLQVLMPOVLYHYAVYVLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
 QY 481 SQDKEAIQAYSESLSMSPAAGTVOLEAKL 509
 DB 481 SQDKEAIQAYSESLSMSPAAGTVOLEAKL 509
 RESULT 2
 Q4FK30_MOUSE
 ID Q4FK30_MOUSE PRELIMINARY; PRT; 509 AA.
 AC Q4FK30;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Scarb1 protein.
 GN Name=Scarb1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
 RT "Cloning of mouse full open reading frames in Gateway (R) system entry

RT vector (pDONR201);
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CTO10222; CAJ18430.1; -; mRNA.
 SQ SEQUENCE 509 AA; 56754 MW; 5CFCD62D62D6ECB1C CRC64;
 Query Match 100.0%; Score: 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSSRRARWALGALGALLFAALGVNMLVPSLIKKQVLKNVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGALLFAALGVNMLVPSLIKKQVLKNVRIDPSSLSFGMWKEIP 60
 Qy 61 VPFLSVYFFVVPVNPVNEVNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSLSH 120
 Db 61 VPFLSVYFFVVPVNPVNEVNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSLSH 120
 Qy 121 POPDKSHGSESDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGORAPMNRVTGSEIL 180
 Db 121 POPDKSHGSESDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGORAPMNRVTGSEIL 180
 Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNPFSRIHLVDKWNGL 240
 Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNPFSRIHLVDKWNGL 240
 Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
 Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
 Qy 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTRCFAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTRCFAPLFLSHPHFNADPVLSEAVLG 360
 Qy 361 LNPFPKHSFLDHPVTGIPMNCVSKMQLSLYKSVKIGQTKIBPVVPLPLWFQSG 420
 Db 361 LNPFPKHSFLDHPVTGIPMNCVSKMQLSLYKSVKIGQTKIBPVVPLPLWFQSG 420
 Qy 421 AMGCKPLSTFTVQLVLPQVLYHYAQYVLLGLGALLLVPIICQLRSQEKCFLPWGSKKG 480
 Db 421 AMGCKPLSTFTVQLVLPQVLYHYAQYVLLGLGALLLVPIICQLRSQEKCFLPWGSKKG 480
 Qy 481 SODKEATQAYSESLSMPAAKTVLQEAKL 509
 Db 481 SODKEATQAYSESLSMPAAKTVLQEAKL 509
 RESULT 3
 SCRB1 RAT STANDARD; PRT; 509 AA.
 ID SCRB1 RAT
 AC P97943;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
 GN Name=Scarb1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RA Johnson S.C.M., Svensson P.A., Carlsson B.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Ovary;
 RA Mizutani T., Sonoda Y., Minegishi T., Wakabayashi K., Miyamoto K.;
 RT "Cloning, characterization, and cellular distribution of rat scavenger
 receptor class B type I (SRBI) in the ovary."
 RL Biochem. Biophys. Res. Commun. 234:499-505(1997).

RN RP NUCLEOTIDE SEQUENCE, AND GLYCOSYLATION.
 RC STRAIN=Donryu; TISSUE=Testis;
 RX MEDLINE=22128898; PubMed=12016218; DOI=10.1074/jbc.M202879200;
 RA Kawasaki Y., Nakagawa A., Nagaosa K., Shiratsuchi A., Nakanishi Y.;
 RT "Phosphatidylserine binding of class B scavenger receptor type I, a
 phagocytosis receptor of testicular Sertoli cells."
 RL J. Biol. Chem. 277:27559-27566(2002).
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN RP INTERACTION WITH PDZK1.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=20309936; PubMed=10829064; DOI=10.1073/pnas.100114397;
 RA Ikemoto M., Arai H., Feng D., Tanaka K., Aoki J., Dohmae N., Takio K.,
 RA Adachi H., Tsujimoto M., Inoue K.;
 RT "Identification of a PDZ-domain-containing protein that interacts with
 the scavenger receptor class B type I."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:6538-6543(2000).
 CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
 cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
 cells. Probable receptor for HDL, located in particular region of
 the plasma membrane, called caveolae. Facilitates the flux of free
 and esterified cholesterol between the cell surface and
 extracellular donors and acceptors, such as HDL and to a lesser
 extent, apoB-containing lipoproteins and modified lipoproteins.
 CC Probably involved in the phagocytosis of apoptotic cells, via its
 phosphatidylserine binding activity (By similarity).
 CC -1- SUBUNIT: The C-terminal region binds to PDZK1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
 the plasma membrane, called caveolae (by similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the CD36 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 EMBL; U76205; BAB19203.1; -; mRNA.
 EMBL; D89655; BAA14004.1; -; mRNA.
 EMBL; AB002151; BAA74541.1; -; mRNA.
 EMBL; BC076504; AAH76504.1; -; mRNA.
 PIR; JC5533; JC5533.
 Ensembl; ENSRNOG0000000981; Rattus norvegicus.
 InterPro; IPR002159; CD36.
 InterPro; IPR005428; CD36_antigen.
 PANTHER; PTHR11923; CD36; 1.
 Pfam; PF01130; CD36; 1.
 PRINTS; PR01610; CD36ANTIGEN.
 PRINTS; PR01609; CD36FAMILY.
 Glycoproteins; Receptor; Transmembrane.
 TOPO_DOM 1 11 Cytoplasmic (Potential).
 TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 440 Extracellular (Potential).
 FT TRANSMEM 441 461 Potential.
 FT TOPO_DOM 462 509 Cytoplasmic (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 509 AA; 56957 MW; 792A0BB8D11A105 CRC64;

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Query Match 93.4%; Score 2504; DB 1; Length 509;
Best Local Similarity 92.3%; Pred. No. 1.1e-181;
Matches 470; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMILWPSLIKQVLRIDPSSLSFGMKKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMILWPSLIKQVLRIDPSSLSFGMKKEIP 60

Qy 61 VPYLSYVFEVNPSEVLNGQPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120
Db 61 VPYLSYVFEVNPSEVLNGQPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120

Qy 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMTMLALVTMGQAFNMRTVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMTMLALVTMGQAFNMRTVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLVDKXNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLVDKXNGL 240

Qy 241 SKIDYHSEQCNNMGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300
Db 241 SEVNYHSEQCNNMGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300

Qy 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPDPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGVGQTKIEPVPVPLPLWFQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGVGQTKIEPVPVPLPLWFQSG 420

Qy 421 AMGKPLSTFTYQLVLMPOVHYAQVYLLGLGGLLLVPIICQLRSEKCFLWMSGSKG 480
Db 421 MMGKTLNTFTYQLVLMPOVHYAQVYLLGLGGLLLVPIICQLRSEKCFLWMSGSKG 480

Qy 481 SODKEAIAQYSESILMSPAAGTGLVQEA 509
Db 481 SODKEAIAQYSESILMSPAAGTGLVQEA 509

RESULT 4
Q6SR89 RAT PRELIMINARY; PRT; 509 AA.
ID Q6SR89 RAT PRELIMINARY; PRT; 509 AA.
AC Q6SR89;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scavenger receptor class B type 1.
DE Name=Scarb1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=9236778; PubMed=10221589; DOI=10.1385/ENDO.9.3.243;
RA McLean M.P., Sandhoff T.W.;
RT "Expression and hormonal regulation of the high-density lipoprotein
RT (HDL) receptor scavenger receptor class B type I messenger ribonucleic
RT acid in the rat ovary."
RL Endocrine 9:243-252(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=20043932; PubMed=10579331; DOI=10.1210/en.140.12.5669;
RA Lopez D., McLean M.P.;
RT "Sterol regulatory element-binding protein-1a binds to cis elements in
RT the promoter of the rat high density lipoprotein receptor SR-BI
RT gene.";
```

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RL Endocrinology 140:5669-5681(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RA McLean M.P., Sandhoff T.W., Lopez D.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV451993; AAR18387.1; -; mRNA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR GO; GO:0007155; P.cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 56859 MW; EA0A76ECD207706C CRC64;

Query Match 92.7%; Score 2484; DB 2; Length 509;
Best Local Similarity 91.7%; Pred. No. 3.6e-180;
Matches 467; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMILWPSLIKQVLRIDPSSLSFGMKKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMILWPSLIKQVLRIDPSSLSFGMKKEIP 60

Qy 61 VPYLSYVFEVNPSEVLNGQPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120
Db 61 VPYLSYVFEVNPSEVLNGQPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120

Qy 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMTMLALVTMGQAFNMRTVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMTMLALVTMGQAFNMRTVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLVDKXNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLHLVDKXNGL 240

Qy 241 SKIDYHSEQCNNMGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300
Db 241 SEVNYHSEQCNNMGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300

Qy 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPDPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGVGQTKIEPVPVPLPLWFQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKGVGQTKIEPVPVPLPLWFQSG 420

Qy 421 AMGKPLSTFTYQLVLMPOVHYAQVYLLGLGGLLLVPIICQLRSEKCFLWMSGSKG 480
Db 421 MMGKTLNTFTYQLVLMPOVHYAQVYLLGLGGLLLVPIICQLRSEKCFLWMSGSKG 480

Qy 481 SODKEAIAQYSESILMSPAAGTGLVQEA 509
Db 481 SODKEAIAQYSESILMSPAAGTGLVQEA 509

RESULT 5
Q6SR548 RAT PRELIMINARY; PRT; 509 AA.
ID Q6SR548 RAT PRELIMINARY; PRT; 509 AA.
AC Q6SR548;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type II pneumocyte CD36-related class B scavenger receptor.
DE Name=SRB1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RN NUCLEOTIDE SEQUENCE.
RP STRAIN-Wistar;
RA Kollack I., Schlame M., Fechner H., Looman A.C., Wissel H.,
RA Ruestow B.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF071495; AAC33892.1; -, mRNA.
DR Ensemble; ENSRNOG0000000981; Rattus norvegicus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57152 MW; 1272E4FE824AD7F8 CRC64;

Query Match 92.5%; Score 2479; DB 2; Length 509;
Best Local Similarity 91.2%; Pred. No. 8.6e-180;
Matches 464; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFLSVVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Qy 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Qy 181 WGYDDPFFHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVTVQVNFRIHLVDKWNGL 240
Db 181 WGYDDPFFHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVTVQVNFRIHLVDKWNGL 240
Qy 241 SKIDYVHSEQCWMINGTSGOMWAPFMTPESSLEFPSPACRSMKLTYNESVPEGIPYR 300
Db 241 SEVKYHSEQCWMINGTAGOMWAPFMTPESSLEFPSPACRSMKLTVOESVPEGIPYR 300
Qy 301 FTAPDTLIFANGSVYPNPGFCPCRESGIONVSTCRFGAPFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPDTLIFANGSVYPNPGFCPCRESGIONVSTCRFGAPFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPDKHSLFLDHPVTGIPMNCVSKMQLSLYKSVKIGQGTGKIIPVLPPLWFOG 420
Db 361 LNPDKHSLFLDHPVTGIPMNCVSKMQLSLYKSVKIGQGTGKIIPVLPPLWFOG 420
Qy 421 AMGKPLSTFTQLVLMPOVLYAQYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQLVLMPOVLYAQYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKCTVLOEAKL 509
Db 481 SODKEATQAYSESLSMPAAKCTVLOEAKL 509

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RESULT 6
SCRB1_CRIGR STANDARD; PRT; 509 AA.
AC Q60417;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI) (HaSR-BI).
GN Name=SCARB1;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Cricetinae; Cricetulus.

```

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NCBI_TaxID=10029;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovarian carcinoma;
RX MEDLINE=94342261; PubMed=7520436;
RA Acton S.L., Scherer P.E., Lodish H.F., Krieger M.;
RT "Expression cloning of SR-BI, a CD36-related class B scavenger receptor.";
RL J. Biol. Chem. 269:21003-21009(1994).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apoB-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the CD36 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U11453; AAA61572.1; -, mRNA.
CC PIR; A53920; A53920.
CC InterPro; IPR002159; CD36.
CC InterPro; IPR005428; CD36_antigen.
CC PANTHER; PTHR11923; CD36; 1.
CC Pfam; PF01130; CD36; 1.
CC PRINTS; PR01610; CD36ANTIGEN.
CC PRINTS; PR01609; CD36FAMILY.
CC Glycoprotein; Receptor; Transmembrane.
CC TOPO_DOM 1 11 Cytoplasmic (Potential).
CC TRANSHEM 12 32 Potential.
CC TOPO_DOM 33 440 Extracellular (Potential).
CC TRANSHEM 441 461 Potential.
CC TOPO_DOM 462 509 Cytoplasmic (Potential).
CC CARBOHYD 102 108 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 509 AA; 56735 MW; 1A7C0F5F6CB61A17 CRC64;

Query Match 91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 2.3e-177;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFLSVVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPSVSLKMTLALVTMGQAFMNRVTGEIL 180
Qy 181 WGYDDPFFHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVTVQVNFRIHLVDKWNGL 240

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Db 181 WGYEDPFWNFSLKYPGMFPPIKGFGLFVGMNDSGLFTVFTGVQNFQSKIHLDVKNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNDSRVFEGIPTYR 300
Db 241 SKVNYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Db 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTGVLOEAKL 509
Db 481 SODKEAIQAYSESLSMSPAAGTGVLOEAKL 509

RESULT 7

Q6B417 RAT PRELIMINARY; PRT; 506 AA.
ID Q6B417 RAT PRELIMINARY; PRT; 506 AA.
AC Q6B417;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Scavenger receptor class B type 2.
GN Name=Scarb2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Sprague-Dawley;
RA Lopez D., Rubin D., McLean M.P.;
RT "Regulation of the Rat SR-B Isoforms";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY682847; AAT85567.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 506 AA; 56342 MW; 6FDE625301320E2E CRC64;

Query Match 84.9%; Score 2275.5; DB 2; Length 506;
Best Local Similarity 86.4%; Pred. No. 2.5e-164;
Matches 432; Conservative 27; Mismatches 26; Indels 15; Gaps 2;

Qy 1 MCGSRARWALGICGALGLLFAALGVNMLVPSLIKKOVLKNVIRDPSSLSFGWKEIP 60
Db 1 MGVSSRARWALGLGVLLCAALGVITMLVPSLIKKOVLKNVIRDPSSLSFGWKEIP 60
Qy 61 VPFYLSVVFVFEVNVNEVLNGKPVVRERGPPVYREFRQKNVITDNDNDTVSFVNRSLH 120
Db 61 VPFYLSVVFVFEVNVNEVLNGKPVVRERGPPVYREFRQKNVITDNDNDTVPIENRSLR 120
Qy 121 FQPKSHGSESDYIVLPNIIVLGSGILMESKPVSLKLMNTLALVTGQRAFPMNRTVGIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGSGILMESKPVSLKLMNTLALVTGQRAFPMNRTVGIL 180
Qy 181 WGYDDPFWHFLNTYLPDMLPIKGFGLFVGMNDSGLFTVFTGVQNFQSKIHLDVKNGL 240

Db 181 WGYEDPFWNFSLKYPGMFPPIKGFGLFVGMNDSGLFTVFTGVQNFQSKIHLDVKNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNDSRVFEGIPTYR 300
Db 241 SEVNYHSEOCNMINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQSRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Db 421 MMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Qy 481 SODKEA---IQAYSESLSMSP 497
Db 469 PEDTTPPNLIAMSDQPPSP 488

RESULT 8

SCRBI_PIG STANDARD; PRT; 509 AA.
ID SCRBI_PIG STANDARD; PRT; 509 AA.
AC Q8SQCL;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-B1) (High density lipoprotein receptor SR-B1).
GN Name=SCRBI;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9923;
RN NUCLEOTIDE SEQUENCE.
RP Kim J.G., Vallet J.L., Christenson R.K.;
RA "Characterization of porcine high density lipoprotein (HDL) receptor SR-B1";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for different ligands such as phospholipids, cholesterol ester, lipoproteins, phosphatidylserine and apoptotic cells. Probable receptor for HDL, located in particular region of the plasma membrane, called caveolae. Facilitates the flux of free and esterified cholesterol between the cell surface and extracellular donors and acceptors, such as HDL and to a lesser extent, apob-containing lipoproteins and modified lipoproteins. Probably involved in the phagocytosis of apoptotic cells, via its phosphatidylserine binding activity (By similarity).
CC -!- SUBUNIT: The C-terminal region binds to PDZK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly localized to cholesterol and sphingomyelin-enriched domains within the plasma membrane, called caveolae (By similarity).
CC -!- PTM: N-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the CD36 family.

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EMBL; AF467889; AAL75567.1; -; mRNA.
InterPro; IPR002159; CD36.
InterPro; IPR005428; CD36_antigen.
PANTHER; PTHR11923; CD36; 1.
Pfam; PF01130; CD36; 1.
PRINTS; PR01610; CD36ANTIGEN.
PRINTS; PR01609; CD36FAMILY.

Glycoprotein; Receptor; Transmembrane.
 FT TOPO DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO DOM 33 439 Extracellular (Potential).
 FT TRANSMEM 440 460 Potential.
 FT TOPO DOM 461 509 Cytoplasmic (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 212 212 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 383 383 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 509 AA; 57514 MW; F7421796C391C4C1 CRC64;

Query Match 82.6%; Score 2215; DB 1; Length 509;
 Best Local Similarity 80.2%; Pred. No. 1e-159;
 Matches 408; Conservative 48; Mismatches 53; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Qy 61 VPFYLSVYFPEVVPNEVLNGOKPVRRGPGYVYRERQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFPEVVPNEVLNGOKPVRRGPGYVYRERQKVNITFNDNDTVSFVENRSLH 120
 Qy 121 FQPKSHGSESDYIVLPNIIVLGSLIMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGSLIMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
 Qy 181 WGYDDPVPFHINTLTPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPVPFHINTLTPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFSPSEACSMKLIYKEQVFGIPTFR 300
 Db 241 SKVNFHSDQCNMINGTSGQWAPFMTPESSLEFSPSEACSMKLIYKEQVFGIPTFR 300
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Db 301 FVAENTLTFANGSVYPPNEGFCPCRESGIONVSTCRFNAPLFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIPEVPLPLLPFQSG 420
 Db 361 LHPNTEHSLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIPEVPLPLLPFQSG 420
 Qy 421 AMGGKPLSTFTYQLVLPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Db 421 AMEGETLQTFYQLVLPQVLYHYAQVYLLGLGGLLLVPIIVYQIRSOEKCYLFWSSKKG 480
 Qy 481 SODKEATQAYSESIMSPAAGTGLQEARL 509
 Db 481 SODKEATQAYSESIMSPAAGTGLQEARL 509

RESULT 9
 Q6T8F1_TUPGB
 ID Q6T8F1_TUPGB PRELIMINARY; PRT; 509 AA.
 AC Q6T8F1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Scavenger receptor class B member 1.
 GN Name=SCARB1;
 OS Tupia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupia.
 NCBI_TaxID=37347;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Barth H., Cerino R., Arcuri M., Hoffmann M., Schurmann P., Adah M.I.,

Gissler B., Zhao X., Chisetti V., Lavezzo B., Blum H.E.,
 von Weizsacker F., Vicelli A., Scarselli E., Baumert T.F.;
 RT "Scavenger Receptor Class B Type I and Hepatitis C Virus Infection of
 Primary Tupaia Hepatocytes.";
 J. Virol. 79:5774-5785(2005).
 RL EMBL; AY428553; AAR12144.1; -; mRNA.
 DR GO: 0016020; C.membrane; IEA.
 DR GO: 0004872; F.receptor activity; IEA.
 DR GO: 0007155; P.cell adhesion; IEA.
 DR InterPro: IPR002159; CD36.
 DR Pfam: PF01130; CD36; 1.
 DR PRINTS; PRO1610; CD36ANTIGEN.
 DR PRINTS; PRO1609; CD36FAMILY.
 KW Receptor.
 SQ SEQUENCE 509 AA; 57369 MW; F0A3FBB1431PFB18 CRC64;

Query Match 82.5%; Score 2212; DB 2; Length 509;
 Best Local Similarity 80.0%; Pred. No. 1.7e-159;
 Matches 407; Conservative 49; Mismatches 53; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Qy 61 VPFYLSVYFPEVVPNEVLNGOKPVRRGPGYVYRERQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFPEVVPNEVLNGOKPVRRGPGYVYRERQKVNITFNDNDTVSFVENRSLH 120
 Qy 121 FQPKSHGSESDYIVLPNIIVLGSLIMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGSLIMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
 Qy 181 WGYDDPVPFHINTLTPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPVPFHINTLTPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFSPSEACSMKLIYKEQVFGIPTFR 300
 Db 241 SKVNFHSDQCNMINGTSGQWAPFMTPESSLEFSPSEACSMKLIYKEQVFGIPTFR 300
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Db 301 FVAENTLTFANGSVYPPNEGFCPCRESGIONVSTCRFNAPLFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIPEVPLPLLPFQSG 420
 Db 361 LHPNTEHSLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIPEVPLPLLPFQSG 420
 Qy 421 AMGGKPLSTFTYQLVLPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Db 421 AMEGETLQTFYQLVLPQVLYHYAQVYLLGLGGLLLVPIIVYQIRSOEKCYLFWSSKKG 480
 Qy 481 SODKEATQAYSESIMSPAAGTGLQEARL 509
 Db 481 SODKEATQAYSESIMSPAAGTGLQEARL 509

RESULT 10
 Q52LZ5_HUMAN
 ID Q52LZ5_HUMAN PRELIMINARY; PRT; 509 AA.
 AC Q52LZ5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Scavenger receptor class B, member 1.
 GN Name=SCARB1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC093732; AAH03732.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 509 AA; 56973 MW; 0184AE9CEC595374 CRC64;

Query Match 82.1%; Score 2200; DB 2; Length 509;
Best Local Similarity 79.6%; Pred. No. 1.4e-158;
Matches 405; Conservative 49; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVWILMPSLIKQVVKVIRIDPSSLSFGWKKEIP 60
Db 1 MGCSAKARWAGALGVGLLCAVLGAVMIVMPSLIKQVVKVIRIDPSSLSFGWKKEIP 60
Qy 61 VPFLSVVFFVWVNPVNLGQPKVRRGYPVYRFRQKNITFDNDITVSFVENSLSH 120
Db 61 IPFLSVVFFVWVNPVNLGQPKVRRGYPVYRFRQKNITFDNDITVSFLEYRTFQ 120
Qy 121 FQPKSHGSESDYVLPNLYLGGSIILMESKPSVSLKMLMTLALVTMGQAPMNRVTGEIL 180
Db 121 FQPKSHGSESDYVLPNLYLGGSIILMESKPSVSLKMLMTLALVTMGQAPMNRVTGEIM 180
Qy 181 WGYDDPFVHFLNTVLPDMLPTKGKFLVGNNGNSGVFTVGTQVQNPSTRHLVDKNGKL 240
Db 181 WGYDDPLVNLINKYPPGMPFPDQKPLPAELNNSDGLFTVGTQVQNPSTRHLVDKNGKL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPMPTPESSILEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKVDFHSDQNMINGTSGQWAPMPTPESSILEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPPTLFPANGSVYPNPGFCPCRESGIQNVSTRCFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FVAPKTLFPANGSIYPNPGFCPCLESGIQNVSTRCFGAPLFLSHPHFNADPVLSEAVTG 360
Qy 361 LNPNPKEHSLFLDHPVTGIPMNCSSVKMOLSIYTKSVKIGIGOTKIEPVLPLLWFEOG 420
Db 361 LHPNQEAHSLFLDHPVTGIPMNCSSVKMOLSIYTKSVKIGIGOTKIEPVLPLLWFEOG 420
Qy 421 AMGQPLSTFTYQLVLMQVLYHAYVLLGLGLLLVPIICQLRSQKCFLWFGSKGK 480
Db 421 AMEGTILFTYQLVLMQVLYHAYVLLGLGLLLVPIICQLRSQKCFLWFGSKGK 480
Qy 481 SODKEAIQAYSLSLMSPAKGTVLOEAKL 509
Db 481 SKDKEAIQAYSLSLMSAPKGSVLQEAKL 509
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RESULT 11
SCRB1_BOVIN STANDARD; PRT; 509 AA.
ID SCRB1_BOVIN
AC O18824;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
DE Name=SCARB1;
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Corpus luteum;
RX MEDLINE=98068685; PubMed=9406850; DOI=10.1016/S0303-7207(97)00173-1;
RX Rajapaksha W.R.A.K.J.S., McBride M., Robertson L., O'Shaughnessy P.J.;
RT "Sequence of the bovine HDL-receptor (SR-BI) cDNA and changes in
RT receptor mRNA expression during granulosa cell luteinization in vivo
RT and in vitro."
RL Mol. Cell. Endocrinol. 134:59-67(1997).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apoB-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the CD36 family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; AF019384; AAB70920.1; -, mRNA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR PANTHER; PTHR11923; CD36; 1.
DR Pfam; PF011130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Glycoprotein; Receptor; Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 440 Extracellular (Potential).
FT TRANSMEM 441 461 Potential.
FT TOPO_DOM 462 509 Cytoplasmic (Potential).
FT CARBOHYD 102 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 509 AA; 57610 MW; B3B7FD368C22C12F CRC64;

Query Match 81.3%; Score 2180; DB 1; Length 509;
Best Local Similarity 78.6%; Pred. No. 4.6e-157;
Matches 400; Conservative 50; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVWILMPSLIKQVVKVIRIDPSSLSFGWKKEIP 60
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Db 1 MGNLRARVTAALGICLLFAVLGIMVWPSLIKQOVLKNVRIDPNSLFWNKWEIP 60
Qy 61 VPFYLSVYFVFNVEVNGOKPVYRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFVFNVEVNGOKPVYRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHSGESDYIVLPNVLGSGILMESKPVSLKLMNTLALVTMGORAFMNRVTGAIL 180
Db 121 FQPKSHSGESDYIVLPNVLGSGILMESKPVSLKLMNTLALVTMGORAFMNRVTGAIL 180
Qy 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTGVONFSRHLVDKWNGL 240
Db 181 WGYDDPLHLNQFPNSLPKGFGLFAELNNSDGLFTFTGVONFSRHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPMPTPESSLEFSPACRSMKLYKESVFGGIPYR 300
Db 241 SKVNYHSDQCNMNGTSGQWAPMPTPESSLEFSPACRSMKLYKESVFGGIPYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
Db 301 FVAPSTLTFANGSVYPPNEGFCPCRESGIONVSTCRFNAFLFLSHPHFYNDPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGOTGKIEPVVLPVLLWFEQSG 420
Db 361 LHPNEBEHALFDHPVTGIPMNCVKQLSLYKSVKGIGOTGKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMQVHLHYAQVLLGGLLVPILCOLRSQKCFLFWGSKKG 480
Db 421 AMEGTLETFTYQLVLMQVHLHYAQVLLGGLLVPILCOLRSQKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAEL 509
Db 481 SKDKEAVQAYSEFLMTSAPKGTVLQEARL 509

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RESULT 12

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Q6WIW9 RABIT PRELIMINARY; PRT; 509 AA.
ID Q6WIW9 RABIT PRELIMINARY; PRT; 509 AA.
AC Q6WIW9;
DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
DE Scavenger receptor class B type I.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Fatsch J.R.;
RT Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.
RL J. Lipid Res. 45:214-222(2004).
DR ENBL: AY283277; AAP40266.1; - mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR002159; CD36.
DR InterPro: IPR005428; CD36_antigen.
DR Pfam: PF01130; CD36.1.
DR PRINTS: PR01610; CD36ANTIGEN.
DR PRINTS: PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57052 MW; 00DD47F1AF2DB4E0 CRC64;

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Query Match 80.1%; Score 2148; DB 2; Length 509;
Best Local Similarity 77.6%; Pred. No. 1.2e-154;
Matches 395; Conservative 55; Mismatches 59; Indels 0; Gaps 0;

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Qy 1 MGSSRARWVALGIGALGLLFAALGVVMILWVPSLIKQOVLKNVRIDPNSLFWNKWEIP 60
Db 1 MGGRARRAAAGLVGVGLLCAVGVALLAAVPLIRQVVLKNVRIDPNSLFWNKWEIP 60
Qy 61 VPFYLSVYFVFNVEVNGOKPVYRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 APPYLSVYFVFNVEVNGOKPVYRERGYPVYRERQKVNITFNDNDTVSFLEHRSFQ 120
Qy 121 FQPKSHSGESDYIVLPNVLGSGILMESKPVSLKLMNTLALVTMGORAFMNRVTGAIL 180
Db 121 FQPKSHSGESDYIVLPNVLGSGILMESKPVSLKLMNTLALVTMGORAFMNRVTGAIL 180
Qy 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTGVONFSRHLVDKWNGL 240
Db 181 WGYEDPLMLNLINKYLPGVFPFKGLFAEMNDSGVTFTGVONFSRHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPMPTPESSLEFSPACRSMKLYKESVFGGIPYR 300
Db 241 SKVNYHSDQCNMNGTSGQWAPMPTPESSLEFSPACRSMKLYKESVFGGIPYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
Db 301 FVAPKTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGOTGKIEPVVLPVLLWFEQSG 420
Db 361 LHPNEBEHALFDHPVTGIPMNCVKQLSLYKSVKGIGOTGKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMQVHLHYAQVLLGGLLVPILCOLRSQKCFLFWGSKKG 480
Db 421 AMEGTLETFTYQLVLMQVHLHYAQVLLGGLLVPILCOLRSQKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAEL 509
Db 481 SKDKEAVQAYSEFLMTSAPKGTVLQEARL 509

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RESULT 13

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SCRB1 HUMAN STANDARD; PRT; 552 AA.
ID SCRB1 HUMAN STANDARD; PRT; 552 AA.
AC Q8WTU0; Q14016; Q6KFX4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-B1) (CD36 antigen-like
DE 1) (CD36 and LIMP2II analogous 1) (CLA-1) (Collagen type I receptor,
DE thrombospondin receptor-like 1).
GN Name=SCARB1; Synonyms=CD36L1, CLA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Promyelocyte;
RX MEDLINE=93366811; PubMed=7689561;
RA Calvo D.; Vega M.;
RT "Identification, primary structure and distribution of CLA-1, a novel
RT member of the CD36/LIMP2II gene family."
J. Biol. Chem. 268:18929-18935(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA Hirano K.-I., Yamashita S., Matsuzawa Y.;
RL Submitted (MAY 2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3).
RC TISSUE=Prostate, and Rhabdomyosarcoma;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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FT SVLQRAKL (in isoform 1, isoform 2 and
FT isoform 4).
FT /FTID=VSP_008554.
FT G -> S (in dbSNP:4238001).
FT /FTID=VAR_017098.
FT V -> I.
FT /FTID=VAR_017099.
FT G -> S.
FT /FTID=VAR_017100.
FT S -> G (in dbSNP:10396213).
FT /FTID=VAR_019507.
FT C -> R (in dbSNP:2293440).
FT /FTID=VAR_017101.
FT F -> L (in Ref. 2).
FT F -> S (in Ref. 1).
FT CONFLICT 70 70
FT CONFLICT 97 97
FT CONFLICT 97 97
SQ SEQUENCE 552 AA; 60878 MW; 06B0BD771FEA284F CRC64;

Query Match 75.4%; Score 2022.5; DB 1; Length 552;
Best Local Similarity 74.6%; Pred. No. 4.8e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

QY 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSARARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVYFVFNPNVNEVLNGKQPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
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RESULT 14
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AC Q59FM4;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Scavenger receptor class B member 1 variant (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.

SVLQRAKL (in isoform 1, isoform 2 and
isoform 4).
/FTID=VSP_008554.
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/FTID=VAR_017098.
V -> I.
/FTID=VAR_017099.
G -> S.
/FTID=VAR_017100.
S -> G (in dbSNP:10396213).
/FTID=VAR_019507.
C -> R (in dbSNP:2293440).
/FTID=VAR_017101.
F -> L (in Ref. 2).
F -> S (in Ref. 1).
CONFLICT 70 70
CONFLICT 97 97
CONFLICT 97 97
SEQUENCE 552 AA; 60878 MW; 06B0BD771FEA284F CRC64;

Query Match 75.4%; Score 2022.5; DB 1; Length 552;
Best Local Similarity 74.6%; Pred. No. 4.8e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

QY 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSARARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVYFVFNPNVNEVLNGKQPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFVFNPNVNEVLNGKQPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
QY 121 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
QY 149 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIM 208
Db 149 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIM 208
QY 181 WGYDDPFVHFLNTYLPDMPLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMPLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
QY 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
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Db 301 FTAPDTLTFANGSVYPPNPGFCPCRESGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
QY 361 LNPMPKHSFLDIIHPVTGIPMNCVKMQLSLYKSVKIGIGOTGKIHPVLPVLLWFEOG 420
Db 361 LNPMPKHSFLDIIHPVTGIPMNCVKMQLSLYKSVKIGIGOTGKIHPVLPVLLWFEOG 420
QY 421 AMGKPLSTFTYQLVLMPOVLYHAQYVLLGLGGLLLVPIICQLRSQKCFKFLWFSKKG 480
Db 421 AMGKPLSTFTYQLVLMPOVLYHAQYVLLGLGGLLLVPIICQLRSQKCFKFLWFSKKG 480
QY 481 SODKEATQAY-----SESLSMPAA 499
Db 481 SODKEATQAY-----SESLSMPAA 499
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Db 476 RADSHSLACWGKSGASDRTLWPTA 498

RESULT 15
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AC Q6W1W8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RP NUCLEOTIDE SEQUENCE.
RA Ritsch A., Tancevski I., Schoger W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patech J.R.;
RA "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RT J. Lipid Res. 45:214-222(2004).

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RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209436; BAD92673.1; -, mRNA.
KW Receptor.
FT NON TER
SQ SEQUENCE 581 AA; 64186 MW; 795810C1C2FA75A3 CRC64;

Query Match 75.4%; Score 2022.5; DB 2; Length 581;
Best Local Similarity 74.6%; Pred. No. 5.1e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

QY 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 29 MGSARARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 88
QY 61 VPFYLSVYFVFNPNVNEVLNGKQPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
Db 89 VPFYLSVYFVFNPNVNEVLNGKQPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 148
QY 121 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 149 FQPKSHGSESDYIVLPNLIIVLGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIM 208
QY 181 WGYDDPFVHFLNTYLPDMPLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
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Db 449 AMGKPLSTFTYQLVLMPOVLYHAQYVLLGLGGLLLVPIICQLRSQKCFKFLWFSKKG 503
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Db 504 RADSHSLACWGKSGASDRTLWPTA 526

RESULT 15
Q6W1W8 RABIT PRELIMINARY; PRT; 501 AA.
AC Q6W1W8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RP NUCLEOTIDE SEQUENCE.
RA Ritsch A., Tancevski I., Schoger W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patech J.R.;
RA "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RT J. Lipid Res. 45:214-222(2004).

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DR EMEL; AY283278; AAP40267.1; -: mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR02159; CD36.
DR InterPro; IPR05428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
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KW Receptor.
SQ SEQUENCE 501 AA; 55675 MW; 9A839B31C49F4C71 CRC64;

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Best Local Similarity 77.3%; Pred. No. 4.2e-141;
Matches 361; Conservative 51; Mismatches 55; Indels 0; Gaps 0;

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Qy 61 VPFYLSVYFFEVNPNNEVLNGQKPVVRERGYPVYRERQKNITFDNDTVSFVENRSLH 120
Db 61 APFYLSVYFFDVNPNNEILKGEKQVRERGYPVYRERHKKNITFDNDTVSFLEHRSFQ 120

Qy 121 FQPKSHSSESDYIVLNLVLGSLILWESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
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Qy 301 FTAPDTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDADPVLSEAVLG 360
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Search completed: February 23, 2006, 12:45:06
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:45:24 ; Search time 34 Seconds
(without alignments)
1237.704 Million cell updates/sec

Title: US-08-765-108-8

Perfect score: 2681

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pdp.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pdp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2681	100.0	509	1 US-08-559-505-4	Sequence 4, Appli
2	2681	100.0	509	1 US-08-749-907-4	Sequence 4, Appli
3	2681	100.0	509	2 US-09-241-581B-8	Sequence 8, Appli
4	2681	100.0	509	2 US-09-385-799-4	Sequence 4, Appli
5	2681	100.0	509	4 PCT-US95-07721-8	Sequence 8, Appli
6	2447	91.3	509	1 US-08-559-505-2	Sequence 2, Appli
7	2447	91.3	509	1 US-08-749-907-2	Sequence 2, Appli
8	2447	91.3	509	1 US-08-890-980-4	Sequence 4, Appli
9	2447	91.3	509	2 US-08-890-979-4	Sequence 4, Appli
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11	2447	91.3	509	2 US-09-031-626-4	Sequence 4, Appli
12	2447	91.3	509	2 US-09-241-581B-4	Sequence 4, Appli
13	2447	91.3	509	2 US-08-265-428-4	Sequence 4, Appli
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27	568	21.2	412	2 US-09-949-016-11488	Sequence 11488, A

28 436 16.3 458 2 US-09-270-767-43768 Sequence 43768, A
29 431 16.1 310 2 US-09-270-542-90 Sequence 90, Appli
30 346 12.9 332 2 US-09-270-767-46306 Sequence 46306, A
31 295 11.0 462 2 US-09-270-767-45262 Sequence 45262, A
32 267 10.0 158 2 US-09-270-767-61875 Sequence 61875, A
33 230 8.6 301 2 US-09-270-767-33112 Sequence 33112, A
34 229 8.6 301 2 US-09-270-767-48329 Sequence 48329, A
35 229 8.5 248 2 US-09-270-767-59167 Sequence 59167, A
36 189 7.0 74 2 US-09-513-999C-6528 Sequence 6528, Ap
37 181 6.8 181 2 US-09-270-767-42865 Sequence 42865, A
38 106 4.0 172 2 US-09-270-767-60022 Sequence 60022, A
39 106 4.0 205 2 US-09-270-767-44571 Sequence 44571, A
40 100.5 3.7 45 2 US-09-161-939A-4 Sequence 4, Appli
41 99 3.7 320 2 US-09-134-000C-4950 Sequence 4950, Ap
42 98.5 3.7 414 2 US-10-104-047-2031 Sequence 2031, Ap
43 97.5 3.6 45 2 US-09-161-939A-21 Sequence 21, Appli
44 97.5 3.6 924 2 US-09-583-110-3216 Sequence 3216, Ap
45 97.5 3.6 928 2 US-09-107-433-2917 Sequence 2917, Ap

ALIGNMENTS

RESULT 1

US-08-559-505-4
; Sequence 4, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/559,505
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabat, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class BI."

US-08-559-505-4

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
DB 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
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DB 61 VPFYLSVYFFVVPNEVNLGKQPVVRERGYPVYFRQKVNITFNDNDTVSFVNRSLH 120
QY 121 FQPKSHGSESDYIVLPNIIIVLGGSIIMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGGSIIMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
DB 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
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DB 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
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DB 421 AMGKPLSTFTYTLVLPQVLYHYAQQVLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
QY 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
DB 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 2

US-08-749-907-4
; Sequence 4, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class B1."
US-08-749-907-4

Query Match 100.0%; Score 2691; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
DB 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
QY 61 VPFYLSVYFFVVPNEVNLGKQPVVRERGYPVYFRQKVNITFNDNDTVSFVNRSLH 120
DB 61 VPFYLSVYFFVVPNEVNLGKQPVVRERGYPVYFRQKVNITFNDNDTVSFVNRSLH 120
QY 121 FQPKSHGSESDYIVLPNIIIVLGGSIIMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGGSIIMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
DB 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
QY 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
DB 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
DB 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
QY 361 LNPMPKHSFLDHPVTGIPMNCVVMQSLYIKSVKGIGQTKIEBPVVLPLLPFQSG 420
DB 361 LNPMPKHSFLDHPVTGIPMNCVVMQSLYIKSVKGIGQTKIEBPVVLPLLPFQSG 420
QY 421 AMGKPLSTFTYTLVLPQVLYHYAQQVLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
DB 421 AMGKPLSTFTYTLVLPQVLYHYAQQVLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
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DB 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 3

US-09-241-581B-8
; Sequence 8, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B

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; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for
; the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-241-581B-8

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120

Qy 121 POPDKSHGESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGORAFNRTVGIL 180
Db 121 POPDKSHGESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGORAFNRTVGIL 180

Qy 181 WGYDDPPFVHFLNTLYPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSTRHLVDKKNGL 240
Db 181 WGYDDPPFVHFLNTLYPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSTRHLVDKKNGL 240

Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPYR 300

Qy 301 FTAPDTLPANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLPANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPMPKHSFLDHPVTGIPMNCVKMOLSLYIKSVKGIGOTGKIHPVVLPLLWFEQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVKMOLSLYIKSVKGIGOTGKIHPVVLPLLWFEQSG 420

Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
Db 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480

Qy 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509

RESULT 4
US-09-385-799-4
; Sequence 4, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385.799
; FILING DATE: 30-Aug-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-385-799-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120

Qy 121 POPDKSHGESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGORAFNRTVGIL 180
Db 121 POPDKSHGESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGORAFNRTVGIL 180

Qy 181 WGYDDPPFVHFLNTLYPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSTRHLVDKKNGL 240
Db 181 WGYDDPPFVHFLNTLYPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSTRHLVDKKNGL 240

Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPYR 300

Qy 301 FTAPDTLPANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLPANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPMPKHSFLDHPVTGIPMNCVKMOLSLYIKSVKGIGOTGKIHPVVLPLLWFEQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVKMOLSLYIKSVKGIGOTGKIHPVVLPLLWFEQSG 420

Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
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Db 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQKCFLEWGSCKG 480
QY 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
RESULT 5
PCT-US95-07721-8
; Sequence 8, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /function = "Amino acid sequence for
; OTHER INFORMATION: the murine Scavenger Receptor Class BI."
PCT-US95-07721-8
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGGSSRARVAGLGGALLFAALGVMLVPSLIQOVLKVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRARVAGLGGALLFAALGVMLVPSLIQOVLKVRIDPSSLSFGMWKEIP 60
QY 61 VPFLSVYVFFVAVNPVNEVLNGQKPVVRERGPYVYRFRQKVNITFDNDITVSFVENSRLH 120
Db 61 VPFLSVYVFFVAVNPVNEVLNGQKPVVRERGPYVYRFRQKVNITFDNDITVSFVENSRLH 120
QY 121 FQPKSHGSESDYVLPNVLGGSILMESKPVSLKLMNTLALVTMGORAPMNTVGEIL 180
Db 121 FQPKSHGSESDYVLPNVLGGSILMESKPVSLKLMNTLALVTMGORAPMNTVGEIL 180
QY 181 WGYDDPFVHFTLVLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGYDDPFVHFTLVLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKNGL 240
QY 241 SKIDYWHSEQCNINGTSGQWMAFPMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300

Db 241 SKIDYWHSEQCNINGTSGQWMAFPMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPDITLFANGSVYPNEGFCPCRESGIONVSTCRGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDITLFANGSVYPNEGFCPCRESGIONVSTCRGAPLFLSHPHFYNNADPVLSEAVLG 360
QY 361 LNPNPKEHSLFLDIHPVTGIPMNCVSMQVLSYIKSVKGIGQTKIEPVVLPPLWFEQSG 420
Db 361 LNPNPKEHSLFLDIHPVTGIPMNCVSMQVLSYIKSVKGIGQTKIEPVVLPPLWFEQSG 420
QY 421 AMGGKPLSTFTYQLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQKCFLEWGSCKG 480
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Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
RESULT 6
US-08-559-505-2
; Sequence 2, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /function = "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note = "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464


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; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175,
; OTHER INFORMATION: 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 repre
; OTHER INFORMATION: N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21, 251,
; OTHER INFORMATION: 280, 321, 323, 334, 384 and 470 represent potential disulfide
US-08-559-505-2

Query Match          91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVWMLVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Db 1 MGSRRARWAVGLGVGGLCAVLGVWMLVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Qy 61 VPVYLSVYFFVWVNPNEVNGKPVRRERGPVYVREPRQKNIITFNDNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFVWVNPNEVNGKPVRRERGPVYVREPRQKNIITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIIVLPNVLVGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIIVLPNVLVGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEPSPACSKMLTYNESRVFSGIPTYR 300
Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEPSPACSKMLTYNESRVFSGIPTYR 300
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Db 301 FTAPDTTLFANGSVYPPNEGFCFCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360
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Db 361 LNPMPKSHSLFDLHPVTGIPMNCVSKQLSIYKSVKIGQTKIEPVLPLLWFQSG 420
Qy 421 AMGCKPLSTFTVTLVMPQVLYAQVLLGLGILLVPIICOLRSQEKCLFWSGSKG 480
Db 421 AMGCKPLSTFTVTLVMPQVLYAQVLLGLGILLVPIICOLRSQEKCLFWSGSKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEATQAYSESLSMPAAKGTVLQEAKL 509

RESULT 7
US-08-749-907-2
; Sequence 2, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-3
; OTHER INFORMATION: potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; OTHER INFORMATION: 251, 280, 321, 323, 334, 384 and 470 represent potential disul
; OTHER INFORMATION: linkages."
US-08-749-907-2

Query Match          91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVWMLVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Db 1 MGSRRARWAVGLGVGGLCAVLGVWMLVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Qy 61 VPVYLSVYFFVWVNPNEVNGKPVRRERGPVYVREPRQKNIITFNDNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFVWVNPNEVNGKPVRRERGPVYVREPRQKNIITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIIVLPNVLVGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIIVLPNVLVGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEPSPACSKMLTYNESRVFSGIPTYR 300
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Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDTHPVTGIPMNCVSMQSLYKSVKGIGQTKIEPVVPLLLWFEQSG 420
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Db 421 AMGGKPLSTFYTQVLVMPQVLYHQAQVYVLLGLGGLLLVPIICOLRSQKCFLFWGSKKG 480
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Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
RESULT 8
US-08-890-980-4
; Sequence 4, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-890-980-4
Query Match 91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWAVGLGVVGLLCAVLGVVMIWVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYVFFVNPVNEVLNGQKPVVRGYPVYVREFRQKNITFDNDTIVSFVENSRLH 120
Db 61 VPFYLSVYVFFVNPVNEVLNGQKPVVRGYPVYVREFRQKNITFDNDTIVSFVENSRLH 120
Qy 121 FQPKSHGSESDYVILNVLVGLSILMESKPSVILKMTLALVTMGQAFMRTVGEIL 180
Db 121 FQPKSHGSESDYVILNVLVGLSILMESKPSVILKMTLALVTMGQAFMRTVGEIL 180
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Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVEMNNSDGLFTVFTGVQNFRIHLVDKNGL 240
Qy 241 SKIDYHSSQCNMINTSGOMWAPFMTPESSLEFFSPACRSKMLTYNBSRVFEGIPTYR 300
Db 241 SKYNYHSSQCNMINTSGOMWAPFMTPESSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDTHPVTGIPMNCVSMQSLYKSVKGIGQTKIEPVVPLLLWFEQSG 420
Db 361 LNPDPKHSFLDTHPVTGIPMNCVSMQSLYKSVKGIGQTKIEPVVPLLLWFEQSG 420
Qy 421 AMGGKPLSTFYTQVLVMPQVLYHQAQVYVLLGLGGLLLVPIICOLRSQKCFLFWGSKKG 480
Db 421 AMGGKPLSTFYTQVLVMPQVLYHQAQVYVLLGLGGLLLVPIICOLRSQKCFLFWGSKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
RESULT 9
US-08-890-979-4
; Sequence 4, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-890-979-4
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWAVGLGVVGLLCAVLGVVMIWVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60


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Qy 421 AMGKPLSTFTYQLVLPMPVLYHYAYVLLGLGGLLLVPIICQLRSQKCFLWFSQSGKKG 480
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Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 12
US-09-241-581B-4
; Sequence 4, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane
; domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane
; domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257,
; 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
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;
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions
; 21, 251, 280, 321, 323, 334, 384 and
; 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-241-581B-4

Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGGSSRARWALGIGLGLLFAALGVVMILWPSLKKQVLKQVLRIDPSSISFGMWKEIP 60
Db 1 MGGSSRARWAVAGLVGVVGLLCAVLGVVMILWPSLKKQVLKQVLRIDPSSISFGMWKEIP 60
Qy 61 VPFYLSVYFVFNPNNEVLNGQKPVVRERGPYVYRFRQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFVFNPNSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVEHRS 120
Qy 121 FQPKSHGSESXYIVLPNLIIVLGSILMESKPVSLKLMMTLALVTMGQRAFMNRTVGEIL 180
Db 121 FQPKSHGSESXYIILPNLIIVLGSILMESKPVSLKLMMTLGLATLQRAFMNRTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGCVFTFTGVQNFSLHLVDKWNGL 240
Db 181 WGYDDPFVFNPKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLSFFSPEACRSKMLTYNESRVPEGIPTYR 300
Db 241 SKVNYHSEOCNMINGTSGOMWAPFMTPESSLSFFSPEACRSKMLTYHDSGVPEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360
Db 301 FTAPKTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDTHPVVTGIPMNCVKMQLSLYIKSVKGIGTGKIBPVVLPVLLWFSQSG 420
Db 361 LNPDPREHSLFDHPVTGIPMNCVKLIQISLYIKAVKIGIGTGKIBPVVLPVLLWFSQSG 420
Qy 421 AMGKPLSTFTYQLVLPMPVLYHYAYVLLGLGGLLLVPIICQLRSQKCFLWFSQSGKKG 480
Db 421 AMGGEPLNTFTYQLVLPMPVLYHYAYVLLGLGGLLLVPIIYQLRSQKCFLWFSQSGKKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 13
US-08-265-428-4
; Sequence 4, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
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;; FILING DATE: 530
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: MIT6620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 815-6508
;; TELEFAX: (404) 815-6555
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 509 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..509
;; OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger
;; FEATURE:
;; NAME/KEY: Domain
;; LOCATION: 9..32
;; OTHER INFORMATION: /note= "Putative transmembrane
;; OTHER INFORMATION: domain."
;; FEATURE:
;; NAME/KEY: Domain
;; LOCATION: 440..464
;; OTHER INFORMATION: /note= "Putative transmembrane
;; OTHER INFORMATION: domain."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..385
;; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
;; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312,
;; OTHER INFORMATION: 330-332 and 383-385 represent potential N-linked glycosylation
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 21..470
;; OTHER INFORMATION: /note= "The cysteines at positions
;; OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and 470 represent
;; OTHER INFORMATION: potential disulfide linkages."
US-08-265-428-4
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSRRARWALGLGALLFAALGVVNMILWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVGLGVVGLLCAVLGVVNMILWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFFVFNPNVNEVNGQKPVRRERGYPVTRFRQKNVITFNNDTVSFVENRSLH 120
Db 61 VPFLSVYFFVFNPNVNEVNGQKPVRRERGYPVTRFRQKNVITFNNDTVSFVENRSLH 120
Qy 121 FQPKSHGSDYIVLPNVLVGLSILMESVPVSLKMTLALVTMGORAFMNTVGEIL 180
Db 121 FQPKSHGSDYIVLPNVLVGLSILMESVPVSLKMTLALVTMGORAFMNTVGEIL 180
Qy 181 WGYDDPPVHFLNTLPLDMLPIKGFGLFVGNMNSGVFTVFTGVQNFSPRIHLVDKNGL 240
Db 181 WGYDDPPVHFLNTLPLDMLPIKGFGLFVGNMNSGVFTVFTGVQNFSPRIHLVDKNGL 240
Qy 241 SKIDYHSEQNMGNTSGQWAPMTPESSLEFPSPACRSMKLTYNESVFGIPTYR 300
Db 241 SKVNYHSEQNMGNTSGQWAPMTPESSLEFPSPACRSMKLTYNESVFGIPTYR 300
Qy 301 FTAPDTLPANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPDTLPANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360

Qy 361 LNPMPKHSLSFLDIHPVTGIPMNCVQMLSLYIKSVKGIGQTKIIPVVLPLLWFSQSG 420
Db 361 LNPMPKHSLSFLDIHPVTGIPMNCVQMLSLYIKSVKGIGQTKIIPVVLPLLWFSQSG 420
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Db 421 AMGCKPLSTFTVLVMPQVLYHAQYVLLGGLLAVPIICQLRSQEKCFLWSSGSKKG 480
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Db 481 SQDKEAIOAYSESLSMSPAAGTGVLEAKL 509
RESULT 14
US-09-385-799-2
; Sequence 2, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,799
; FILING DATE: 30-Aug-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
;

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173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
potential N-linked glycosylation sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions 21,
251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
linkages."
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Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLFAALGVVMILVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVLLCAVLGVVMILVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFFVVPNEVLNGKPVRRERGPVYVREPRQKNITFNDNDTVSFVNRSLH 120
Db 61 VPFLSVYFFVVPNEVLNGKPVRRERGPVYVREPRQKNITFNDNDTVSFVNRSLH 120
Qy 121 FQPKSHGSESDYIILPNILVGLGSIILMESKPSVSLKMLMTLALVTMGQAFPMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVGLGSIILMESKPSVSLKMLMTLALVTMGQAFPMNRVTGEIL 180
Qy 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Db 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Qy 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Db 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNREGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNREGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
Qy 361 LNPDPKSHSLFDHPVTGIPMNCVSMQSLYIKSVKIGIQGTGKIIEPVVLPILWFEQSG 420
Db 361 LNPDPKSHSLFDHPVTGIPMNCVSMQSLYIKSVKIGIQGTGKIIEPVVLPILWFEQSG 420
Qy 421 AMGKPLSTFTQLVLMPOVLHYAQVLLGLGILLVPIICQLRSQEKCFLWFGSKKG 480
Db 421 AMGKPLSTFTQLVLMPOVLHYAQVLLGLGILLVPIICQLRSQEKCFLWFGSKKG 480
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; Sequence 4, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US95/07721
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the
Hamster Scavenger Receptor Class B-I."
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane
domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane
domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..385
OTHER INFORMATION: /note= "Positions 102-104, 108-110,
173-175, 212-214, 227-229, 255-257,
310-312, 330-332 and 383-385 represent
potential N-linked glycosylation sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions
21, 251, 280, 321, 323, 334, 384 and
470 represent potential disulfide
linkages."
PCT-US95-07721-4
Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLFAALGVVMILVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVLLCAVLGVVMILVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFFVVPNEVLNGKPVRRERGPVYVREPRQKNITFNDNDTVSFVNRSLH 120
Db 61 VPFLSVYFFVVPNEVLNGKPVRRERGPVYVREPRQKNITFNDNDTVSFVNRSLH 120
Qy 121 FQPKSHGSESDYIILPNILVGLGSIILMESKPSVSLKMLMTLALVTMGQAFPMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVGLGSIILMESKPSVSLKMLMTLALVTMGQAFPMNRVTGEIL 180
Qy 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Db 181 WGYDDPFVHNTLTPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKRWGL 240
Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACRSKMLTYNESRVFEGIPTYR 300
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Job time : 35 secs

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OM protein - protein search, using sw model

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Title: US-08-765-108-8

Perfect score: 2881

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2681	100.0	509	4	US-10-164-863-4
4	2681	100.0	509	4	US-10-706-073-4
5	2681	100.0	509	5	US-10-933-037-4
6	2605	97.2	513	4	US-10-322-281-565
7	2447	91.3	509	3	US-09-148-012-2
8	2447	91.3	509	3	US-09-779-152-4
9	2447	91.3	509	4	US-10-023-610-4
10	2447	91.3	509	4	US-10-178-611-2
11	2447	91.3	509	4	US-10-164-863-2
12	2447	91.3	509	4	US-10-212-848-4
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18	2200	82.1	509	5	US-10-494-555-1
19	2193	81.8	532	4	US-10-276-774-2382
20	2192	81.8	509	4	US-10-648-593-219
21	2192	81.8	509	5	US-10-794-198A-12
22	2160	80.6	509	4	US-10-210-172-116
23	2068.5	77.2	537	5	US-10-450-763-52676
24	2022.5	75.4	552	4	US-10-313-641-12
25	2022.5	75.4	552	4	US-10-428-551-12
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27	1844	68.8	416	4	US-10-210-172-118

28 741.5 27.7 478 4 US-10-408-765A-657 Sequence 657, Appl
29 741.5 27.7 478 4 US-10-794-899-90 Sequence 90, Appl
30 727.5 27.1 531 4 US-10-403-571-158 Sequence 158, Appl
31 682.5 25.5 520 6 US-11-097-143-4890 Sequence 4890, Ap
32 677 25.3 471 4 US-10-048-917-1 Sequence 1, Appli
33 677 25.3 472 3 US-09-836-544-21 Sequence 21, Appl
34 677 25.3 472 4 US-10-372-683-45 Sequence 45, Appl
35 677 25.3 472 4 US-10-398-593-2 Sequence 44, Appl
36 645 24.1 472 4 US-10-196-703-44 Sequence 3022, Ap
37 642.5 24.0 471 4 US-10-408-765A-3022 Sequence 8385, Ap
38 585 21.8 491 6 US-11-097-143-8385 Sequence 24735, A
39 572 21.3 534 6 US-11-097-143-24735 Sequence 12084, A
40 537 20.0 861 6 US-11-097-143-12084 Sequence 2697, Ap
41 530.5 19.8 513 6 US-11-097-143-2697 Sequence 16122, A
42 518.5 19.3 553 6 US-11-097-143-16122 Sequence 355, App
43 518.5 19.3 589 4 US-10-108-605-355 Sequence 6, Appli
44 518.5 19.3 589 6 US-11-013-314-6 Sequence 7293, Ap
45 510 19.0 589 6 US-11-097-143-7293

ALIGNMENTS

RESULT 1

US-09-148-012-4
; Sequence 4, Application US/09148012
; Patent No. US2002009040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: In the Treatment Of Steroidal Overproduction
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-09-148-012-4

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 7 1e-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWALGALGALLFAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPFYLSVYFVEVNPNEVLNGQKQVYRERGYPVYRFRQKVNITFNDNDTYSFVENRSLH 120
Db 61 VPFYLSVYFVEVNPNEVLNGQKQVYRERGYPVYRFRQKVNITFNDNDTYSFVENRSLH 120

Qy 121 FQPKSHGSSDYLVLPNLIIVLGGSIILMESKPSVLKLMVTLALVTMGORAPMNRVTGBIL 180
Db 121 FQPKSHGSSDYLVLPNLIIVLGGSIILMESKPSVLKLMVTLALVTMGORAPMNRVTGBIL 180

Qy 181 WGYDDPFPVHFLNTYLPDKLPIKGFGLFVGKNNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db 181 WGYDDPFPVHFLNTYLPDKLPIKGFGLFVGKNNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240

Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSEACRSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSEACRSMKLTYNESRVFEGIPYR 300

Qy 301 FTAPDTTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPDTTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360

Qy 361 LNPMPKSHSLFDIHPVTGTIPMNCVSRMQLSLYIKSVKIGIQGTGKIEFPVLLPWFQSG 420

Db 361 LNPKEHSLFLDIHPVTGIPMNCVKMQLSLYKSVKGIQTCKIEPVLPLLWFEQSG 420
Qy 421 AMGKPLSTFTTQVLVMPQVHLHYAQVLLGLGGLLLVPIICQIRSQEKCFLEWGSKKG 480
Db 421 AMGKPLSTFTTQVLVMPQVHLHYAQVLLGLGGLLLVPIICQIRSQEKCFLEWGSKKG 480
Qy 481 SODKEATQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEATQAYSESLMSPAAGTIVLQEAKL 509

RESULT 2

US-10-178-611-4
; Sequence 4, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; marine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-178-611-4
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.1e-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFCMWKEIP 60
Db 1 MGGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFCMWKEIP 60
Qy 61 VPFYLSVYFFVVPVNPNEVLNGQKPVYRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFYLSVYFFVVPVNPNEVLNGQKPVYRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120

Qy 121 FQPKDGHGSESDYIVLPNLIIVLGSSILMESKPSVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKDGHGSESDYIVLPNLIIVLGSSILMESKPSVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Qy 181 WGYDDPFFVHFNTYLPDMLPIKGFGLFVGMNNSNGVFTFTGVQNFSSIHILVDKWNGL 240
Db 181 WGYDDPFFVHFNTYLPDMLPIKGFGLFVGMNNSNGVFTFTGVQNFSSIHILVDKWNGL 240
Qy 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPPEACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPPEACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLIFANGSVYPPNEGFCPCREGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLIFANGSVYPPNEGFCPCREGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPKEHSLFLDIHPVTGIPMNCVKMQLSLYKSVKGIQTCKIEPVLPLLWFEQSG 420
Db 361 LNPKEHSLFLDIHPVTGIPMNCVKMQLSLYKSVKGIQTCKIEPVLPLLWFEQSG 420
Qy 421 AMGKPLSTFTTQVLVMPQVHLHYAQVLLGLGGLLLVPIICQIRSQEKCFLEWGSKKG 480
Db 421 AMGKPLSTFTTQVLVMPQVHLHYAQVLLGLGGLLLVPIICQIRSQEKCFLEWGSKKG 480
Qy 481 SODKEATQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEATQAYSESLMSPAAGTIVLQEAKL 509

RESULT 3

US-10-164-863-4
; Sequence 4, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-164-863-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.1e-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFCMWKEIP 60
Db 1 MGGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFCMWKEIP 60
Qy 61 VPFYLSVYFFVVPVNPNEVLNGQKPVYRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFYLSVYFFVVPVNPNEVLNGQKPVYRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKDGHGSESDYIVLPNLIIVLGSSILMESKPSVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKDGHGSESDYIVLPNLIIVLGSSILMESKPSVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Qy 181 WGYDDPFFVHFNTYLPDMLPIKGFGLFVGMNNSNGVFTFTGVQNFSSIHILVDKWNGL 240
Db 181 WGYDDPFFVHFNTYLPDMLPIKGFGLFVGMNNSNGVFTFTGVQNFSSIHILVDKWNGL 240
Qy 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPPEACRSMKLTYNESRVFEGIPTYR 300

Db 241 SKIDYHSEQCNMINGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSRMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVSRMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Qy 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLFWGSKKG 480
Db 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLFWGSKKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
RESULT 4
US-10-706-073-4
; Sequence 4, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-10-706-073-4
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.le-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVNPNVNLGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFEVNPNVNLGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKRGKFLFVGMNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKRGKFLFVGMNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
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Db 241 SKIDYHSEQCNMINGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSRMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420

Db 361 LNPMPKHSFLDHPVTGIPMNCVSRMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Qy 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLFWGSKKG 480
Db 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLFWGSKKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
RESULT 5
US-10-933-037-4
; Sequence 4, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-933-037-4
Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.le-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVNPNVNLGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFEVNPNVNLGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180

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Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLPLMFEQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLPLMFEQSG 420
Qy 421 AMGGKPLSTFTYQVLMPQVLYHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
Db 421 AMGGKPLSTFTYQVLMPQVLYHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
Qy 481 SODKEAIOAYSLSMSPAAGTGLVQEA 509
Db 481 SODKEAIOAYSLSMSPAAGTGLVQEA 509

RESULT 6
US-10-322-281-565
; Sequence 565, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-565

Query Match 97.2%; Score 2605; DB 4; Length 513;
Best Local Similarity 98.4%; Pred. No. 2.2e-247;
Matches 501; Conservative 0; Mismatches 2; Indels 6; Gaps 3;

Qy 1 MGSSRRARWV--GLGALGLLFAALGVVIMLVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Db 11 MGSSRRARWV--GLGALGLLFAALGVVIMLVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 68
Qy 61 VPFYLSVYFVFNPNNEVLNQKPVVRERGYPVYRERQKVNITFDNDNTVSVFVNRSLH 120
Db 69 VPFYLSVYFVFNPNNEVLNQKPVVRERGYPVYRERQKVNITFDNDNTVSVFVNRSLH 128
Qy 121 FQPKSHGSDYLVNLNVLGSLIMESKPVSLKMTLALVTMQRAPMRTVCEIL 180
Db 129 FQPKSHGSDYLVNLNVLGSLIMESKPVSLKMTLALVTMQRAPMRTVCEIL 188
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Db 189 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 248
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 249 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIP--Y 306
Qy 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Db 307 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPFLSHPHFYNADPVLSEAV-- 364
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLPLMFEQSG 420
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Db 365 LQPNPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLPLMFEQSG 424
Qy 421 AMGGKPLSTFTYQVLMPQVLYHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
Db 425 AMGGKPLSTFTYQVLMPQVLYHYAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 484
Qy 481 SODKEAIOAYSLSMSPAAGTGLVQEA 509
Db 485 SODKEAIOAYSLSMSPAAGTGLVQEA 513

RESULT 7
US-09-148-012-2
; Sequence 2, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MTT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; FEATURES:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (310)..(312)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
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LOCATION: (383)..(385)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (21)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (251)
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LOCATION: (321)
OTHER INFORMATION: Potential
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NAME/KEY: DISULFID
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OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (334)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (384)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (470)
OTHER INFORMATION: Potential

US-09-148-012-2

Query Match 91.3%; Score 2447; DB 3; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGGSSRARWALGALGLLFAALGVVMIWVPSLIIKQVLLKNNVRIDPSSLSFGMWKEIP 60
DB 1 MGGSSRARWAVAGLVGVVGLLCAVLGVVMIWVPSLIIKQVLLKNNVRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFEVVNPNEVLNGOKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
DB 61 VPFLSYVFFEVVNPNEVLNGOKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
QY 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKLMNTLALVTMGQRAFMRNTVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKLMNTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFVHFLNTLYLDMPLPIKGFGLFVGMNNSGVTFTVQVQNFSLHLDVKNGL 240
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QY 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPSEACRSMKLTYNESRVPFGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPSEACRSMKLTYNESRVPFGIPTYR 300
QY 301 FTAPDTLFGANGSVVYPNNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLFGANGSVVYPNNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDPREHSLFLDHPVTGIPMNCVSKVQVLSLYIKAVKGIGQTKIEBPVVLPLLPFQSG 420
DB 361 LNPDPREHSLFLDHPVTGIPMNCVSKVQVLSLYIKAVKGIGQTKIEBPVVLPLLPFQSG 420
QY 421 AMGGKPLSTFTQLVLPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
DB 421 AMGGKPLSTFTQLVLPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESLSMSPAAGTGLQEA 509

RESULT 9
US-10-023-610-4
Sequence 4, Application US/10023610
Publication No. US20030023059A1
GENERAL INFORMATION:

DB 481 SQDKEAIQAYSESLSMSPAAGTGLQEA 509
RESULT 8
US-09-779-152-4
Sequence 4, Application US/09779152
Publication No. US20030044782A1
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Ordovas, Jose M.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
FILE REFERENCE: WNI-172CP2
CURRENT APPLICATION NUMBER: US/09/779,152
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 08/890,979
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 509
TYPE: PRI
ORGANISM: Human
US-09-779-152-4

Query Match 91.3%; Score 2447; DB 3; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGGSSRARWALGALGLLFAALGVVMIWVPSLIIKQVLLKNNVRIDPSSLSFGMWKEIP 60
DB 1 MGGSSRARWAVAGLVGVVGLLCAVLGVVMIWVPSLIIKQVLLKNNVRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFEVVNPNEVLNGOKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
DB 61 VPFLSYVFFEVVNPNEVLNGOKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
QY 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKLMNTLALVTMGQRAFMRNTVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKLMNTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFVHFLNTLYLDMPLPIKGFGLFVGMNNSGVTFTVQVQNFSLHLDVKNGL 240
DB 181 WGYDDPFVHFLNTLYLDMPLPIKGFGLFVGMNNSGVTFTVQVQNFSLHLDVKNGL 240
QY 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPSEACRSMKLTYNESRVPFGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPSEACRSMKLTYNESRVPFGIPTYR 300
QY 301 FTAPDTLFGANGSVVYPNNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLFGANGSVVYPNNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDPREHSLFLDHPVTGIPMNCVSKVQVLSLYIKAVKGIGQTKIEBPVVLPLLPFQSG 420
DB 361 LNPDPREHSLFLDHPVTGIPMNCVSKVQVLSLYIKAVKGIGQTKIEBPVVLPLLPFQSG 420
QY 421 AMGGKPLSTFTQLVLPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
DB 421 AMGGKPLSTFTQLVLPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESLSMSPAAGTGLQEA 509

RESULT 9
US-10-023-610-4
Sequence 4, Application US/10023610
Publication No. US20030023059A1
GENERAL INFORMATION:

APPLICANT: Acton, Susan L.
TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: MIA-005.03
CURRENT APPLICATION NUMBER: US/10/023.610
CURRENT FILING DATE: 2001-12-17
EARLIER APPLICATION NUMBER: 09/686,106
EARLIER FILING DATE: 2000-10-10
EARLIER APPLICATION NUMBER: 09/032,894
EARLIER FILING DATE: 1998-02-27
EARLIER APPLICATION NUMBER: 08/890,980
EARLIER FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 4
LENGTH: 509
TYPE: PRT
ORGANISM: Human
US-10-023-610-4

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVAGLVGVLCAVLGVVMIILVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYVFFVVPVNPNEVLNGKQPVVRRGPPVYVRRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPFLSVYVFFVVPVNPSEILKGEKPVVRRGPPVYVRRFRHKANITFDNDTVSFVEHRSLSH 120
Qy 121 FQPKSHGSESDYIILPNILVLGSIILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVLGAVVMESKAGLKMMTLGLATLQRAFMRNRTVGEIL 180
Qy 181 WGYDDPFVHFLNTLPDMLPTKKGFLFVGMNNSGVTFTVGTQVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVFNKYLDPDMPFKKGFLFVEMNNSDGLFTVGTQVQNFRIHLVDKWNGL 240
Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPACRSKMLTYNSRVFEGIPTYR 300
Db 241 SKVNYHSEQCNMNGTSGQWAPFMTQSSLEFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNFGFCPCRESQVNSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNFGFCPCLESQVNSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDIHPVTGIPMNCVSKVQSLYIKSVKIGIGQTKIIPPVVLPLLWFFQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKIGIGQTKIIPPVVLPLLWFFQSG 420
Qy 421 AMGSKPLSTFTQVLMPQVLYHAYQVLLGLGGLLLVPIICQSRQSKCFLFWGSGKKG 480
Db 421 AMGGEPLNTFTQVLMPQVLYHAYQVLLGLGGLLLVPIIYQSRQSKCFLFWGSGKKG 480
Qy 481 SODKEATQAVSESLMSPAAGTIVLQEAAL 509
Db 481 SODKEATQAVSESLMSPAAGTIVLQEAAL 509

RESULT 10
US-10-178-611-2
Sequence 2, Application US/10178611
Publication No. US20030167475A1
GENERAL INFORMATION:
APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta

STATE: Georgia.
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/178.611
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,907
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT/538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger Receptor Class B-I."
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..385
OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent potential N-linked glycosylation sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide linkages."
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-178-611-2

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVAGLVGVLCAVLGVVMIILVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYVFFVVPVNPNEVLNGKQPVVRRGPPVYVRRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPFLSVYVFFVVPVNPSEILKGEKPVVRRGPPVYVRRFRHKANITFDNDTVSFVEHRSLSH 120
Qy 121 FQPKSHGSESDYIILPNILVLGSIILMESKPVSLKLMMTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVLGAVVMESKAGLKMMTLGLATLQRAFMRNRTVGEIL 180


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QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
Db 181 WGYDDPFVNFINKYLPDMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKHLVDKWNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPMTPESSLEPSPACRSMKLTYNESRVFEGIPYR 300
Db 241 SKVNYHSEOCNMINGTSGQWAPMTPOSSLEPSPACRSMKLTYHDSGVFEGIPYR 300
QY 301 FTAPDTLFGANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFGANGSVYPPNEGFCPCLESIGNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSYIKSVKIGQGTGKIEPVVLPVLLWFQSG 420
Db 361 LNPDPREHSLFDHPVTGIPMNCVSKLQISLYIKAVKIGQGTGKIEPVVLPVLLWFQSG 420
QY 421 AMGGKPLSTFTVTLVLMPOVLHYAOVLLGLGLLLVPIICOLBSQKCPFWGSKKG 480
Db 421 AMGGEPLNTFTVTLVLMPOVLQYVQVLLGLGLLLVPIYQLRSQSKCFLFWGSKKG 480
QY 481 SODKEAIOAYSESLMSPAAGTVLQEAKL 509
Db 481 SODKEAIOAYSESLMSPAAGTVLQEAKL 509

RESULT 11
US-10-164-863-2
; Sequence 2, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
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; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (310)..(312)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (383)..(385)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (21)..(21)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (251)..(251)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (280)..(280)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (321)..(321)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (323)..(323)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (334)..(334)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (384)..(384)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (470)..(470)
; OTHER INFORMATION: Potential
US-10-164-863-2
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Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSRRARWVALGALGALLFAALGVVMIILVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Db 1 MGSRRARWVALGALGALLFAALGVVMIILVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
QY 61 VPFLYSVYFVFNPNVNLNGQKPVVRERGYPVYVREFRQKVNITFDNDTYSFVENRSLH 120
Db 61 VPFLYSVYFVFNPNVNLNGQKPVVRERGYPVYVREFRQKVNITFDNDTYSFVENRSLH 120
QY 121 POPKSHGSSDYIVLNPILVGLGSIILMESKPVSLKLMNTLALVTMGORAPMNTVGEIL 180
Db 121 POPDRSHGSSDYIILNPILVGLGAVVMESKAGLKLMTLGLATLQORAPMNTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
Db 181 WGYDDPFVNFINKYLPDMFPPIKGFGLFVGMNNSDGLFTVFTGVQNFSKHLVDKWNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPMTPESSLEPSPACRSMKLTYNESRVFEGIPYR 300
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Db 241 SKNYWHEQCNMNGTSGQWAPFMTPOSSLEFFSPEACRSMKLTVDHSGVFEGITPYR 300
Qy 301 FTAPDTLFPANGSVYPNPEGFCPCRESGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPKTLFPANGSVYPNPEGFCPCLESIGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVVMQSLYIKSVKGIGOTGKIIEPVVLPILWPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVVKLQISLYIKAVKGIGOTGKIIEPVVLPILWPFQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGGLLLVPIICQLRSQEKCFLEFWSGSKKG 480
Db 421 AMGGEPLNTFTYQLVLMPOVLHYQYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 12
US-10-212-848-4
; Sequence 4, Application US/10212848
; Publication No. US2004002325A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: MMI-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-848-4

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGGSSRABWALGALGALIPALGVMLVPSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
Db 1 MGGSSARARWAVGLGVGLLCAVLGVMLVPSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYFVFNPNVNEVINGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFVFNPNVNEVINGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSES DYI L PNLVILGGSILMESKVLKMMTLALVTMGRAPMNRVTGEIL 180
Db 121 FQPKSHGSES DYI L PNLVILGGSILMESKVLKMMTLALVTMGRAPMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGGELFVGNVNSGVFTVFTGVQNESRIHLVDKNGL 240
Db 181 WGYDDPFVFNKLYLPDMPFIKGRFGLFVGNVNSDGLFTVFTGVQNFKTHLVDKNGL 240
Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFFSPEACRSMKLTYNESRVFEGITPYR 300
Db 241 SKNYWHEQCNMNGTSGQWAPFMTPOSSLEFFSPEACRSMKLTVDHSGVFEGITPYR 300
Qy 301 FTAPDTLFPANGSVYPNPEGFCPCRESGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPKTLFPANGSVYPNPEGFCPCLESIGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVVMQSLYIKSVKGIGOTGKIIEPVVLPILWPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVVKLQISLYIKAVKGIGOTGKIIEPVVLPILWPFQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGGLLLVPIICQLRSQEKCFLEFWSGSKKG 480
Db 421 AMGGEPLNTFTYQLVLMPOVLHYQYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKKG 480
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Db 421 AMGGEPLNTFTYQLVLMPOVLHYQYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEA 509

RESULT 13
US-10-706-073-2
; Sequence 2, Application US/10706073
; Publication No. US2004007526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
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; NAME/KEY: CARBOHYD
; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
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; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (310)..(312)
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; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (383)..(385)
; OTHER INFORMATION: Potential
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FEATURE: DISULFID
NAME/KEY: (21)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (251)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (280)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (321)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (323)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (334)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (384)
OTHER INFORMATION: Potential
FEATURE: DISULFID
NAME/KEY: (470)
OTHER INFORMATION: Potential
US-10-706-073-2

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232; Indels 0; Gaps 0;
Matches 453; Conservative 35; Mismatches 21;

Qy 1 MGSRRARWALGALGALLFAALGVNMLVPSLIKKOVLKNVRIDPSSLSFGWKEIP 60
Db 1 MGSRRARWAVGLGVGLCAVLGVNMLVPSLIKKOVLKNVRIDPSSLSFGWKEIP 60
Qy 61 VPFYLSVYFFVFNPNVNLNGOKPVVRERGPVYVREFRQKNVITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFVFNPNVNLNGOKPVVRERGPVYVREFRQKNVITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGESDYILPNILVGLGSLMESKPVSLKAMTLALVTMGORAPMNRVTGAIL 180
Db 121 FQPKSHGESDYILPNILVGLGSLMESKPVSLKAMTLALVTMGORAPMNRVTGAIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKNGNL 240
Db 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKNGNL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPMPTPSSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKVNYWHSEQCNMINGTSGQWAPMPTPSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTADTLPFANGSVYPPNPGFCRESGTONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNPGFCRESGTONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPMPKSHSLFDHPVTGIPMNCVKMOLSIYTKSVKIGOTGKIBPVLPVLLWFEOG 420
Db 361 LNPDPREHSLFDHPVTGIPMNCVKMOLSIYTKSVKIGOTGKIBPVLPVLLWFEOG 420
Qy 421 AMGGKPLSTFTYQLVMPQVLYHQAQYVLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
Db 421 AMGGEPLNTFTYQLVMPQVLYHQAQYVLLGLGGLLLVPIIVQLRSQKCFLFWSGSKG 480
Qy 481 SQDKAIOAYSLSMSPAAGTGLQEAKL 509
Db 481 SQDKAIOAYSLSMSPAAGTGLQEAKL 509

RESULT 14

US-10-933-037-2
; Sequence 2, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933.037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-933-037-2

Query Match 91.3%; Score 2447; DB 5; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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Db 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
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Db 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIHPVTGIPMNCVVMQSLYIKSVKIGIGTGKIEPVPVLPILWFEOQS 420
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Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
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RESULT 15
US-09-779-152-2
; Sequence 2, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890, 979
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-2
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Query Match 82.1%; Score 2200; DB 3; Length 509;
Best Local Similarity 79.6%; Pred. No. 1.9e-207;
Matches 405; Conservative 49; Mismatches 55; Indels 0; Gaps 0;

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Db 1 MGGSRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSISFGMWKEIP 60
Qy 61 VPFYLSVYFFVFNPNVNEVLNGQKPVVRERGYPVYRFRQKNITFNNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFVFNPNVNEVLNGQKPVVRERGYPVYRFRQKNITFNNDNDTVSFVENRSLH 120
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Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEOCNMINGTSGOMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIHPVTGIPMNCVVMQSLYIKSVKIGIGTGKIEPVPVLPILWFEOQS 420
Db 361 LNPDPKHSFLDIHPVTGIPMNCVVMQSLYIKSVKIGIGTGKIEPVPVLPILWFEOQS 420
Qy 421 AMGGKPLSTFTYTLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLFWSGSKKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVLLGLGILLVPIICOLRSQEKCFLFWSGSKKG 480
Qy 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
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Search completed: February 23, 2006, 12:51:25
Job time : 123 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:47:29 ; Search time 11.5 Seconds
(without alignments)
658.923 Million cell updates/sec

Title: US-08-765-108-8
Perfect score: 2681
Sequence: 1 MGSSRRARWALGALGALL.....YSESLMSPAAGTGLQEAFL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA-New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2192	81.8	509	7 US-11-055-309A-12	Sequence 12, Appl
2	2192	81.8	509	7 US-11-072-175-219	Sequence 219, App
3	2192	81.8	532	6 US-10-821-234-918	Sequence 918, App
4	98.5	3.7	414	7 US-11-072-512-2031	Sequence 2031, Ap
5	97	3.6	1075	7 US-11-098-686-10295	Sequence 10295, A
6	90	3.4	909	7 US-11-076-187-4	Sequence 4, Appli
7	88	3.3	890	7 US-11-072-512-2992	Sequence 2992, Ap
8	86.5	3.2	379	6 US-10-793-626-1512	Sequence 1512, Ap
9	85	3.2	320	7 US-11-142-700-6	Sequence 6, Appli
10	84.5	3.2	453	7 US-11-185-878-5	Sequence 5, Appli
11	84.5	3.2	455	7 US-11-182-946-3	Sequence 3, Appli
12	84	3.1	1130	7 US-11-086-482-1	Sequence 1, Appli
13	84	3.1	1130	7 US-11-192-341-23	Sequence 23, Appl
14	84	3.1	1735	7 US-11-040-472-13	Sequence 13, Appl
15	83.5	3.1	636	7 US-11-098-686-10289	Sequence 10289, A
16	82.5	3.1	687	6 US-10-055-877-200	Sequence 200, App
17	82	3.1	400	7 US-11-077-386-26	Sequence 26, Appl
18	82	3.1	610	7 US-11-142-700-16	Sequence 16, Appl
19	81	3.0	803	7 US-11-098-686-10461	Sequence 10461, A
20	81	3.0	1332	7 US-11-091-643-18	Sequence 18, Appl
21	81	3.0	3716	7 US-11-052-554A-141	Sequence 141, App
22	80.5	3.0	813	6 US-10-509-950-1	Sequence 1, Appli
23	80.5	3.0	1206	6 US-10-995-561-709	Sequence 709, App
24	80.5	3.0	1307	6 US-10-995-561-711	Sequence 711, App
25	80.5	3.0	2256	7 US-11-144-368-4	Sequence 4, Appli

26	80.5	3.0	2458	7 US-11-186-999-6	Sequence 6, Appli
27	80.5	3.0	2458	7 US-11-186-999-13	Sequence 13, Appl
28	80	3.0	420	6 US-10-935-494-3	Sequence 3, Appli
29	80	3.0	1394	6 US-10-935-494-31	Sequence 31, Appl
30	79.5	3.0	1167	6 US-10-942-072-6	Sequence 6, Appli
31	79.5	3.0	1167	6 US-10-942-072-13	Sequence 13, Appl
32	79.5	3.0	1168	6 US-10-942-072-11	Sequence 11, Appl
33	79.5	3.0	2455	7 US-11-186-999-4	Sequence 4, Appli
34	79.5	3.0	2515	7 US-11-113-424-53	Sequence 53, Appl
35	79	2.9	254	7 US-11-054-515-1259	Sequence 1259, Ap
36	79	2.9	857	7 US-11-052-554A-218	Sequence 218, App
37	79	2.9	1081	7 US-11-142-700-23	Sequence 23, Appl
38	79	2.9	1089	7 US-11-098-686-10150	Sequence 10150, A
39	78.5	2.9	555	7 US-11-072-512-2011	Sequence 2011, Ap
40	78.5	2.9	685	7 US-11-142-700-25	Sequence 25, Appl
41	78.5	2.9	952	7 US-11-207-626A-45	Sequence 45, Appl
42	78.5	2.9	1342	7 US-11-113-202-14	Sequence 14, Appl
43	78	2.9	304	7 US-11-142-700-2	Sequence 2, Appli
44	78	2.9	685	7 US-11-098-686-10574	Sequence 10574, A
45	78	2.9	1390	6 US-10-957-351-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-055-309A-12
; Sequence 12, Application US/11055309A
; Publication No. US20050282750A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P0235IUS
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 509
; TYPE: PRT
; ORGANISM: HUMAN
US-11-055-309A-12

Query Match 81.8%; Score 2192; DB 7; Length 509;
Best Local Similarity 79.4%; Pred. No. 4.5e-199;
Matches 404; Conservative 49; Mismatches 56; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLFAALGVVMILWPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVMIVMPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFFLSYTFEVVNPNEVLNGQKPVYRERGYPVYRERQKVNITFNDNDTVSFVENSILH 120
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Qy 121 FQPKSHGSSSDYLVLPNIILVGLSSILWESKPSVLKUMTLALVTMGSORAFMNRITVCEIL 180
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Qy 181 WGYDDPFPVHFINTYLPDMLPIKGFGLFVGMMNSNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFPVHFINTYLPDMLPIKGFGLFVGMMNSNSGVFTVFTGVQNFRIHLVDKWNGL 240

Db 181 WGYKDPVLNLINKYFPGMFPFKGFLFAELNNSDGLFTVFTGVQNISRIHLVDKWNGL 240
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Db 241 SKVDFWHSDDQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
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Qy 481 SQDKEAIQAYSESLSMSPAAGTGLQEAKL 509
Db 481 SKDKEAIQAYSESLSMTSAPKGSVLQEAKL 509

RESULT 2
US-11-072-175-219
; Sequence 219, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; PRIOR FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-219

Query Match 81.8%; Score 2192; DB 7; Length 509;
Best Local Similarity 79.4%; Pred. No. 4.5e-199;
Matches 404; Conservative 49; Mismatches 56; Indels 0; Gaps 0;

Qy 1 MGGSSRARWVALGALGALLFAALGVMMILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGCsAKARWAAGALGAVGLCAVLGAVMIWVPSLIKQVLKNVRIDPSSLSFNMWKEIP 60
Qy 61 VPFYLSVVFVFNPNVNEVLNGKPVRRGPGVYVREPRQKVNITFNDNDTVSFVENSILH 120
Db 61 IPFYLVSVYFFDVMPNPSILKGEKQVRRGPGVYVRESRHKSNITFNNNDTVSFLEYRTFQ 120
Qy 121 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
Db 121 FQPSKSHGSES DYI VMPN ILV LGA AVNMENKPM TLKIMTLAFTTLGERAFMNRITVGEIM 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKKGKGLFVGMNNSGVFTVFTGVQNSRIHLVDKWNGL 240
Db 181 WGYKDPVLNLINKYFPGMFPFKGFLFAELNNSDGLFTVFTGVQNTSRHLVDKWNGL 240
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKVDFWHSDDQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
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Db 301 FVAPKTLFANGSIYPPNEGFCPCLESIGQNVSTCRFSAPFLSHPHFLNADPVLAEAVTG 360
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Db 481 SKDKEAIQAYSESLSMTSAPKGSVLQEAKL 509

RESULT 3
US-10-821-234-918
; Sequence 918, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 918
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-918

Query Match 81.8%; Score 2192; DB 6; Length 532;
Best Local Similarity 79.4%; Pred. No. 4.8e-199;
Matches 404; Conservative 49; Mismatches 56; Indels 0; Gaps 0;

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Db 24 MGCsAKARWAAGALGAVGLCAVLGAVMIWVPSLIKQVLKNVRIDPSSLSFNMWKEIP 83
Qy 61 VPFYLSVVFVFNPNVNEVLNGKPVRRGPGVYVREPRQKVNITFNDNDTVSFVENSILH 120
Db 84 IPFYLVSVYFFDVMPNPSILKGEKQVRRGPGVYVRESRHKSNITFNNNDTVSFLEYRTFQ 143
Qy 121 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRITVGEIL 180
Db 144 FQPSKSHGSES DYI VMPN ILV LGA AVNMENKPM TLKIMTLAFTTLGERAFMNRITVGEIM 203
Qy 181 WGYDDPFVHFLNTYLPDMLPIKKGKGLFVGMNNSGVFTVFTGVQNSRIHLVDKWNGL 240
Db 204 WGYKDPVLNLINKYFPGMFPFKGFLFAELNNSDGLFTVFTGVQNTSRHLVDKWNGL 263
Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 264 SKVDFWHSDDQCNMNGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 323
Qy 301 FTAPDTTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
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Qy 361 LNPMPKEHSLFLDIHPVTGIPMNCVKMOLSLYIKSVKGIGQTKIEPVVPLPLWFQSG 420
Db 384 LHPNQEAHSLFLDIHPVTGIPMNCVKQLSLYMKSVAGIGQTKIEPVVPLPLWFAESG 443
Qy 421 AMGKPLSTFTQVLMPQVLYHAQVYLLGGLLLVPIICOLRSQEKCFLWSSGSKG 480
Db 444 AMEGTLLHTFTQVLMPKVMHYAQVYLLGCVLLLPVICQIRSQEKCFLWSSSKG 503

OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-10-793-626-1512

Query Match 3.2%; Score 86.5; DB 6; Length 379;
Best Local Similarity 21.8%; Pred. No. 2.2; Indels 95; Gaps 19;
Matches 83; Conservative 49; Mismatches 153; Indels 95; Gaps 19;
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QY 155 LKAMWTLALVTMGQAFNRTVGEILMGYDDPPVHF-INTYLPDMLPIKGFGLFVGNN 213
DB 61 ILLINAMALVLYGFTGLEGLVARIMOGVCTAFFMSLQGLIIDLPEK-----YRS 112
QY 214 SNSGVFTVFTGVQNFRIHLVDKMGNSKIDYHSEOCNMLNGTSGOMWAPFMTPESSLE 273
DB 113 EGVSLYSLSFSTIPNL-----LGPLIANGIHWVE-----NWTIFAIVMIFIAVTTLF 159
QY 274 FSPSPACRSMLKTYNESRVFEGIPYRFTAPDTLFPANGSVYPPNMGFCPCRESG-IQNV 332
DB 160 GYRTTFANTQEVAPKEV---LPFNAMTVYVQFPKAKL-----FC---SGMIMILS 206
QY 333 TCRCA-----PLFLSHPHFYNADPVLSEAVLGNPNKHSLSLFDHPVTGIPMNCVK 387
DB 207 SIVFGAMSTFPLTYVREGFANA-----GIFLTIQAITV---IAR 244
QY 388 MQLSLYIKSVGIGQTKIEPVLPLLMFEQ-SGAMGKPLSTR-----YQLVLM 437
DB 245 FYLRKYVPS-DGLWH-HRFMMIVLTLLMASIIIVAFGQILSIFVYISAIFIGITQALVY 302
QY 438 PQVLHYAQYVLLGLGLLLL 457
DB 303 PTLTLYLSFVLPKIGRNMLL 322

RESULT 9

US-11-142-700-6
Sequence 6, Application US/11142700
Publication No. US20060026721A1
GENERAL INFORMATION:
APPLICANT: Stephen M. Allen
APPLICANT: Gary M. Fader
APPLICANT: Saverio Carl Falco
APPLICANT: Anthony J. Kinney
APPLICANT: Jonathan E. Lightner
APPLICANT: Quo-Hua Miao
APPLICANT: J. Antoni Rafalski
APPLICANT: Catherine J. Thorpe
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB-1170
CURRENT APPLICATION NUMBER: US/11/142,700
PRIOR FILING DATE: 2005-06-01
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 320
TYPE: PRT
ORGANISM: Zea mays
US-11-142-700-6

Query Match 3.2%; Score 85; DB 7; Length 320;
Best Local Similarity 23.5%; Pred. No. 2.4;
Matches 43; Conservative 31; Mismatches 81; Indels 28; Gaps 8;
QY 150 SKPVSL--KLMWTLALVTMGQAFNRTV-----GBILM-----GYDDPPVHFINTY--194
DB 46 SAPINLSRDLHQVLRWALGVSVEIFMSRHCPLWYAGGRLKWLRFAYNTNIVYPTFTSIPL 105

QY 195 -----LPDMLPIKGFGLFVGNNNSGVF-TVFTGVQNFRIHLVDKMGNSKIDYVHS 248
DB 106 LAYCTIPAVCLLTCKF-IIPTLNNLASIWFTALFLSIATSVLEL--RWSGVSIEDWNRN 162
QY 249 EQCNMNGTSGOMWAPFMTPESSLEFPSPACRSMLKTYNESRVFEGIPYRFT--P 304
DB 163 EQFVIGGVSAHLFAVFGFLKVLGGVDTSFTVTSKAAGDEADAFGLDLYLFKWTLLVPP 222
QY 305 DTL 307
DB 223 TTL 225
RESULT 10
US-11-185-878-5
Sequence 5, Application US/11185878
Publication No. US20050282217A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
FILE REFERENCE: PE379PDI
CURRENT APPLICATION NUMBER: US/11/185,878
PRIOR FILING DATE: 2005-07-21
PRIOR FILING DATE: 2002-10-25
PRIOR FILING DATE: 2002-10-25
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 453
TYPE: PRT
ORGANISM: human
US-11-185-878-5

Query Match 3.2%; Score 84.5; DB 7; Length 453;
Best Local Similarity 26.1%; Pred. No. 4.4;
Matches 48; Conservative 19; Mismatches 60; Indels 57; Gaps 12;
QY 195 LPDMLPIKGFGLFVGNNNSGV-----FTVFTGVQNFRIHLVDKMGNSKIDYVHS 248
DB 194 LPQIENVKG-----TEDSGTTLVLLPLVIFFGCLLSLLFT-----GLMYRYQRWKS 239
QY 249 EQCNMNGTSGOMWAPFMTPESSLEFPSPACRSMLKTYNESRVFEGIPYRFT--302
DB 240 KLYSIVCGKS-----TPEKEGEL---EGTTTKPLAPNPS--FS--PTFGFTTLTGFS 284
QY 303 -APDTLFPANGSVYPPNMGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLGL 361
DB 285 PVPSSTFTSSSTYTP--GDGP-----NFAAPREVAPPYQCADPILATA-LAS 329
QY 362 NPNP 365
DB 330 DPIP 333
RESULT 11
US-11-182-946-3
Sequence 3, Application US/11182946

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; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-3

Query Match      3.2%; Score 84.5; DB 7; Length 455;
Best Local Similarity 26.1%; Pred. No. 4.4;
Matches 48; Conservative 19; Mismatches 60; Indels 57; Gaps 12;

Qy 195 LPDMLPIKGKGLFVGMNNSGV-----FTVTVGVQNFRIHLVDKNGLS-KIDYHWS 248
Db 196 LPQENVRKG-----TEDSGTTLVLPLVIFFGCLLSLLFI-----GLMRYQRWKS 241
Qy 249 EQCMMNINGSQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYRFT----- 302
Db 242 KLYSIVCGKS-----TPEKEGEL---EGTTTKPLAPNPS--FS--PTPGFTPTLGF 286
Qy 303 -APDTLFGANGVYPNPEGFCPCRESGIONVSTCFGAPLFUSHPHFYNADPVLSEAVLGL 361
Db 287 PVPSTSTSSSTYTP--GDGP-----NFAAPRREVAPPYQADPILATA-LAS 331
Qy 362 NPNP 365
Db 332 DPDP 335

RESULT 12
US-11-086-482-1
; Sequence 1, Application US/11086482
; Publication No. US20060030017A1
; GENERAL INFORMATION:
; APPLICANT: Novartis Pharmaceutical
; APPLICANT: Friedrich, Gabriele
; TITLE OF INVENTION: Three-Dimensional Structure of c-Abl
; FILE REFERENCE: 4-33710A
; CURRENT APPLICATION NUMBER: US/11/086,482
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-086-482-1

Query Match      3.1%; Score 84; DB 7; Length 1130;
Best Local Similarity 21.1%; Pred. No. 18;
Matches 64; Conservative 36; Mismatches 98; Indels 106; Gaps 14;

Qy 204 KFGLFVGMNNSGVFT-----VFTGVQNFRIHLVDKNGLSKIDYHWSQCNMNGTS 258
Db 51 KENLLAGSENDNLFVALYDFVAGDNTLS-----ITKGEKLVLYGNHNGEWCEAQTKN 106
Qy 259 QMWAP--FMTPESSLE-----PF-----SPEACRSKMLT 286
Db 107 GQGWVPSNYITPVNSLEKHSWYHGPVSRNAAYLLSSGINGSFLVRESSESPGQRSISLR 166
Qy 287 YNESRVFEGIPTYRFTAPDTLFGANGVYPNPEGFCPCRESGIONVSTCFGAPLFSLHP 345
Db 167 Y-EGRVH-----YRINTASD-----GKLYVSSS-----RFTLAELVHH 201
Qy 346 HFYNADPVL-----EAVLGLNPNPKHSLFLDHPVTGIPMNCVSKMQLSLYI 394
Db 202 HSTVADGLITTLHYPAKRNKPTVYGVSPNYDKWEM-----ERTDITM 244
Qy 395 KSVKIGIGOTGKIIEPVVLPVLLWPEQSGAMGKPL-----STFYTQLVLMPOVLHYAQYV 447
Db 245 KHKLGQGYGEVYEGV-----WKYSLSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQ 300

US-11-192-341-23
; Sequence 23, Application US/11192341
; Publication No. US20060030583A1
; GENERAL INFORMATION:
; APPLICANT: SGX Pharmaceuticals, Inc.
; APPLICANT: Arnold, William D.
; APPLICANT: Bounaud, Pierre
; APPLICANT: Goeborg, Andreas
; APPLICANT: Li, Zhe
; APPLICANT: McDonald, Ian
; APPLICANT: Steensma, Ruo W.
; APPLICANT: Wilson, Mark E.
; TITLE OF INVENTION: Pyrrolo-Pyridine Kinase Modulators
; FILE REFERENCE: 022132-004510US
; CURRENT APPLICATION NUMBER: US/11/192,341
; CURRENT FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: 60/683,510
; PRIOR FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/591,888
; PRIOR FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: 60/591,887
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-192-341-23

Query Match      3.1%; Score 84; DB 7; Length 1130;
Best Local Similarity 21.1%; Pred. No. 18;
Matches 64; Conservative 36; Mismatches 98; Indels 106; Gaps 14;

Qy 204 KFGLFVGMNNSGVFT-----VFTGVQNFRIHLVDKNGLSKIDYHWSQCNMNGTS 258
Db 51 KENLLAGSENDNLFVALYDFVAGDNTLS-----ITKGEKLVLYGNHNGEWCEAQTKN 106
Qy 259 QMWAP--FMTPESSLE-----PF-----SPEACRSKMLT 286
Db 107 GQGWVPSNYITPVNSLEKHSWYHGPVSRNAAYLLSSGINGSFLVRESSESPGQRSISLR 166
Qy 287 YNESRVFEGIPTYRFTAPDTLFGANGVYPNPEGFCPCRESGIONVSTCFGAPLFSLHP 345
Db 167 Y-EGRVH-----YRINTASD-----GKLYVSSS-----RFTLAELVHH 201
Qy 346 HFYNADPVL-----EAVLGLNPNPKHSLFLDHPVTGIPMNCVSKMQLSLYI 394
Db 202 HSTVADGLITTLHYPAKRNKPTVYGVSPNYDKWEM-----ERTDITM 244
Qy 395 KSVKIGIGOTGKIIEPVVLPVLLWPEQSGAMGKPL-----STFYTQLVLMPOVLHYAQYV 447
Db 245 KHKLGQGYGEVYEGV-----WKYSLSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQ 300
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Qy 448 LGLL 451
Db 301 LGLV 304

RESULT 14

US-11-040-472-13

; Sequence 13, Application US/11040472

; Publication No. US20050283857A1

; GENERAL INFORMATION:

; APPLICANT: Adang, Michael

; APPLICANT: Hua, Gang

; APPLICANT: Chen, Jiang

; APPLICANT: Abdullah, Mohd

; TITLE OF INVENTION: Peptides for Inhibiting Insects

; FILE REFERENCE: UGR-105CP

; CURRENT APPLICATION NUMBER: US/11/040,472

; CURRENT FILING DATE: 2005-01-21

; PRIOR APPLICATION NUMBER: US 60/538,715

; PRIOR FILING DATE: 2004-01-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 1735

; TYPE: PRT

; ORGANISM: Anopheles gambiae

US-11-040-472-13

Query Match 3.1%; Score 84; DB 7; Length 1735;

Best Local Similarity 20.8%; Pred. No. 33;

Matches 100; Conservative 54; Mismatches 147; Indels 180; Gaps 27;

Qy 32 VPSLIKQOVLKNVRIDPSSLSFGMWK--EI-----PVPFVLSVYFVFNPN 76

Db 829 IPPIDK--VLQNVII--SDMKSNWHVFEIIVLMDTNKQPVHDPFNDGQVYQEKIPSN 884

Qy 77 EVLNGQKPVVRERG-----PY-----VYREFROKVNITFNDNDTVSV--ENRSLHP 121

Db 885 TA-----IVRVEGKDQDRDVPYHTVSVEINRDPFQQLRYFEVDSTGRATYKENNDL-- 936

Qy 122 QPKSHGSESDYIVLPNLTVL--GSSILMESKPVSLKMTLALVTMQRQAFMRTVGEI 179

Db 937 -LDRDAGLES---IMINIVLMDNAGGYDIQNR--VSTNINLTLL----- 974

Qy 180 LMWYDDPFVHPFLNTPLDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNQ 239

Db 975 -----DINDHTP-KLPELADELKVS-ENAKQG-YIVKT---PFAALDLDKRT 1018

Qy 240 LSKIDYHSEQNMGNTSGQMWAPPMTPESSLEFFGPE---ACRSKMLTYNESRVFEGI 296

Db 1019 NAKINYIEE-----MTPEPETPLFSLNIDYNAVPRVAQDLKGFVGT 1062

Qy 297 PTYRFTAPDTLFPANGSVYPPNEGCPCEBSGIONVSICTP-----G 337

Db 1063 WTLKAKACD---RGSEYEP---IPLTEPKONCETRDYELTVPEFNNTPTSPSR 1115

Qy 338 APLFLSHPHFYNADPVLS-----EAV-----LGLNPNKEHSLF--- 371

Db 1116 AOLRLKYESLQNGRLPVTETNGSPLPKFAIDDDGGIYGDVTFSLTNDGEQDHEVFRVD 1175

Qy 372 -----LDIHPVTGIPMNCV-----KMLSLYIKSVKGIQGTGKIE 407

Db 1176 KVDNKTGLLVLENSLAVQP---PPKNYSITVIARDGGDRQSEAAIHVVFINMTGEPAPLE 1232

Qy 408 P 408

Db 1233 P 1233

RESULT 15

US-11-098-686-10289

; Sequence 10289, Application US/11098686

; Publication No. US20060024696A1

; GENERAL INFORMATION:

; APPLICANT: Kapur, Vivek and Gebhart, Connie J.

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

; FILE REFERENCE: 09531-128001

; CURRENT APPLICATION NUMBER: US/11/098,686

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: PCT/US03/31318

; PRIOR FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: US 60/416,395

; PRIOR FILING DATE: 2002-10-04

; NUMBER OF SEQ ID NOS: 11433

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10289

; LENGTH: 636

; TYPE: PRT

; ORGANISM: Lawsonia intracellularis

US-11-098-686-10289

Query Match 3.1%; Score 83.5; DB 7; Length 636;

Best Local Similarity 18.8%; Pred. No. 8.9;

Matches 74; Conservative 54; Mismatches 145; Indels 121; Gaps 16;

Qy 17 LGLLPAALGVVMIIMVPSLIKQOVLKNVRIDPSSLSFGMWKEIIVPFLSVY----- 68

Db 142 IGIILCSLGVSWILLRPIAKK---INNIPVSVRWFESVW--IILASITTIYSPPTFSNN 196

Qy 69 -----PFEVVNPNNEVLNGO-KPVVRERGPV--VYREFROKVNITENDNDTVS 112

Db 197 ALSQELSKNGIWSLFSFRNNQDYOQFYVIDKKLAFELHHELIENPSVFFNDN---S 253

Qy 113 FVENRSLHPQPKSHGSESDYIVLPNLTVLGSSILMESKPVSLKMTLALVTMQRQAFM 172

Db 254 MEWRRYIH-----SNSPEKHLNVTIIVVESLGSVSLGDRTPHLNDLSKKCLYFTNMKATG 308

Qy 173 NRTV-----GEIL--WGYYDDPFVHPFLNTPLDMLP 200

Db 309 TRTVRGLEAILSLPPTPGASIVRRPNHNLFTGTGLFRQGYDTVIY----- 357

Qy 201 IKGFGLFVGMNNSNG-----VFTVFTGVQNFRIHLVDKWNGLSKIDYWH 247

Db 358 --GGYGFDMNNEFFSNGFRIIDRSTIPDEYKTFNANGICDEDLFDVIREADIYTS 415

Qy 248 SEQCNMINTSGQMWAPPMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYRFTA----- 303

Db 416 NKPPYHVALTTSN-HRPFTYDGRVDVPSGTS-RTGAIKYTDYAI-----HRLFKEAKK 467

Qy 304 -----PDTLF-----ANGSVYPPNEGFCPC 323

Db 468 KPWFSDTIFITIVADHTAGSAGKTVLPDPNDYDIPC 501

Search completed: February 23, 2006, 12:51:54

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